

Amendments to the Specification:

Please delete the following paragraphs from page 10, from line 27, through page 12, line 18,;

~~BRIEF DESCRIPTION OF THE DRAWINGS~~

~~The objects and features of the invention can be better understood with reference to the following detailed description and drawings.~~

~~FIG. 1 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being down regulated in cartilage isolated from patients having mild osteoarthritis, but which are not down regulated in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.~~

~~FIG. 2 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being down regulated in cartilage isolated from patients having severe osteoarthritis, but which are not down regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.~~

~~FIG. 3 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage in patients having mild osteoarthritis, but which are not up regulated in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.~~

~~FIG. 4 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage isolated from patients having severe osteoarthritis, but which are not up regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.~~

~~FIG. 5 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage isolated from patients having severe osteoarthritis, but which are down regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.~~

~~FIG. 6 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for (a) mild OA only, (b) moderate OA only, (c) marked OA only and (d) severe OA only in OA cartilage as compared to cartilage isolated from normal individuals using the 15K ChondroChip.TM. microarray analysis as disclosed herein.~~

~~FIG. 7 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for (a) mild OA only and (b) severe OA only in OA cartilage as compared to cartilage isolated from normal individuals using the Affymetrix.RTM. U133A Array analysis as disclosed herein.~~

Please replace the following 33 paragraphs beginning at page 5, from line 23 through page 10, line 15, with the following 33 paragraphs:



In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a and 7a.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a and 7a.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a and 7a.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Table FIG. 6b.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Table FIG. 6b.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Table FIG. 6b.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Table FIG. 6c.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Table FIG. 6c.

In one embodiment, the invention provides for an isolated biomarker consisting

essentially of the nucleic acids identified in Table FIG. 6c.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d and 7b.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d and 7b.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d and 7b.

In another embodiment, the invention teaches a method of diagnosing mild osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a, 7a, whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of mild osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a, 7a.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a, 7a.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a, 7a.

In another embodiment, the invention teaches a method of diagnosing severe osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d, 7b whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of severe osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d, 7b.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d, 7b.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d, 7b.

In another embodiment, the invention teaches a method of diagnosing moderate osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Table FIG. 6b, whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of moderate osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Table FIG. 6b.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene

selected from the group consisting of the nucleic acids identified in Table FIG. 6b.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Table FIG. 6b.

In another embodiment, the invention teaches a method of diagnosing marked osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Table FIG. 6c, whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of marked osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Table FIG. 6c.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Table FIG. 6c.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Table FIG. 6c.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of mild osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Tables FIGS. 1, 3, 5, 6a and 7a in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of

the efficacy of the drug for treatment of mild osteoarthritis in the patient.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of moderate osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Table FIG. 6b in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of moderate osteoarthritis in the patient.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of marked osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Table FIG. 6c in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of marked osteoarthritis in the patient.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of severe osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Tables FIGS. 2, 4, 5, 6d and 7b in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of severe osteoarthritis in the patient.

In another embodiment, the invention teaches a method of identifying a therapeutic agent for the treatment of osteoarthritis, the method comprising providing a sample from a patient diagnosed with osteoarthritis, measuring the level of expression of a biomarker as set out in Tables FIGS. 1-7 in the presence and the absence of the therapeutic agent; and comparing the level of expression measured in the presence of the therapeutic agent to the level of expression measured in the absence of the therapeutic agent, wherein a decrease in the differential expression of the biomarker is indicative of a therapeutic agent for the treatment of osteoarthritis. –

Please replace the following 8 paragraphs beginning at page 16, line 12 through page 17, line 4, with the following 8 paragraphs:

--In one embodiment, a biomarker for the diagnosis of osteoarthritis consists essentially of the genes as set out in Tables FIGS. 1-7.

In another embodiment, a biomarker for the diagnosis of mild osteoarthritis consists essentially of the genes disclosed in Tables FIGS. 1, 3, 5, 6a or 7a.

In another embodiment, a biomarker for the diagnosis of severe osteoarthritis consists essentially of the genes as set out in Tables FIGS. 2, 4, 5, 6d or 7b.

In another embodiment, a biomarker for the diagnosis of moderate osteoarthritis consists essentially of the genes disclosed in Table FIG. 6b.

In another embodiment, a biomarker for the diagnosis of marked osteoarthritis consists essentially of the genes disclosed in Table FIG. 6c.

A “gene”, as used herein, refers to DNA encoding mRNA and does not include promoters and enhancers upstream of the coding region.

As used herein, “polypeptide sequences encoded by” refers to the amino acid sequences

obtained after translation of the protein coding region of a gene, as defined herein. The mRNA nucleotide sequence for each gene is identified by its Genbank Accession number (see Tables FIGS. 1-7) and the corresponding polypeptide sequence is identified by a Protein Accession Number or GenSeq or RefSeq (see Tables FIGS. 1-7). The Genbank Accession numbers identified in Tables FIGS. 1-7 provide the location of the 5' UTR, protein coding region (CDS) and 3' UTR within the mRNA nucleotide sequence of each gene. --

Please replace the following 3 paragraphs beginning at page 36, line 16 through line 22, with the following 3 paragraphs:

*--Identification of Biomarkers Useful in Diagnosis of OA*

~~*--Identification of Biomarkers Useful in Diagnosis of OA*~~

The invention provides stage-specific genes identifiable in a sample (Tables FIGS. 1-7) whose level of expression is indicative of the existence of some degree of mild, moderate, marked or severe osteoarthritis when compared with the level of expression of the same one or more genes in a normal individual. These genes, or the products of these genes, in combination are therefore useful as biomarkers to identify individuals having OA. --

Please replace the paragraph at page 37, from line 4 through line 10, with the following paragraph:

--For example there are

$$\frac{21!}{2! (21-2)!} = \frac{5.1 \cdot 10^{19}}{2.432 \cdot 10^{17}} = 210$$

$$2! (21-2)! = 2.432 \cdot 10^{17}$$

possible combinations of two genes amongst the 21 genes that are down regulated in severe OA (~~Figure~~ Table 2).

Similarly there are  $21!/3!(21-3)!$  Possible combinations of three genes amongst the 21 genes that are down regulated in severe OA (Figure Table 2). –

Please replace the paragraph at page 37, from line 12 through line 26, with the following paragraph:

--The invention further provides genes as set forth in Tables FIGS. 1-7 whose level of expression is distinctive for at least one stage of osteoarthritis as compared with another stage of osteoarthritis. For example, the invention provides for genes which have been identified as being down regulated (Table FIG. 1) or up-regulated (Table FIG. 3) in cartilage isolated from patients having mild osteoarthritis, but which are not neither down-regulated (Table FIG. 1) or up-regulated (Table FIG. 3) in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. Similarly, the invention provides for genes which have been identified as being down regulated (Table FIG. 2) or up-regulated (Table FIG. 4) in cartilage isolated from patients having severe osteoarthritis, but which are not down regulated (Table FIG. 2) or up-regulated (Table FIG. 4) in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. The invention also provides for genes that are differentially expressed at specific stages of OA e.g. mild OA only (Tables FIGS. 6a and 7a), moderate OA only (Table FIG. 6b), marked OA only (Table FIG. 6c) or severe OA only (Tables FIGS. 6d and 7b). The invention further provides for genes that are up-regulated in severe OA and down regulated in mild OA (Table FIG. 5). –

Please replace the paragraph at page 38, from line 7 through line 13, with the following paragraph:

-- The invention contemplates the use of the genes set out in Tables FIGS. 1-7 as biomarkers of OA whose level of expression is indicative of the existence of osteoarthritis when compared with the level of expression of the same gene in a normal individual. The level of expression of the biomarkers of the invention can be determined by measuring the level of the protein products of the genes, or may be determined by measuring the expression of mRNA utilizing oligonucleotides, ESTs, cDNA, DNA or



RNA, or portions thereof, corresponding to one or more genes of the invention to measure the level of expression. --

Please replace the paragraph at page 40, from line 1 through line 8, with the following paragraph:

-- The invention contemplates the use of genes as set out in Tables ~~FIGS.~~ 1-7, or combinations thereof, whose level of expression is indicative of the existence of a certain stage of osteoarthritis. The expression levels of the marker genes in a sample may be determined by any means known in the art. For example, the level of expression of the biomarkers of the invention can be determined by measuring the level of the protein products of the genes, or may be determined utilizing oligonucleotides, ESTs, cDNA, DNA or RNA, or portions thereof, corresponding to one or more genes of the invention to measure the level of expression.--

Please replace the paragraph at page 43, from line 3 through line 11, with the following paragraph:

-- In order to classify cartilage according to disease state, a scoring system is used, whereby subjective decisions by the arthroscopist are minimized. The scoring system which defines disease states described herein is that of Marshall, supra, incorporated herein by reference. According to this method, each of the 6 articular surfaces (patella, femoral trochlea, medial femoral condyle, medial tibial plateau, lateral femoral condyle and lateral tibial plateau) is assigned a cartilage grade based on the worst lesion present on that specific surface. A scoring system is then applied in which each articular surface receives an osteoarthritis severity number value that reflects the cartilage severity grade for that surface, as described in Table 8 ~~Table 1~~.

Table [[1]] 8. Articular Cartilage Grading System		
Grade	Articular Cartilage	Points

0	Normal	0
I	Surface intact-softening, edema	1
II	Surface-disrupted-partial thickness lesions (no extension to bone)	2
III	Full thickness lesions-extensions to intact bone	3
IV	Bone erosion or eburnation	4

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Please replace the following 3 paragraphs beginning at page 50, from line 21 through page 51 line 14, with the following 3 paragraphs:

-- In one aspect, the invention provides for antibodies that are bound to an array and selectively bind to the polypeptides encoded by two or more of the genes of an isolated biomarker (e.g., labelled proteins encoded by the nucleotide sequences of Tables FIGS. 1-7). The invention also provides for the production and purification of the polypeptides encoded by the genes of an isolated biomarker as well as the isolation, characterization and production of monoclonal antibodies that bind to the polypeptides encoded by the genes described in Tables FIGS. 1-7.

#### Protein Production

Standard recombinant nucleic acid methods can be used to express a polypeptide or antibody of the invention. Generally, a nucleic acid sequence encoding the polypeptide is cloned into a nucleic acid expression vector. Of course, if the protein includes multiple polypeptide chains, each chain must be cloned into an expression vector, e.g., the same or different vectors, that are expressed in the same or different cells. If the protein is sufficiently small, i.e., the protein is a peptide of less than 50 amino acids, the protein can be synthesized using automated organic synthetic methods. Polypeptides comprising the 5' region, 3' region or internal coding region of a gene of an isolated biomarker as defined herein, are expressed from nucleic acid expression vectors containing only those nucleotide sequences corresponding to the 5' region, 3' region or internal coding region of

a gene of an isolated biomarker. Methods for producing antibodies directed to full length polypeptides encoded by the genes described in Tables FIGS. 1-7 or polypeptides encoded by the 5' region, 3' region or internal coding regions of the genes described in Tables FIGS. 1-7 are provided below. --

Please replace the paragraph at page 61, from line 16 through line 22, with the following paragraph:

-- The invention provides for known and novel nucleic acid sequences that are uniquely expressed in mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic cartilage. Tables FIGS. 6 and 7 shows OA stage specific markers with Genbank Accession numbers and corresponding Protein Accession Numbers that are diagnostic for mild OA only (Tables FIGS. 6a, 7a), moderate OA only (Table FIG. 6b), marked OA (Table FIG. 6c) and severe OA (Tables FIGS. 6d, 7b) as identified in cartilage cDNA libraries using the methods according to the invention. --

Please replace the paragraph at page 97, from line 3 through line 5, with the following paragraph:

-- This example demonstrates the use of the claimed invention to detect either mild OA specific or severe OA specific biomarkers utilizing the ChondroChip™ as demonstrated in Tables FIGS. 1-4. --

Please replace the paragraph at page 97, on line 18, with the following paragraph:

-- Tables FIGS. 1-4 provide those genes identified as unique to either mild or severe OA. --

Please replace the paragraph at page 97, on lines 21-23, with the following paragraph:

-- This example demonstrates the use of the claimed invention to detect stage specific OA biomarkers utilizing the ChondroChip™ or the Affymetrix® U133A as demonstrated in Table FIG. 6 and Table FIG. 7 respectively.--

Please replace the paragraph at page 99, from line 1 through line 24, with the following paragraph:

-- Total cellular protein from a cartilage sample taken from each patient is first isolated and labelled using the BD Clontech Protein Extraction and labelling kit (Catalogue #K1848-1 or #631786). Briefly, the Extraction Protocol consists of three main steps: mechanically disrupting the cells, solubilizing the cells, and centrifuging the extract. The process may start with a cell pellet or frozen tissue and may use any method of mechanical disruption--French press, sonication, mincing, or grinding. Once disrupted, the sample is solubilized by adding the Extraction/Labeling Buffer (1:20 w/v). Because the Buffer is formulated for labeling with N-hydroxysuccinimide (NHS)-ester dyes (e.g. Cy3 and Cy5 dyes), it does not contain any protease inhibitors or reducing agents that would compete for reaction with the dye. After extraction, the sample is centrifuged to pellet insoluble material such as chromosomal DNA. The soluble extract is then labelled with Cy3 and Cy5 Fluorescent Dyes (monofunctional NHS-esters). The labelled proteins are then incubated with an array of monoclonal antibodies which are directed to full length polypeptides encoded by the genes described in Tables FIGS. 1, 3, 6a, 7a (mild OA) or Tables FIGS. 2, 4, 6d or 7b (Severe OA). Detection of specific binding to the array is then measured by scanning with a GMS Scanner 418 and processing of the experimental data with Scanalyzer software (Michael Eisen, Stanford University), followed by GeneSpring software (Silicon Genetics, CA) analysis. Differential expression of the mild OA specific of severe OA-specific genes in the samples from patients with mild and severe osteoarthritis respectively as compared to healthy patients is determined by statistical analysis using the Wilcoxon Mann Whitney rank sum test (Glantz S A. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002). Differential expression of each of the genes described in Tables FIGS. 1, 3, 6a, 7a is diagnostic for mild osteoarthritis. Differential expression of each of the genes described in Tables FIGS. 2, 4, 6d or 7b is diagnostic of severe OA. --

Please add the following 5 new paragraphs (Tables) at page 97, between lines 18 and 19:

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**Table 1** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being down regulated in cartilage isolated from patients having mild osteoarthritis, but which are not down-regulated in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.

SEQ ID No	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
1	FCR1090;Novel;					1 (0.725 to 1.275)	0.499	0.556 (0.504 to 0.608)
	MIOA2900;ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY ;P39188	BC035122.1		Hs.382273		1 (0.686 to 1.314)	0.497	1.53 (1.205 to 1.854)
	seob7176;U50' snoRNA and U50 snoRNA ;AB017710.1	AB017710.1				1 (0.837 to 1.163)	0.497	0.651 (0.572 to 0.731)
2	miob0185;DNA sequence (clone RP11-38M8 from 7q31) ;AC009275.5	AC009275.8				1.000 (0.696 to 1.304)	0.497	0.585 (0.568 to 0.601)
	seoa5479;EST( aa89a04.r1 Stratagene fetal retina 937202 clone 838446 5') ;AA457594	AA457594	NM_024843	Hs.31297	NP_079119	1 (0.977 to 1.023)	0.495	0.832 (0.561 to 1.102)
	seob3694;hypothetical protein FLJ10147 (FLJ10147)(OR F) ;NM_018010.1	NM_018010.1	NM_018010	Hs.170318	NP_060480	1 (0.927 to 1.073)	0.493	0.934 (0.808 to 1.060)

3	MIOA1763;MHC class 1 region ;AF055066	AF055066			AAC24825.	1 (0.523 to 1.477)	0.493	0.88 (0.815 to 0.945)
	ncrc1999;INTERFERON-INDUCED TRANSMEMBRANE PROTEIN 3 (INTERFERON-INDUCIBLE PROTEIN 1-8U) ;Q01628	NM_021034.1	NM_021034.1	Hs.433414	NP_066362.1	1.000 (0.529 to 1.471)	0.492	0.711 (0.638 to 0.784)
	MIOA6236;EST(qr24f06.x1 NCI_CGAP_GC 6 clone IMAGE:1941827 3') ;AI203343	AI203343	NM_016586	Hs.16755	NP_057670	1 (0.716 to 1.284)	0.492	0.61 (0.567 to 0.653)
4	SEOA6643a;DNA sequence (chromosome 16 cloneRPCI-11_567P19, WORKING DRAFT SEQUENCE, 63 unordered pieces) ;AC009152.1	AC009152.7				1 (0.794 to 1.206)	0.491	0.774 (0.611 to 0.938)
5	fcrb5788;H19, imprinted maternally expressed untranslated ;Hs.334822	AF087017.1				1 (0.848 to 1.152)	0.491	1.191 (1.007 to 1.375)
	SEOA3908;elongation factor-1-gamma ;Z11531	Z11531	NM_001404	Hs.256184	NP_001395	1 (0.833 to 1.167)	0.49	0.742 (0.683 to 0.802)
	FCR6188;hypothetical protein (KIAA0121) ;D50911	D50911	XM_052386	Hs.155584		1 (0.846 to 1.154)	0.49	0.704 (0.580 to 0.827)

MIOB2691;HRI HFB2072 (=AF115778 M.musculus short coiled coil protein SCOCO (Scoc)) ;AB015335.1	AB015335.1	NM_032547	Hs.286013	NP_11593 6	1 (0.686 to 1.314)	0.486	1.157 (1.108 to 1.207)
seoa3242;EST zp96a07.r1 Stratagene muscle 937209 cDNA clone 628020 5' ;AA196423	AA196423		Hs.374621		1 (0.85 to 1.150)	0.486	0.885
SEOA5977a;hyp othetical protein (KIAA0569) ;AB011141	AB011141	NM_014795	Hs.34871	NP_05561 0	1.000 (0.959 to 1.041)	0.485	0.960 (0.88 to 1.041)
ncrb7403;EST (EST390300 MAGE resequences, MAGO cDNA) ;AW978191.1	AW978191.1		Hs.117927		1 (0.831 to 1.169)	0.485	0.613 (0.61 to 0.616)
seob6836;hXBP -1 transcription factor DNA (=TREB protein) ;L13850.1	L13850.1				1 (0.933 to 1.067)	0.485	0.616 (0.554 to 0.678)
miob3968;gamm a-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4) ;NM_000809.1	NM_000809. 1	NM_000809	Hs.248112	NP_00080 0	1 (0.747 to 1.253)	0.484	0.926 (0.898 to 0.954)
SEOA2970a:maj or histocompatibilit y class II antigen gamma chain ;K01144	K01144	NM_004355	Hs.84298	NP_00434 6	1 (0.615 to 1.385)	0.48	1.777 (1.256 to 2.297)

SEOA9357;hypothetical protein, estradiol-induced (E2IG5), (ORF) ;NM_014367.1	NM_014367.1	NM_014367	Hs.5243	NP_055182	1 (0.783 to 1.217)	0.48	0.658 (0.528 to 0.788)
MIOA8338;Hep G2 ;D17039	D17039	NM_004048	Hs.48516	NP_004039	1 (0.525 to 1.475)	0.48	0.635 (0.529 to 0.742)
SEOB1273;CGI-129 protein ;AF151887.1	AF151887.1	NM_016098	Hs.108725	NP_057182	1 (0.963 to 1.037)	0.474	0.909 (0.823 to 0.995)
SEOA9433;fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA ;NM_013231.1	NM_013231.1	NM_013231	Hs.48998	NP_037363	1 (0.910 to 1.09)	0.473	0.598 (0.489 to 0.707)
seoa1431;EST (wg57e08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 clone IMAGE:23692223') ;AI760043.1	AI760043.1	NM_019000	Hs.82273	NP_061873	1 (0.569 to 1.431)	0.472	0.866 (0.862 to 0.870)
ncr0238;EST tt13f10.x1 NCI_CGAP_GC6 IMAGE:22406833' similar to TR:P97434 P97434 P116RIP. ;contains element A3R repetitive element ;AI655514	AI655514	NM_007032	Hs.40342	NP_619538	1 (0.639 to 1.361)	0.472	0.968 (0.778 to 1.158)



	SEOB1513;T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene ;S72931.1	S72931.1				AAB30469	1 (0.81 to 1.190)	0.469	0.567 (0.483 to 0.651)
	seob7039;high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha (=AB007900 KIAA0440) ;AF090989.1	AF090989.1	NM_015556	Hs.172180	NP_05637 1		1 (0.735 to 1.265)	0.469	0.702 (0.665 to 0.738)
	ncrc6072;testis specific ankyrin-like protein 1 (LOC51281) ;NM_016552.1	NM_016552.1	NM_016552	Hs.122275	NP_06031 4		1 (0.846 to 1.154)	0.463	0.846 (0.748 to 0.944)
	ncrb0045;chitinase 3-like 1(cartilage glycoprotein-39) (CHI3L1) ;NM_001276.1	NM_001276.1	NM_001276	Hs.75184	NP_00126 7		1 (0.764 to 1.236)	0.454	0.644 (0.608 to 0.681)
	miob4752;EST(aa17g07.r1 Soares_NhHMP u_S1 clone IMAGE:813564 5') ;AA455459.1	AA455459.1		Hs.445247			1 (0.905 to 1.095)	0.452	0.77 (0.511 to 1.029)
	seob5203;microvascular endothelial differentiation gene 1 product ;AB026908.1	AB026908.1	NM_012328	Hs.6790	NP_03646 0		1	0.451	0.525 (0.374 to 0.675)
	SEOB1411;KIAA0879 protein (KIAA0879) ;NM_014936.1	NM_014936.1	NM_014936	Hs.54037	NP_05575 1		1 (0.706 to 1.294)	0.449	0.614 (0.558 to 0.669)

	MIOA6207;EST(an41g01.s1 Gessler Wilms tumor clone IMAGE:1701264 3') ;AI174629	AI174629		Hs.6634		1 (0.537 to 1.463)	0.447	0.517 (0.467 to 0.567)
6	miob4692;dJ93 K22.1 (novel protein (contains DKFZP564B116 )) ;AL050333	AL050333				1 (0.315 to 1.685)	0.447	0.588 (0.426 to 0.749)
	ncrc4864;fibroblast activation protein, alpha;seprase (RefSeq aa 6e-91) ;NP_004451.1	NM_004460.2	NM_004460.2	Hs.418	NP_004451.1	1 (0.353 to 1.647)	0.446	0.738 (0.515 to 0.960)
	SEOB2750;PGK1=phosphoglycerate kinase 1 ;S75476.1	S75476.1				1 (0.994 to 1.006)	0.445	1.370 (1.174 to 1.567)
7	miob5780;DNA sequence (clone 24_A_9) ;AC007371.16	AC007371.16				1 (0.796 to 1.204)	0.443	0.522 (0.498 to 0.547)
	fcrb1731;NDUFV3 gene for mitochondrial NADH-Ubiquinone oxidoreductase ;AB038163.1	AB038163.1			BAB13732	1 (0.975 to 1.025)	0.439	1.555 (0.334 to 2.775)

seob5880;EST zx48b06.r1 Soares_testis_N HT cDNA clone IMAGE:795443 5' similar to contains Alu repetitive element;contain s element MER13 repetitive element ; ;AA454038.1	AA454038.1	NM_017925	Hs.29032	NP_06039 5	1 (0.676 to 1.324)	0.428	0.740 (0.646 to 0.834)
miob2355;NAD H dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) (NDUFB3) ;NM_002491.1	NM_002491. 1	NM_002491	Hs.109760	NP_00248 2	1 (0.865 to 1.135)	0.428	0.739 (0.669 to 0.808)
ncr0644;EST(A V724328 HTB cDNA clone HTBAYE08 5') ;AV724328.1	AV724328.1	NM_007111	Hs.79353	NP_00904 2	1 (0.664 to 1.336)	0.427	0.549 (0.546 to 0.553)
fcrb5537;slug (chicken homolog), zinc finger protein, clone MGC:10182 IMAGE:3908245 , mRNA, complete cds /cds=(152,958) /gb=BC014890 /gi=15928855 /ug=Hs.93005 /len=2010 ;Hs.93005	BC014890	NM_003068	Hs.93005	NP_00305 9	1 (0.329 to 1.671)	0.42	0.52 (0.482 to 0.558)

	fcrb3691;FLJ22066 fis, clone HEP10611 /cds=UNKNOWN /gb=AK025719 /gi=10438328 /ug=Hs.251664 /len=2281 ;Hs.251664	AK025719		Hs.251664		1 (0.582 to 1.418)	0.419	1.101 (0.419 to 1.783)
	MIOA4076a;AR P2/3 COMPLEX 20 KD SUBUNIT (P20-ARC), putative ;Q18491	NM_020154.1	NM_020154.1	Hs.4245	NP_06453 9.1	1 (0.383 to 1.617)	0.418	2.909 (2.011 to 3.806)
8	SEOB1449;C-type lectin ;BAA95671.1	no significant match				1 (0.833 to 1.167)	0.393	0.572 (0.517 to 0.626)
	ncrb4957;WNT1 inducible signalling pathway protein 2 (WISP2) ;NM_003881.1	NM_003881.1	NM_003881	Hs.194679	NP_00387 2	1 (0.769 to 1.231)	0.387	0.722 (0.646 to 0.798)
	SEOB3360;dual specificity phosphatase 1 (DUSP1) ;NM_004417.2	NM_004417.2	NM_004417	Hs.171695	NP_00440 8	1 (0.821 to 1.179)	0.386	0.646 (0.573 to 0.719)
	seob1967;hypothetical protein (FLJ11041 fis, clone PLACE1004405 ) ;AK001903.1	AK001903.1		Hs.28792		1 (0.217 to 1.783)	0.384	2.451 (1.884 to 3.019)
	SEOB1385;hypothetical protein (KIAA0907) ;AB020714.1	AB020714.1	NM_014949	Hs.24656	NP_05576 4	1 (0.749 to 1.251)	0.377	0.601 (0.527 to 0.676)
	mioa4318;embryonic lung protein (HUEL) ;AF006621.1	AF006621.1	NM_006345	Hs.270956	NP_00633 6	1 (0.924 to 1.076)	0.377	0.601 (0.536 to 0.667)

seob4726;differentiation-related gene 1 (nickel-specific induction protein) (RTP) ;NM_006096.1	NM_006096.1	NM_006096	Hs.75789	NP_006087	1 (0.637 to 1.363)	0.359	0.710 (0.479 to 0.941)
SEOA8195a;SOX9 ;Z46629	Z46629	NM_000346	Hs.2316	NP_000337	1 (0.386 to 1.614)	0.356	0.516 (0.381 to 0.651)
ncrc0981;EST (cDNA clone HEMBA1000915 3' HEMBA1) ;AU144114.1	AU144114.1		Hs.453087		1 (0.976 to 1.024)	0.35	1.322 (0.621 to 2.022)
miob2375;H3 histone, family 3B (H3.3B) (H3F3B) ;NM_005324.1	NM_005324.1	NM_005324	Hs.393660	NP_005315	1 (0.850 to 1.15)	0.339	0.632 (0.580 to 0.684)
SEOB1322;fos proto-oncogene (c-fos) ;K00650.1	K00650.1			AAA52471	1 (0.688 to 1.312)	0.289	0.643 (0.622 to 0.665)
SEOA1079a;chitinase (HUMTCHIT) ;U58515	U58515	NM_004000	Hs.154138	NP_003991	1 (0.172 to 1.828)	0.282	2.606 (2.244 to 2.969)
ncrc2705;EST(wr53g02.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2491442 3') ;AI973251.1	AI973251.1	NM_031461	Hs.182364	NP_113649	1 (0.261 to 1.739)	0.269	0.748 (0.252 to 1.243)
MIOA7395a;SOD-2 manganese superoxide dismutase ;X65965	X65965				1 (0.218 to 1.782)	0.232	0.595 (0.273 to 0.916)

**Table 2:** FIG. 2 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being down regulated in cartilage isolated from patients having severe osteoarthritis, but which are not down regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.

SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
	FCR1566;EST (np83a06.s1 NCI_CGAP_Th y1 clone IMAGE:113288 2 gb:L06505 60S RIBOSOMAL PROTEIN L12);AA632687	AA632687	NM_000976	Hs.378011	NP_000967	1 (0.401 to 1.599)	0.694	0.42 (0.341 to 0.499)
	fcrb1690;EST (7n15h06.x1 NCI_CGAP_Brn 23 DNA clone IMAGE:356489 9 3') ;BF195152.1	BF195152.1		Hs.451373		1 (0.667 to 1.333)	0.523	0.412 (0.328 to 0.497)
	ncrc3541;EST(x n38h02.x1 NCI_CGAP_Kid 11 cDNA clone IMAGE:269601 9 3') ;AW195479.1	AW195479.1	NM_005398	Hs.303090	NP_005389	1 (0.943 to 1.057)	0.832	0.489 (0.489 to 0.489)
	ncrb8425;EST(6 01463665F1 NIH_MGC_67 cDNA clone IMAGE:386680 1 5') ;BE777895.1	BE777895.1	NM_021639	Hs.169854	NP_067652	1 (0.806 to 1.194)	0.554	0.48 (0.474 to 0.485)

ncrb8303;Hypothetical protein(cDNA FLJ11339 fis, clone PLACE1010743 , weakly similar to myosin-IXb splice variant mRNA) ;AK002201.1	AK002201.1	NM_004145	Hs.159629	NP_004136	1 (0.319 to 1.681)	0.528	0.394 (0.305 to 0.482)
ncr1204;promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds ;AF060568	AF060568			AAD03619	1	0.824	0.402 (0.324 to 0.48)
MIOA0090;EST (wh87a08.x1 NCI_CGAP_CL L1 clone IMAGE:238770 2 3' WP:B0035.2 CE05160 DNAJ PROTEIN LIKE) ;AI760344.1	AI760344.1	NM_004125	Hs.433898	NP_004116	1 (0.606 to 1.394)	0.6	0.442 (0.425 to 0.459)
seoa8384;EST(t h76e02.x1 Soares_NhHMP u_S1 clone IMAGE:212460 2 3') ;AI434978.1	AI434978.1		Hs.164315		1	NO DATA	0.424 (0.418 to 0.431)
MIOA3760a;zinc finger transcription factor GKLF ;AF105036.1	AF105036.1	NM_004235	Hs.356370	NP_004226	1 (0.831 to 1.169)	NO DATA	0.384 (0.367 to 0.402)
FCR1580;EST (zs83g12.s1 NCI_CGAP_GC B1 clone IMAGE:704134 3');AA279281	AA279281	NM_004089	Hs.75450	NP_004080	1 (0.288 to 1.712)	0.676	0.336 (0.272 to 0.399)

	miob4857;EST(DKFZp434O157 2 clone DKFZp434O157 2) ;AL137333.1	AL137333.1	XM_042234	Hs.194478		1 (0.918 to 1.082)	0.659	0.411 (0.391 to 0.432)
	miob6713;zinc finger protein (ZNF-U69274) ;NM_014415.1	NM_014415.1	NM_014415	Hs.301956	NP_055230	1 (0.892 to 1.108)	0.539	0.41 (0.373 to 0.447)
	seoa3815;EST(oj25g11.s1 NCI_CGAP_Kid 5 clone IMAGE:149325 2 3') ;AA886870	AA886870	NM_018359	Hs.107381	NP_060829	1 (0.642 to 1.358)	NO DATA	0.359 (0.345 to 0.373)
	ncrc9528;nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha;Nuclear factor of kappa light chain gene enhancer in B-cells (RefSeq aa 4e-38) ;NP_065390.1	NM_020529			NP_065390.1	1 (0.458 to 1.542)	NO DATA	0.38 (0.356 to 0.403)
	ncrb8237;TSC-22-like Protein mRNA, ;AF183393.1	AF183393.1	NM_004089	Hs.75450	NP_004080	1 (0.286 to 1.714)	0.707	0.326 (0.297 to 0.355)
9	miob2933;DNA sequence PAC clone RP5-1060B11 from 7q11.23-q21.1, complete sequence ;AC006322.2	AC006322.2				1 (0.714 to 1.286)	1.088	0.388 (0.352 to 0.424)



	MIOA1025;myleoid differentiation primary response protein MyD88 ;U70451	U70451	NM_002468	Hs.82116	NP_002459	1 (0.912 to 1.088)	0.554	0.366 (0.331 to 0.401)
	miob0762;EST(tc01c04.x1 NCI_CGAP_Co 16 cDNA clone IMAGE:206256 6 3') ;AI343957.1	AI343957.1				1	NO DATA	0.325 (0.320 to 0.33)
	FCR6730;DNA sequence (Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST)) ;U80460	U80460				1 (0.331 to 1.669)	1.621	0.329 (0.320 to 0.337)
10	miob4228;DNA sequence (PAC 121G13 chromosome 6) ;Z86062.1	Z86062.1				1 (0.969 to 1.031)	NO DATA	0.398 (0.3 to 0.497)
	ncr6316;selenium binding protein 1 (RefSeq aa 8e-40) ;NP_003935.1	NM_003944.2	NM_003944.2	Hs.334841	NP_003935.1	1 (0.454 to 1.546)	0.519	0.202 (0.189 to 0.214)

**Table 3:** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage in patients having mild osteoarthritis, but which are not up regulated in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.

SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
	MIOA8106;D NA sequence(HS_5573_B1_E05_SP6 RPCI-11 Male BAC Library genomic clone Plate=1149 Col=9 Row=J) ;AQ750872.1	AQ750872.1				1 (0.871 to 1.129)	3.168	1.018 (0.964 to 1.072)
	FCR4376;ES T (ol15b11.s1 Soares_NFL_T_GBC_S1 clone IMAGE:15235 17 3') ;AA904355	AA904355	NM_032682	Hs.27434 4	NP_11607 1	1 (0.871 to 1.129)	3.047	0.901 (0.798 to 1.005)
11	hfc8691;No significant match;					1 (0.823 to 1.177)	2.727	1.791 (1.729 to 1.852)
	SEOA0824;alpha-tubulin ;K00557	K00557	NM_006009	Hs.43339 4	NP_00600 0	1 (0.728 to 1.272)	2.688	1.151 (1.051 to 1.252)
12	FCR6361;DNA sequence (12p13.3 BAC RPCI11-500M8 (Roswell Park Cancer Institute Human BAC Library) ;AC005832	AC005832				1 (0.977 to 1.023)	2.625	1.3 (1.254 to 1.345)
	hfc3990;Novel;	U48696.1				1 (0.808 to 1.192)	2.614	1.784 (1.553 to 2.015)

	SEOA0114;MacMarcks ;X70326	X70326	NM_023009	Hs.75061	NP_075385	1 (0.742 to 1.258)	2.556	1.125 (0.872 to 1.378)
	ncrb4428;Ras association (RalGDS/AF-6) domain family 2 (RASSF2)(= KIAA0168) ;NM_014737.1	NM_014737.1	NM_014737	Hs.80905	NP_739580	1 (0.635 to 1.365)	2.507	1.304 (1.298 to 1.309)
	ncrb4154;glucosamine-6-phosphate ;AJ002231.1	AJ002231.1	NM_005471	Hs.278500	NP_005462	1 (0.609 to 1.391)	2.35	1.386 (0.950 to 1.823)
	ncr0679;membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA	NM_001932.2	NM_001932.2	Hs.423809	NP_001923.2	1 (0.935 to 1.065)	2.277	0.871 (0.840 to 0.901)
	fcrb1982;hypothetical protein MGC3047 (MGC3047) ;XM_027710.1	NM_032348	NM_032348	Hs.59384		1 (0.547 to 1.453)	2.272	1.714 (1.584 to 1.844)
	MIOA8952;erythrocyte membrane protein band 4.1-like 2 (EPB41L2) ;NM_001431.1	NM_001431.1	NM_001431	Hs.7857	NP_001422	1 (0.627 to 1.373)	2.268	1.793 (1.761 to 1.826)
13	bfcn0190n;Homo sapiens chromosome 15, clone CTD1-2291N1, complete	AC107908.3				1 (0.987 to 1.013)	2.248	1.309 (1.124 to 1.494)

	sequence							
	fcr3730;EST xb22e11.x1 NCI_CGAP_ Kid13 cDNA clone IMAGE:25770 68 3' ;AW075553	AW075553		Hs.24327 8		1 (0.999 to 1.001)	2.241	1.33 (0.973 to 1.687)
	fcrb5705;kine sin-like 5 (mitotic kinesin-like protein 1) (KNLSL5), mRNA /cds=(117,26 87) /gb=NM_0048 56 /gi=13699831 /ug=Hs.27084 5 /len=3323 ;Hs.270845	NM_00485 6	NM_138555	Hs.27084 5	NP_61256 5	1 (0.911 to 1.089)	2.203	1.190 (1.054 to 1.326)
	seoa0387;ma trix Gla protein (MGP) ;M55270	M55270			AAB53765	1 (0.775 to 1.225)	2.202	1.174 (0.889 to 1.458)
	hfc0439;alph a-1- antitrypsin mRNA, complete cds ;K01396.1	K01396.1	NM_000295	Hs.29768 1	NP_00028 6	1 (0.945 to 1.055)	2.192	1.028 (0.879 to 1.178)
	miob1269;ES T (an12d12.s1 Stratagene schizo brain S11 IMAGE:16853 99 3') ;AI003217.1	AI003217.1				1	2.187	1.813 (1.454 to 2.173)
	miob3252;CIL P gene for cartilage intermediate	AB022430. 1			BAA76692	1 (0.901 to 1.099)	2.18	0.993 (0.958 to

	layer protein, complete cds ;AB022430.1							1.028)
	ncrb4477;Ho mo sapiens serine (or cysteine) proteinase inhibitor, clade A  (alpha-1 antiproteinase , antitrypsin), member 1 (SERPINA1), mRNA	NM_00029 5.2	NM_000295. 2	Hs.29768 1	NP_00028 6.2	1 (0.756 to 1.244)	2.179	1.224 (0.773 to 1.674)
14	cr0517;Homo sapiens 12 BAC RP13- 820C6 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC137590. 2				1	2.178	1.082 (1.035 to 1.128)
	FCR2743;ES T (qa21e02.x1 NCI_CGAP_ Brn23 clone IMAGE:16874 18 3");AI088910	AI088910	NM_017714	Hs.88367	NP_06018 4	1 (0.961 to 1.039)	2.175	1.231 (1.213 to 1.249)
	fcr6308;EST df54g09.y1 Morton Fetal Cochlea cDNA clone IMAGE:24873 53 5' ;AW023432	AW023432		Hs.18837 5		1 (0.871 to 1.129)	2.159	1.332 (1.179 to 1.486)
	ncrb4843;repl ication protein A1 (70kD) (RPA1) ;NM_002945.	NM_00294 5.1	NM_002945	Hs.84318	NP_00293 6	1	2.154	1.158 (1.098 to 1.218)

	1							
15	seob4891;DN A sequence (BAC clone RP11-15J24 chromosome 2) ;AC007736.3	AC007736. 3				1 (0.729 to 1.271)	2.147	1.27 (1.145 to 1.394)
16	MI0B2566;D NA sequence (chromosome 4 clone RP11-340K9 map 4, WORKING DRAFT SEQUENCE, 24 unordered pieces) ;AC012205.3	AC012205. 3				1	2.145	1.082 (0.827 to 1.338)
	FCR0620;ES T (oe35b11.s1 NCI_CGAP_ Pr25 clone IMAGE:14105 25 3');AA857238	AA857238		Hs.4248		1 (0.946 to 1.054)	2.13	0.849 (0.828 to 0.869)
	FCR6069;ES T (zf01g11.s1 Soares fetal heart NbHH19W clone 375716 3') ;AA033743	AA033743	XM_087386	Hs.43345 2		1 (0.908 to 1.092)	2.119	1.418 (1.396 to 1.441)
17	miob4693;DN A sequence (chromosome 6 clone RP11- 780P12, WORKING DRAFT SEQUENCE, 4 unordered pieces)	AC022218. 5				1 (0.767 to 1.233)	2.096	1.812 (1.559 to 2.066)

	;AC022218.4							
	hfc7667;EST (yr10e10.s1 Soares fetal liver spleen 1NFLS clone IMAGE:20490 6 3')(contains Alu repetitive element) ;H57324.1	H57324.1				1	2.087	1.585
	cr0503;EST (PM4- NN0090- 230400-001- d11 NN0090) ;AW899788.1	AW899788. 1				1 (0.882 to 1.118)	2.085	1.001 (0.908 to 1.093)
	FCR5665;ES T (yd33h08.r1 clone 110079 5') ;T85246	T85246		Hs.45250 9		1 (0.880 to 1.12)	2.081	1.408 (1.393 to 1.423)
	ncr7382;prote ase inhibitor 1 (anti- elastase),alph a-1- antitrypsin (RefSeq aa 3e-43) ;NP_000286. 1	NM_00029 5			NP_00028 6.1	1 (0.783 to 1.217)	2.076	0.893 (0.68 to 1.105)
	fcr4642;EST (integral membrane protein 2A, clone IMAGE:41499 10, mRNA);BC01 0511	BC010511	NM_004867	Hs.17109	NP_00485 8	1 (0.764 to 1.236)	2.068	1.172 (1.144 to 1.200)
	SEOA4017a;r etinoic acid- induced protein (RAI2)	AF136587. 1			AAD33688	1 (0.882 to 1.118)	2.059	1.718 (1.634 to 1.801)

	;AF136587.1							
18	hfc1438;No significant match;					1 (0.933 to 1.067)	2.052	1.294 (1.100 to 1.489)
	hfc0263;paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein) (PACE) ;NM_002569.1	NM_002569.1	NM_002569	Hs.59242	NP_002560	1 (0.975 to 1.025)	2.049	0.884 (0.882 to 0.885)
	ncr7477;cDNA A sequence (cDNA sequence FLJ11736 fis, clone HEMBA1005468) ;AK021798.1	AK021798.1			BAB13899	1	2.045	1.602 (1.422 to 1.783)
	ncr2015;G protein-coupled receptor 23 (GPR23) ;NM_005296.1	NM_005296.1	NM_005296	Hs.27812	NP_005287	1 (0.765 to 1.235)	2.044	1.973 (1.816 to 2.131)
	mioa9984;EST wm09d08.x1 NCI_CGAP_cDNA clone IMAGE:2435439 3' similar to contains Alu repetitive element;contains element THR repetitive element ;	AI859280	NM_017523	Hs.139262	NP_059993	1 (0.722 to 1.278)	2.036	1.245 (1.202 to 1.287)



	;AI859280							
	FCR1427;EST (zt75e12.r1 Soares testis NHT clone 728206 5');AA393418	AA393418	NM_014335	Hs.381137	NP_055150	1 (0.958 to 1.042)	2.023	0.914 (0.852 to 0.977)
	MIOA2551;EST(vz29h10.r1 Soares 2NbMT clone 1327939 5') (low match);AA915413	AA915413				1 (0.860 to 1.14)	2.022	1.988 (1.462 to 2.514)
	FCR6039;protein kinase Dyrk2;Y13493	Y13493	NM_006482	Hs.173135	NP_006473	1 (0.868 to 1.132)	2.02	1.177 (1.157 to 1.197)
	miob1165;DNA sequence (clone 23698);AF052094.1	AF052094.1	NM_001430	Hs.8136	NP_001421	1 (0.611 to 1.389)	2.013	1.761 (1.745 to 1.777)
	fcrb3863;cDNA, 3' end /clone=IMAG E:2504281 /clone_end=3' /gb=AW009305 /gi=5858083 /ug=Hs.337337 /len=456;Hs.337337	AW009305		Hs.337337		1 (0.941 to 1.059)	2.007	1.217 (1.002 to 1.432)
	fcrb1183;tubulin-specific chaperone d (TBCD)=AJ006417 beta-tubulin cofactor D;NM_005993.2	NM_005993.2	NM_005993	Hs.12570	NP_005984	1	2.004	0.781

hcr6052;EST hi90a09.x1 Soares_NFL_ T_GBC_S1 cDNA clone IMAGE:29795 44 3' ;AW665381.1	AW665381. 1	Hs.44532 4	1 (0.889 to 1.111)	2.002	1.354 (1.19 to 1.519)
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**Table 4 :** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage isolated from patients having severe osteoarthritis, but which are not up regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.

SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
	FCR1346;receptor of retinoic acid (=M73779 PML-RAR protein (PML-RAR));X06614	X06614	NM_000964	Hs.361071	NP_000955	1 (0.804 to 1.196)	1.577	2.651 (2.19 to 3.113)
	MIOA5404a;actin-like 6 (ACTL6)=A F041474 =BAF53a (BAF53a)(ORF);NM_004301.1	NM_004301.1	NM_178042	Hs.274350	NP_829888	1	1.011	2.975 (2.785 to 3.165)

SEOA6743; EST(ze26h0 9.r1 Soares retina N2b4HR clone 360161 5') ;AA013461	AA013461		Hs.161598		1 (0.953 to 1.047)	1.442	2.349 (2.297 to 2.401)
FCR5026;6- phosphofruc to-2- kinase/fruct ose-2,6- bisphosphat ase (PF2K) (=AB00790 2 KIAA0442) ;AF041832	AF041832				1 (0.944 to 1.056)	1.46	2.289 (2.269 to 2.309)
miob4484;h ypothetical protein (KIAA0584) ;AB011156. 1	AB011156. 1	NM_015101	Hs.106794	NP_055916	1	1.547	3.424 (2.207 to 4.641)
seob7571;E ST (qh03a05.x1 Soares_NF L_T_GBC_ S1 IMAGE:184 3568 3') ;AI222189.1	AI222189.1	NM_002556	Hs.24734	NP_002547	1 (0.945 to 1.055)	1.615	2.080 (2.041 to 2.12)

**Table 5:** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage isolated from patients having severe osteoarthritis, but which are down regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100 Kb or that are novel are identified by SEQ ID NO.

SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
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	MIOA4076a;ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC), putative ;Q18491	NM_020154.1	NM_020154.1	Hs.4245	NP_064539.1	1 (0.383 to 1.617)	0.418	2.909 (2.011 to 3.806)
	seob1967;hypothetical protein (FLJ11041 fis, clone PLACE1004405) ;AK001903.1	AK001903.1		Hs.28792		1 (0.217 to 1.783)	0.384	2.451 (1.884 to 3.019)

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Please add the following 2 new paragraphs (Tables) at page 98, between lines 19 and 20:

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Table 6a: depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for mild OA only					
Common name	Genbank	Description	RefSeq	UniGene	Rep_Prot
ncrc6905	AB007916	mRNA for KIAA0447 protein, partial cds. /cds=(234,1634) /gb=AB007916 /gi=6683704 /ug=Hs.214646 /len=5932		Hs.214646	NP_878258
seoa9924	AB007960	chromosome 1 specific transcript KIAA0491	NM_016009	Hs.136309	NP_057093
ncrc2701	AB011110	mRNA for KIAA0538 protein, partial cds	NM_006989	Hs.184367	NP_008920
seoc4468	AB014540	mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824		Hs.153026	NP_055870
seob7030	AB023420	mRNA for heat shock protein apg-2, complete cds. /cds=(279,2801) /gb=AB023420 /gi=4579908 /ug=Hs.90093 /len=2839		Hs.90093	NP_002145
seoa8696	AB037754	mRNA for KIAA1333 protein, partial cds	NM_017769	Hs.79828	NP_060239
miob8583	AB037788	mRNA for KIAA1367 protein, partial cds. /cds=(1,1741) /gb=AB037788 /gi=7243114 /ug=Hs.224961 /len=4196		Hs.224961	NP_059133
miob8583	AB037788	mRNA for KIAA1367 protein, partial cds. /cds=(1,1741) /gb=AB037788 /gi=7243114 /ug=Hs.224961 /len=4196		Hs.224961	NP_059133

seob4263	AB040894	mRNA for KIAA1461 protein, partial cds	NM_018328	Hs.94125	NP_060798
seob4263	AB040894	mRNA for KIAA1461 protein, partial cds	NM_018328	Hs.94125	NP_060798
miob2503	AB051541	mRNA for KIAA1754 protein, partial cds. /cds=(32,1816) /gb=AB051541 /gi=12698052 /ug=Hs.28501 /len=4088	NM_033397	Hs.28501	NP_203755
mioc2385	AB067500	mRNA for KIAA1913 protein, partial cds. /cds=(818,2347) /gb=AB067500 /gi=15620884 /ug=Hs.172870 /len=3512	NM_052913	Hs.172870	NP_443145
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
fcrb6309	AF324892	myosin phosphatase target subunit 2 (MYPT2) gene, exons 11 through 24, and complete cds	NM_002481; NM_032103; NM_032104; NM_032105		NP_002472; NP_115286; NP_115287; NP_115288
fcr6564	AF474370	chemokine-like factor super family member 8 (CKLFSF8) mRNA, complete cds /cds=(295,816) /gb=AF474370 /gi=25167350 /ug=Hs.154986 /len=1185		Hs.154986	NP_849199
fcr6564	AF474370	chemokine-like factor super family member 8 (CKLFSF8) mRNA, complete cds /cds=(295,816) /gb=AF474370 /gi=25167350 /ug=Hs.154986 /len=1185		Hs.154986	NP_849199
ncrc0075	AF545571	sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699	NM_015170	Hs.70823	NP_055985
ncr1522	AJ000052	gene encoding splicing factor SF1, exons 2-8	NM_004630		NP_004621
miod7007	AJ251973	partial steerin-1 gene	NM_020443		NP_065176
miod1528	AJ420597	mRNA full length insert cDNA clone EUROIMAGE881791		Hs.34665	NP_775945
seoc5609	AK001419	cDNA FLJ10557 fis, clone NT2RP2002537	NM_014053	Hs.270594	NP_054772
ncr3785	AK001911	cDNA FLJ11049 fis, clone PLACE1004548	NM_020819	Hs.107287	NP_065870
seoc3640	AK021499	cDNA FLJ11437 fis, clone HEMBA1001226	NM_002788; NM_152132		NP_002779

miob9087	AK024433	mRNA for FLJ00023 protein, partial cds	NM_022497	Hs.23450	NP_071942
miod6848	AK026850	cDNA: FLJ23197 fis, clone REC00917	NM_005402	Hs.6906	NP_005393
mioc9655	AK055915	cDNA FLJ31353 fis, clone MESAN2000264. /gb=AK055915 /gi=16550762 /ug=Hs.352554 /len=2192		Hs.352554	NP_006440
miob8096	AK057924	cDNA FLJ25195 fis, clone REC04480, highly similar to Mus musculus exportin 4 mRNA	NM_022459	Hs.117102	NP_071904
seob1782	AK074172	mRNA for FLJ00245 protein		Hs.244343	NP_443068
seob7534	AK075026	cDNA FLJ90545 fis, clone OVARC1000410, weakly similar to angiopoietin Y1 mRNA		Hs.8025	NP_036230
seob5621	AK090874	cDNA FLJ33555 fis, clone BRAMY2009349, moderately similar to Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA		Hs.15303	NP_056070
seoc6732	AK098206	cDNA FLJ40887 fis, clone UTERU2000696, moderately similar to Endoplasmic reticulum resident protein 58		Hs.83286	NP_714916
ncrc1765	AL080156	mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749		Hs.12813	NP_056323
miod7095	AL096734	mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011)	NM_030980	Hs.301904	NP_112242
fcrc6486	AL110153	mRNA; cDNA DKFZp586E0524 (from clone DKFZp586E0524)	NM_000983	Hs.326249	NP_000974
mioc2507	AL137295	mRNA; cDNA DKFZp434M2216 (from clone DKFZp434M2216)	NM_004641	Hs.199429	NP_004632
seoa3357	AL162009	mRNA; cDNA DKFZp586C2117 (from clone DKFZp586C2117)		Hs.356386	NP_004628
miod2065	AL832012	mRNA; cDNA DKFZp451D084 (from clone DKFZp451D084); complete cds	NM_006827	Hs.74137	NP_006818
miob8803	AL833934	mRNA; cDNA DKFZp547F222 (from clone DKFZp547F222)	NM_022458	Hs.107537	NP_071903
ncrc7173	AL834204	mRNA; cDNA DKFZp434J1323 (from clone DKFZp434J1323)	NM_015208		NP_056023
fcrc2573	AL834255	mRNA; cDNA DKFZp586M1819 (from clone DKFZp586M1819) /cds=(1,795) /gb=AL834255 /gi=21739805 /ug=Hs.355753 /len=1723		Hs.355753	NP_848934
ncrb8113	AW182493	xj42g07.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2659932 3', mRNA sequence /clone=IMAGE:2659932 /clone_end=3' /gb=AW182493 /gi=6450953 /ug=Hs.176245 /len=432		Hs.176245	NP_060046

fcr3932	BC011767	clone IMAGE:3609644, mRNA		Hs.56828	NP_006577
ncr7284	BC013088	clone IMAGE:3452986, mRNA	NM_001894; NM_152221	Hs.79658	NP_689407
mioc8879	BC017107	clone IMAGE:3537687, mRNA		Hs.16577	NP_208385
fcrb9161	BC017973	clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946	NM_174896	Hs.288010	NP_777556
miod0057	BC020167	clone IMAGE:3529287, mRNA	NM_152740	Hs.284170	NP_689953
seoc4785	BC022792	Vpr-binding protein, mRNA (cDNA clone MGC:23092 IMAGE:4853730), complete cds	NM_014703	Hs.118738	NP_055518
ncrc2382	BC032405	clone IMAGE:5209850, mRNA		Hs.146428	NP_000084
seob0220	BC032437	clone IMAGE:4432159, mRNA /gb=BC032437 /gi=21595543 /ug=Hs.249247 /len=2309		Hs.249247	
mioa8580	BC032643	Similar to NS1-associated protein 1, clone MGC:45213 IMAGE:5495201, mRNA, complete cds		Hs.373499	NP_006363
fcrb8094	BC034757	Indian hedgehog (Drosophila), clone MGC:34815 IMAGE:5182642, mRNA, complete cds /cds=(74,955) /gb=BC034757 /gi=21961329 /ug=Hs.115274 /len=1760		Hs.115274	
ncrc3706	BC035312	clone MGC:21662 IMAGE:4747440, mRNA, complete cds		Hs.145010	NP_115965
ncrc3089	BC036649	Sec23 A (S. cerevisiae), clone MGC:26267 IMAGE:4821858, mRNA, complete cds	NM_006364	Hs.272927	NP_006355
miob0681	BC037306	Similar to CD47 antigen (Rh-related antigen, integrin-associated signal transducer), clone MGC:33903 IMAGE:5260986, mRNA, complete cds	NM_001777	Hs.313342	NP_001768
ncr3803	BC037492	clone IMAGE:5260578, mRNA		Hs.5518	NP_689971
fcrb4479	BC042102	Similar to RIKEN cDNA 3110032G18 gene, clone IMAGE:4472603, mRNA /gb=BC042102 /gi=27695553 /ug=Hs.432901 /len=2132		Hs.432901	NP_859060
fcr6611	BC042998	Similar to adducin 1 (alpha), clone MGC:44427 IMAGE:5297337, mRNA, complete cds /cds=(869,2857) /gb=BC042998 /gi=28175763 /ug=Hs.183706 /len=4761	NM_001119; NM_014189; NM_014190; NM_176801	Hs.183706	NP_789771
fcr3593	BC044258	clone IMAGE:6068796, mRNA		Hs.11861	NP_005112

seoc5538	BG434947	602507208F1 NIH_MGC_79 cDNA clone IMAGE:4604760 5', mRNA sequence /clone=IMAGE:4604760 /clone_end=5' /gb=BG434947 /gi=13341453 /ug=Hs.382990 /len=677		Hs.382990	NP_060135
mioc7077	BQ649741	AGENCOURT_8493271 NIH_MGC_100 cDNA clone IMAGE:6299336 5', mRNA sequence /clone=IMAGE:6299336 /clone_end=5' /gb=BQ649741 /gi=21773913 /ug=Hs.44701 /len=993		Hs.44701	NP_055301
fcrb4351	BU536672	AGENCOURT_10227215 NIH_MGC_141 cDNA clone IMAGE:6565196 5', mRNA sequence /clone=IMAGE:6565196 /clone_end=5' /gb=BU536672 /gi=22847113 /ug=Hs.380933 /len=1275		Hs.380933	NP_000974
ncrc8884	BU627064	UI-H-FG0-bct-g-21-0-UI.s1 NCI_CGAP_EN1_2 cDNA clone UI-H-FG0-bct-g-21-0-UI 3', mRNA sequence /clone=UI-H-FG0-bct-g-21-0-UI /clone_end=3' /gb=BU627064 /gi=23293278 /ug=Hs.85999 /len=1075		Hs.85999	NP_060312
seoc4779	BU728934	UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aew-e-07-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aew-e-07-0-UI /clone_end=3' /gb=BU728934 /gi=23651308 /ug=Hs.436272 /len=1132		Hs.436272	NP_060312
seob0562	BX094256	BX094256 Soares_fetal_heart_NbHH19W cDNA clone IMAGp998B20783, mRNA sequence /clone=IMAGp998B20783;_IMAGE:342835 /gb=BX094256 /gi=27841884 /ug=Hs.407356 /len=477		Hs.407356	NP_055301
seob6628	BX110894	BX110894 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998F21129, mRNA sequence /clone=IMAGp998F21129;_IMAGE:127124 /gb=BX110894 /gi=27836709 /ug=Hs.309257 /len=612		Hs.309257	T02670
miob0542	CA848700	ir24c06.y1 HR85 islet cDNA clone IMAGE:6546227 5', mRNA sequence /clone=IMAGE:6546227 /clone_end=5' /gb=CA848700 /gi=26999906 /ug=Hs.389121 /len=616		Hs.389121	NP_060312
seob4499	CB050438	NISC_gj17d11.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3272108 3', mRNA sequence /clone=IMAGE:3272108 /clone_end=3' /gb=CB050438 /gi=27788725 /ug=Hs.435309 /len=534		Hs.435309	NP_060265



ncr1150	D83778	mRNA for KIAA0194 gene, partial cds. /cds=(1,4310) /gb=D83778 /gi=1228038 /ug=Hs.216958 /len=5245		Hs.216958	BAA12107
miob6124	L24123	NRF1 protein (NRF1) mRNA	NM_003204		NP_003195
ncr5649	M24095	MHC class I HLA-A10-alpha-2 chain mRNA, partial cds, clone 8/16		Hs.181244	NP_002107
seob7184	M37435	macrophage-specific colony-stimulating factor (CSF-1) mRNA, complete cds	NM_000757; NM_172210; NM_172211; NM_172212		NP_000748; NP_757349; NP_757350; NP_757351
ncrb5537	NM_000014	alpha-2-macroglobulin (A2M), mRNA /cds=(44,4468) /gb=Nm_000014 /gi=6226959 /ug=Hs.74561 /len=4577	NM_000014	Hs.74561	NP_000005
mioa6969	NM_000027	aspartylglucosaminidase (AGA), mRNA /cds=(171,1211) /gb=Nm_000027 /gi=4557272 /ug=Hs.207776 /len=2150	NM_000027	Hs.207776	NP_000018
miob4512	NM_000090	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA /cds=(118,4518) /gb=Nm_000090 /gi=15149480 /ug=Hs.119571 /len=5489	NM_000090	Hs.119571	NP_000081
hfr5232	NM_000095	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA /cds=(26,2299) /gb=Nm_000095 /gi=4557482 /ug=Hs.1584 /len=2439	NM_000095	Hs.1584	NP_000086
fcr0796	NM_000146	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=Nm_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137
mioa7241	NM_000147	fucosidase, alpha-L- 1, tissue (FUCA1), mRNA /cds=(19,1404) /gb=Nm_000147 /gi=24475878 /ug=Hs.576 /len=2035	NM_000147	Hs.576	NP_000138
fcrb2137	NM_000184	hemoglobin, gamma G (HBG2), mRNA /cds=(54,497) /gb=Nm_000184 /gi=28302132 /ug=Hs.386655 /len=583	NM_000184	Hs.386655	NP_000175
ncrc3092	NM_000216	Kallmann syndrome 1 sequence (KAL1), mRNA /cds=(151,2193) /gb=Nm_000216 /gi=4557682 /ug=Hs.89591 /len=6314	NM_000216	Hs.89591	NP_000207
fcr2254	NM_000234	ligase I, DNA, ATP-dependent (LIG1), mRNA /cds=(121,2880) /gb=Nm_000234 /gi=4557718 /ug=Hs.1770 /len=3083	NM_000234	Hs.1770	NP_000225

hfc0439	NM_000295	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA /cds=(233,1489) /gb=NM_000295 /gi=21361197 /ug=Hs.297681 /len=1584	NM_000295	Hs.297681	NP_000286
mioa1277	NM_000313	protein S (alpha) (PROS1), mRNA /cds=(147,2177) /gb=NM_000313 /gi=4506116 /ug=Hs.64016 /len=3309	NM_000313	Hs.64016	NP_000304
fcr4935	NM_000337	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 1, mRNA /cds=(333,1205) /gb=NM_000337 /gi=27477099 /ug=Hs.151899 /len=1440	NM_000337; NM_172244	Hs.151899	NP_758447
ncrc3604	NM_000393	collagen, type V, alpha 2 (COL5A2), mRNA /cds=(158,4648) /gb=NM_000393 /gi=16554580 /ug=Hs.82985 /len=6217	NM_000393	Hs.82985	NP_000384
fcrb4616	NM_000426	laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA /cds=(50,9382) /gb=NM_000426 /gi=4557708 /ug=Hs.75279 /len=9534	NM_000426	Hs.75279	NP_000417
ncrc4376	NM_000454	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1), mRNA /cds=(1,465) /gb=NM_000454 /gi=4507148 /ug=Hs.75428 /len=560	NM_000454	Hs.75428	NP_000445
mioa0577	NM_000574	decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369	NP_000565
seoa8501	NM_000579	chemokine (C-C motif) receptor 5 (CCR5), mRNA /cds=(358,1416) /gb=NM_000579 /gi=4502638 /ug=Hs.54443 /len=3655	NM_000579	Hs.54443	NP_000570
miob7319	NM_000611	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(50,436) /gb=NM_000611 /gi=20127410 /ug=Hs.278573 /len=1946	NM_000611	Hs.278573	NP_000602
ncr9165	NM_000636	superoxide dismutase 2, mitochondrial (SOD2), mRNA /cds=(5,673) /gb=NM_000636 /gi=10835186 /ug=Hs.372783 /len=1026	NM_000636	Hs.372783	NP_000627
miob3618	NM_000693	aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), mRNA /cds=(53,1591) /gb=NM_000693 /gi=4502040 /ug=Hs.75746 /len=3442	NM_000693	Hs.75746	NP_000684
ncr2954	NM_000791	dihydrofolate reductase (DHFR), mRNA /cds=(480,1043) /gb=NM_000791 /gi=7262376 /ug=Hs.83765 /len=3900	NM_000791	Hs.83765	NP_000782

seob1879	NM_000861	histamine receptor H1 (HRH1), mRNA /cds=(179,1642) /gb=Nm_000861 /gi=13435403 /ug=Hs.1570 /len=3870	NM_000861	Hs.1570	NP_000852
seoa9883	NM_000925	pyruvate dehydrogenase (lipoamide) beta (PDHB), mRNA /cds=(19,1098) /gb=Nm_000925 /gi=4505686 /ug=Hs.979 /len=1501	NM_000925	Hs.979	NP_000916
mioa3598	NM_000933	phospholipase C, beta 4 (PLCB4), mRNA /cds=(231,3299) /gb=Nm_000933 /gi=4505866 /ug=Hs.283006 /len=3707	NM_000933	Hs.283006	NP_877949
seob7392	NM_000937	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA /cds=(387,6299) /gb=Nm_000937 /gi=14589948 /ug=Hs.171880 /len=6732	NM_000937	Hs.171880	NP_000928
fcr4319	NM_000941	P450 (cytochrome) oxidoreductase (POR), nuclear gene encoding mitochondrial protein, mRNA /cds=(16,2058) /gb=Nm_000941 /gi=24307876 /ug=Hs.167246 /len=2446	NM_000941	Hs.167246	NP_000932
seob8082	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=Nm_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
seoa1117	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=Nm_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
mioc8016	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=Nm_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
ncr3037	NM_000975	ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=Nm_000975 /gi=15431289 /ug=Hs.388664 /len=609	NM_000975	Hs.388664	NP_000966
seob8311	NM_000985	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=Nm_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
seob3513	NM_001003	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=Nm_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
fcr6708	NM_001003	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=Nm_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
miob9652	NM_001003	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=Nm_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994

seob3326	NM_001004	ribosomal protein, large P2 (RPLP2), mRNA	NM_001004	Hs.297753	NP_000995
seob4140	NM_001004	ribosomal protein, large P2 (RPLP2), mRNA	NM_001004	Hs.297753	NP_000995
fcr4212	NM_001008	ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(13,804) /gb=Nm_001008 /gi=17981706 /ug=Hs.180911 /len=931	NM_001008	Hs.180911	NP_000999
seob4689	NM_001154	annexin A5 (ANXA5), mRNA /cds=(193,1155) /gb=Nm_001154 /gi=4809273 /ug=Hs.300711 /len=1630	NM_001154	Hs.300711	NP_001145
seob5894	NM_001177	ADP-ribosylation factor-like 1 (ARL1), mRNA /cds=(105,650) /gb=Nm_001177 /gi=4755126 /ug=Hs.242894 /len=968	NM_001177	Hs.242894	NP_001168
ncrb2458	NM_001202	bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA /cds=(478,1704) /gb=Nm_001202 /gi=19528648 /ug=Hs.68879 /len=1999	NM_001202; NM_130850; NM_130851	Hs.68879	NP_570912
hfcr6384	NM_001211	BUB1 budding uninhibited by benzimidazoles 1 beta (yeast) (BUB1B), mRNA /cds=(135,3287) /gb=Nm_001211 /gi=20149508 /ug=Hs.36708 /len=3702	NM_001211	Hs.36708	NP_001202
ncrc0696	NM_001280	cold inducible RNA binding protein (CIRBP), mRNA /cds=(81,599) /gb=Nm_001280 /gi=4502846 /ug=Hs.119475 /len=1322	NM_001280	Hs.119475	NP_001271
seob5645	NM_001344	defender against cell death 1 (DAD1), mRNA /cds=(67,408) /gb=Nm_001344 /gi=4503252 /ug=Hs.82890 /len=699	NM_001344	Hs.82890	NP_001335
seob3464	NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA /cds=(166,2082) /gb=Nm_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
mioc3490	NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA /cds=(166,2082) /gb=Nm_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
seoa0743	NM_001387	dihydropyrimidinase-like 3 (DPYSL3), mRNA /cds=(111,1823) /gb=Nm_001387 /gi=4503378 /ug=Hs.74566 /len=5047	NM_001387	Hs.74566	NP_001378
ncr3040	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=Nm_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
fcrb0386	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=Nm_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393

fcrb1741	NM_001416	eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA /cds=(17,1237) /gb=Nm_001416 /gi=4503528 /ug=Hs.129673 /len=1383	NM_001416	Hs.129673	NP_001407
mioa7361	NM_001431	erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=Nm_001431 /gi=4503578 /ug=Hs.7857 /len=4336	NM_001431	Hs.7857	NP_001422
fcrb2710	NM_001541	heat shock 27kDa protein 2 (HSPB2), mRNA /cds=(70,618) /gb=Nm_001541 /gi=4504518 /ug=Hs.78846 /len=874	NM_001541	Hs.78846	NP_001532
miob9529	NM_001689	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(255,683) /gb=Nm_001689 /gi=4502300 /ug=Hs.429 /len=826	NM_001689	Hs.429	NP_001680
seob5767	NM_001690	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=Nm_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
seoc4161	NM_001690	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=Nm_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
seoa2134	NM_001801	cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=Nm_001801 /gi=4502754 /ug=Hs.3229 /len=1556	NM_001801	Hs.3229	NP_001792
fcrb1867	NM_001916	cytochrome c-1 (CYC1), mRNA /cds=(5,982) /gb=Nm_001916 /gi=21359866 /ug=Hs.289271 /len=1273	NM_001916	Hs.289271	NP_001907
hfcr1646	NM_001930	deoxyhypusine synthase (DHPS), transcript variant 1, mRNA /cds=(98,1207) /gb=Nm_001930 /gi=7108341 /ug=Hs.79064 /len=1351	NM_001930; NM_013406; NM_013407	Hs.79064	NP_037539
fcrb2318	NM_002023	fibromodulin (FMOD), mRNA /cds=(21,1151) /gb=Nm_002023 /gi=5016093 /ug=Hs.230 /len=2863	NM_002023	Hs.230	NP_002014
mioa0597	NM_002048	growth arrest-specific 1 (GAS1), mRNA /cds=(411,1448) /gb=Nm_002048 /gi=4503918 /ug=Hs.65029 /len=2828	NM_002048	Hs.65029	NP_002039
fcrb1689	NM_002128	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=Nm_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119

fcrb6464	NM_002135	nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 1, mRNA /cds=(315,2111) /gb=Nm_002135 /gi=27894342 /ug=Hs.1119 /len=2699	NM_002135; NM_173157; NM_173158	Hs.1119	NP_775181
seoa8776	NM_002157	heat shock 10kDa protein 1 (chaperonin 10) (HSP10), mRNA /cds=(42,350) /gb=Nm_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
miod3302	NM_002160	tenascin C (hexabrachion) (TNC), mRNA /cds=(314,6919) /gb=Nm_002160 /gi=4504548 /ug=Hs.289114 /len=7560	NM_002160	Hs.289114	NP_002151
fcr0727	NM_002165	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), mRNA /cds=(36,500) /gb=Nm_002165 /gi=4504568 /ug=Hs.75424 /len=926	NM_002165	Hs.75424	NP_851998
ncrb5595	NM_002318	lysyl oxidase-like 2 (LOXL2), mRNA /cds=(248,2572) /gb=Nm_002318 /gi=4505010 /ug=Hs.83354 /len=3432	NM_002318	Hs.83354	NP_002309
fcr4408	NM_002337	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) (LRPAP1), mRNA /cds=(14,1087) /gb=Nm_002337 /gi=4505020 /ug=Hs.75140 /len=1493	NM_002337	Hs.75140	NP_002328
mioc0760	NM_002355	mannose-6-phosphate receptor (cation dependent) (M6PR), mRNA /cds=(171,1004) /gb=Nm_002355 /gi=10947032 /ug=Hs.134084 /len=2454	NM_002355	Hs.134084	NP_002346
hfcr4462	NM_002388	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA /cds=(45,2471) /gb=Nm_002388 /gi=6631094 /ug=Hs.179565 /len=3061	NM_002388	Hs.179565	NP_002379
fcr6917	NM_002455	metaxin 1 (MTX1), mRNA /cds=(1,954) /gb=Nm_002455 /gi=4505280 /ug=Hs.247551 /len=1065	NM_002455	Hs.247551	NP_002446
seob3670	NM_002488	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa (NDUFA2), mRNA /cds=(57,356) /gb=Nm_002488 /gi=4505354 /ug=Hs.163867 /len=590	NM_002488	Hs.163867	NP_002479
ncr0851	NM_002537	ornithine decarboxylase antizyme 2 (OAZ2), mRNA /gb=Nm_002537 /gi=9845506 /ug=Hs.74563 /len=1906	NM_002537	Hs.74563	NP_002528
seoc1023	NM_002546	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=Nm_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537

miob3315	NM_002634	prohibitin (PHB), mRNA /cds=(74,892) /gb=Nm_002634 /gi=6031190 /ug=Hs.75323 /len=1826	NM_002634	Hs.75323	NP_002625
fcrb2051	NM_002635	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=Nm_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635; NM_005888	Hs.78713	NP_005879
seoa0003	NM_002775	protease, serine, 11 (IGF binding) (PRSS11), mRNA /cds=(49,1491) /gb=Nm_002775 /gi=21327712 /ug=Hs.75111 /len=2039	NM_002775	Hs.75111	NP_002766
mioa3857	NM_002797	proteasome (prosome, macropain) subunit, beta type, 5 (PSMB5), mRNA /cds=(20,811) /gb=Nm_002797 /gi=22538468 /ug=Hs.261927 /len=1050	NM_002797	Hs.261927	NP_002788
miod6835	NM_002802	proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1), mRNA /cds=(49,1371) /gb=Nm_002802 /gi=24430150 /ug=Hs.4745 /len=1586	NM_002802	Hs.4745	NP_002793
seob7465	NM_002819	polypyrimidine tract binding protein 1 (PTBP1), transcript variant 1, mRNA /cds=(89,1762) /gb=Nm_002819 /gi=14165462 /ug=Hs.172550 /len=3322	NM_002819; NM_031990; NM_031991; NM_175847	Hs.172550	NP_787041
ncrc4633	NM_002835	protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(30,2372) /gb=Nm_002835 /gi=18375651 /ug=Hs.62 /len=3161	NM_002835	Hs.62	NP_002826
fcrb0354	NM_002852	pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA /cds=(68,1213) /gb=Nm_002852 /gi=4506332 /ug=Hs.2050 /len=1837	NM_002852	Hs.2050	NP_002843
fcrb2344	NM_002869	RAB6A, member RAS oncogene family (RAB6A), mRNA /cds=(427,1053) /gb=Nm_002869 /gi=19923230 /ug=Hs.5636 /len=3079	NM_002869	Hs.5636	NP_002860
fcrb2756	NM_002904	RD RNA binding protein (RDBP), mRNA /cds=(109,1251) /gb=Nm_002904 /gi=20631983 /ug=Hs.106061 /len=1464	NM_002904	Hs.106061	NP_002895
fcrb9633	NM_002913	replication factor C (activator 1) 1, 145kDa (RFC1), mRNA /cds=(429,3875) /gb=Nm_002913 /gi=15011930 /ug=Hs.166563 /len=5185	NM_002913	Hs.166563	NP_002904

miob3809	NM_002948	ribosomal protein L15 (RPL15), mRNA /cds=(37,651) /gb=Nm_002948 /gi=15431292 /ug=Hs.74267 /len=2018	NM_002948	Hs.74267	NP_002939
fcrb2321	NM_002952	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=Nm_002952 /gi=15055538 /ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943
seoc5858	NM_002964	S100 calcium binding protein A8 (calgranulin A) (S100A8), mRNA /cds=(56,337) /gb=Nm_002964 /gi=21614543 /ug=Hs.416073 /len=428	NM_002964	Hs.416073	NP_002955
fcrb8485	NM_003016	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=Nm_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
hfcr3183	NM_003016	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=Nm_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
fcr7705	NM_003017	splicing factor, arginine/serine-rich 3 (SFRS3), mRNA /cds=(106,600) /gb=Nm_003017 /gi=24025684 /ug=Hs.388623 /len=1403	NM_003017	Hs.388623	NP_003008
fcrb8668	NM_003029	SHC (Src 2 domain containing) transforming protein 1 (SHC1), mRNA /cds=(195,1946) /gb=Nm_003029 /gi=10835030 /ug=Hs.81972 /len=3664	NM_003029	Hs.81972	NP_892113
fcrb6436	NM_003075	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), transcript variant 1, mRNA /cds=(33,3677) /gb=Nm_003075 /gi=21237804 /ug=Hs.236030 /len=4039	NM_003075; NM_139067	Hs.236030	NP_620706
seoa4289	NM_003101	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 (SOAT1), transcript variant 688113, mRNA /cds=(64,1716) /gb=Nm_003101 /gi=24431944 /ug=Hs.14553 /len=3407	NM_003101	Hs.14553	NP_003092
seob2958	NM_003104	sorbitol dehydrogenase (SORD), mRNA /cds=(140,1213) /gb=Nm_003104 /gi=21314633 /ug=Hs.878 /len=2637	NM_003104	Hs.878	NP_003095
seoa7408	NM_003136	signal recognition particle 54kDa (SRP54), mRNA /cds=(225,1739) /gb=Nm_003136 /gi=20149548 /ug=Hs.49346 /len=2164	NM_003136	Hs.49346	NP_003127
ncrb7211	NM_003155	stanniocalcin 1 (STC1), mRNA /cds=(285,1028) /gb=Nm_003155 /gi=4507264 /ug=Hs.25590 /len=3901	NM_003155	Hs.25590	NP_003146



miod3600	NM_003157	NIMA (never in mitosis gene a)-related kinase 4 (NEK4), mRNA /cds=(179,2704) /gb=NM_003157 /gi=4507276 /ug=Hs.1087 /len=3698	NM_003157	Hs.1087	NP_003148
seob4127	NM_003187	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa (TAF9), transcript variant 1, mRNA /cds=(159,953) /gb=NM_003187 /gi=21166375 /ug=Hs.60679 /len=1153	NM_003187; NM_016283	Hs.60679	NP_057367
seoa3296	NM_003239	transforming growth factor, beta 3 (TGFB3), mRNA	NM_003239	Hs.2025	NP_003230
seob4804	NM_003291	tripeptidyl peptidase II (TPP2), mRNA /cds=(24,3773) /gb=NM_003291 /gi=4507656 /ug=Hs.1117 /len=4626	NM_003291	Hs.1117	NP_003282
mioa0059	NM_003297	nuclear receptor subfamily 2, group C, member 1 (NR2C1), mRNA /cds=(57,1868) /gb=NM_003297 /gi=4507672 /ug=Hs.108301 /len=2202	NM_003297	Hs.108301	NP_003288
seob3517	NM_003314	tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407	NM_003314	Hs.7733	NP_003305
miob4803	NM_003316	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(1470,7547) /gb=NM_003316 /gi=21359840 /ug=Hs.118174 /len=9078	NM_003316	Hs.118174	NP_003307
seob6751	NM_003321	Tu translation elongation factor, mitochondrial (TUFM), mRNA /cds=(72,1430) /gb=NM_003321 /gi=21359836 /ug=Hs.12084 /len=1636	NM_003321	Hs.12084	NP_003312
miob2533	NM_003374	voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
seob3197	NM_003374	voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
seob1848	NM_003440	zinc finger protein 140 (clone pHZ-39) (ZNF140), mRNA /cds=(273,1646) /gb=NM_003440 /gi=4507990 /ug=Hs.154205 /len=2407	NM_003440	Hs.154205	NP_003431
fcrb4360	NM_003479	protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925	NM_003479; NM_080391; NM_080392	Hs.82911	NP_536317
mioa0497	NM_003569	syntaxin 7 (STX7), mRNA /cds=(80,865) /gb=NM_003569 /gi=4507294 /ug=Hs.8906 /len=1614	NM_003569	Hs.8906	NP_003560

seoa0792	NM_003676	degenerative spermatocyte lipid desaturase (Drosophila) (DEGS), transcript variant 1, mRNA /cds=(112,1083) /gb=NM_003676 /gi=21614503 /ug=Hs.185973 /len=2058	NM_003676; NM_144780	Hs.185973	NP_659004
fcrb8393	NM_003732	eukaryotic translation initiation factor 4E binding protein 3 (EIF4EBP3), mRNA /cds=(73,375) /gb=NM_003732 /gi=4503536 /ug=Hs.375012 /len=698	NM_003732	Hs.375012	NP_003723
hfcr2850	NM_003769	splicing factor, arginine/serine-rich 9 (SFRS9), mRNA /cds=(53,718) /gb=NM_003769 /gi=4506902 /ug=Hs.77608 /len=1069	NM_003769	Hs.77608	NP_003760
ncr7967	NM_003796	chromosome 19 open reading frame 2 (C19orf2), transcript variant 1, mRNA /cds=(31,1638) /gb=NM_003796 /gi=19924158 /ug=Hs.7943 /len=2295	NM_003796; NM_134447	Hs.7943	NP_604431
ncr1494	NM_003880	WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1, mRNA /cds=(111,1175) /gb=NM_003880 /gi=18491002 /ug=Hs.194678 /len=1307	NM_003880; NM_130396	Hs.194678	NP_569080
mioc6878	NM_003887	development and differentiation enhancing factor 2 (DDEF2), mRNA /cds=(341,3361) /gb=NM_003887 /gi=4502248 /ug=Hs.12802 /len=5711	NM_003887	Hs.12802	NP_003878
fcrb2613	NM_003921	B-cell CLL/lymphoma 10 (BCL10), mRNA /cds=(706,1407) /gb=NM_003921 /gi=20336470 /ug=Hs.193516 /len=2809	NM_003921	Hs.193516	NP_003912
seob2987	NM_003928	CAAX box 1 (CXX1), mRNA /cds=(335,964) /gb=NM_003928 /gi=4503180 /ug=Hs.250708 /len=1209	NM_003928	Hs.250708	NP_003919
seoc6666	NM_003953	myelin protein zero-like 1 (MPZL1), mRNA /cds=(160,969) /gb=NM_003953 /gi=20070164 /ug=Hs.287832 /len=1805	NM_003953	Hs.287832	NP_003944
mioa2213	NM_003973	ribosomal protein L14 (RPL14), mRNA /cds=(38,688) /gb=NM_003973 /gi=16753224 /ug=Hs.235422 /len=843	NM_003973	Hs.235422	NP_003964
mioa1353	NM_003983	solute carrier family 7 (cationic amino acid transporter, y system), member 6 (SLC7A6), mRNA /cds=(262,1809) /gb=NM_003983 /gi=4507052 /ug=Hs.10315 /len=6296	NM_003983	Hs.10315	NP_003974
seoa9377	NM_004036	adenylate cyclase 3 (ADCY3), mRNA /cds=(148,3582) /gb=NM_004036 /gi=10947058 /ug=Hs.8402 /len=4342	NM_004036	Hs.8402	NP_004027
ncrc3415	NM_004075	cryptochrome 1 (photolyase-like) (CRY1), mRNA /cds=(587,2347) /gb=NM_004075 /gi=19923246 /ug=Hs.151573 /len=2999	NM_004075	Hs.151573	NP_004066

miod7011	NM_004083	DNA-damage-inducible transcript 3 (DDIT3), mRNA /cds=(191,700) /gb=Nm_004083 /gi=21361117 /ug=Hs.400353 /len=965	NM_004083	Hs.400353	NP_004074
mioc7152	NM_004120	guanylate binding protein 2, interferon-inducible (GBP2), mRNA /cds=(157,1932) /gb=Nm_004120 /gi=6996011 /ug=Hs.171862 /len=2107	NM_004120	Hs.171862	NP_004111
hfcr2984	NM_004175	small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3), mRNA /cds=(88,468) /gb=Nm_004175 /gi=4759159 /ug=Hs.1575 /len=626	NM_004175	Hs.1575	NP_004166
ncrc4189	NM_004199	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II (P4HA2), mRNA /cds=(188,1795) /gb=Nm_004199 /gi=4758867 /ug=Hs.3622 /len=2194	NM_004199	Hs.3622	NP_004190
seoc7762	NM_004242	high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 1, mRNA /cds=(179,478) /gb=Nm_004242 /gi=23238229 /ug=Hs.77558 /len=935	NM_004242; NM_138730	Hs.77558	NP_620058
hfcr2892	NM_004272	homer 1 (Drosophila) (HOMER1), mRNA /cds=(278,1342) /gb=Nm_004272 /gi=20127465 /ug=Hs.337737 /len=1445	NM_004272	Hs.337737	NP_004263
mioa1410	NM_004290	ring finger protein 14 (RNF14), mRNA /cds=(237,1661) /gb=Nm_004290 /gi=19923285 /ug=Hs.215857 /len=3056	NM_004290	Hs.215857	NP_004281
fcr2089	NM_004404	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=Nm_004404 /gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
miob9393	NM_004404	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=Nm_004404 /gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
fcrb8020	NM_004413	dipeptidase 1 (renal) (DPEP1), mRNA /cds=(296,1531) /gb=Nm_004413 /gi=4758189 /ug=Hs.109 /len=1738	NM_004413	Hs.109	NP_004404
seoa0023	NM_004487	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1), mRNA /cds=(127,9906) /gb=Nm_004487 /gi=4758453 /ug=Hs.7844 /len=10300	NM_004487	Hs.7844	NP_004478

fcrb6220	NM_004555	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), transcript variant 2, mRNA /cds=(211,3417) /gb=Nm_004555 /gi=27886542 /ug=Hs.172674 /len=4005	NM_004555; NM_173163; NM_173164; NM_173165	Hs.172674	NP_775188
ncrc4231	NM_004563	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (PCK2), mRNA /cds=(67,1989) /gb=Nm_004563 /gi=4758885 /ug=Hs.75812 /len=2165	NM_004563	Hs.75812	NP_004554
mioc2872	NM_004577	phosphoserine phosphatase (PSPH), mRNA /cds=(20,697) /gb=Nm_004577 /gi=21614545 /ug=Hs.56407 /len=1432	NM_004577	Hs.56407	NP_004568
fcr1791	NM_004607	tubulin-specific chaperone a (TBCA), mRNA /cds=(50,376) /gb=Nm_004607 /gi=4759211 /ug=Hs.433254 /len=574	NM_004607	Hs.433254	NP_004598
ncr5065	NM_004652	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 1, mRNA /cds=(60,7751) /gb=Nm_004652 /gi=11641424 /ug=Hs.77578 /len=8171	NM_004652; NM_021906	Hs.77578	NP_068706
seob6028	NM_004859	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(173,5200) /gb=Nm_004859 /gi=4758011 /ug=Hs.178710 /len=6111	NM_004859	Hs.178710	NP_004850
mioc7561	NM_004878	prostaglandin E synthase (PTGES), mRNA /cds=(36,494) /gb=Nm_004878 /gi=19923282 /ug=Hs.146688 /len=1846	NM_004878	Hs.146688	NP_004869
seoa7897	NM_004891	mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(60,257) /gb=Nm_004891 /gi=21735607 /ug=Hs.14454 /len=541	NM_004891; NM_145330	Hs.14454	NP_663303
hfc2544	NM_004911	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (ERP70), mRNA /cds=(243,2180) /gb=Nm_004911 /gi=21624646 /ug=Hs.93659 /len=2930	NM_004911	Hs.93659	NP_004902
ncrc8851	NM_004926	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=Nm_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP_004917
ncrc2730	NM_004944	deoxyribonuclease I-like 3 (DNASE1L3), mRNA /cds=(71,988) /gb=Nm_004944 /gi=4826697 /ug=Hs.88646 /len=1079	NM_004944	Hs.88646	NP_004935
seoa4174	NM_004987	LIM and senescent cell antigen-like domains 1 (LIMS1), mRNA	NM_004987	Hs.112378	NP_004978

miod7270	NM_004999	myosin VI (MYO6), mRNA /cds=(140,3997) /gb=Nm_004999 /gi=4826845 /ug=Hs.118483 /len=5212	NM_004999	Hs.118483	NP_004990
ncrc5608	NM_005013	nucleobindin 2 (NUCB2), mRNA /cds=(220,1482) /gb=Nm_005013 /gi=4826869 /ug=Hs.3164 /len=1586	NM_005013	Hs.3164	NP_005004
fcrc1654	NM_005016	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=Nm_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016; NM_031989	Hs.63525	NP_114366
seob0031	NM_005034	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa (POLR2K), mRNA /cds=(67,243) /gb=Nm_005034 /gi=14589955 /ug=Hs.351475 /len=540	NM_005034	Hs.351475	NP_005025
seoa2209	NM_005087	fragile X mental retardation, autosomal 1 (FXR1), mRNA /cds=(13,1878) /gb=Nm_005087 /gi=4826735 /ug=Hs.82712 /len=2132	NM_005087	Hs.82712	NP_005078
seob5147	NM_005146	squamous cell carcinoma antigen recognised by T cells (SART1), mRNA /cds=(43,2445) /gb=Nm_005146 /gi=21327688 /ug=Hs.288319 /len=2536	NM_005146	Hs.288319	NP_005137
seoa1056	NM_005190	cyclin C (CCNC), mRNA /cds=(29,940) /gb=Nm_005190 /gi=7382485 /ug=Hs.118442 /len=1508	NM_005190	Hs.118442	NP_005181
miod1200	NM_005218	defensin, beta 1 (DEFB1), mRNA /cds=(72,278) /gb=Nm_005218 /gi=13124884 /ug=Hs.32949 /len=366	NM_005218	Hs.32949	NP_005209
seoa5743	NM_005218	defensin, beta 1 (DEFB1), mRNA /cds=(72,278) /gb=Nm_005218 /gi=13124884 /ug=Hs.32949 /len=366	NM_005218	Hs.32949	NP_005209
fcrc2306	NM_005259	growth differentiation factor 8 (GDF8), mRNA /cds=(134,1261) /gb=Nm_005259 /gi=4885258 /ug=Hs.41565 /len=2823	NM_005259	Hs.41565	NP_005250
mioc1205	NM_005311	growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=Nm_005311 /gi=19923302 /ug=Hs.81875 /len=5431	NM_005311	Hs.81875	NP_005302
fcrc6650	NM_005348	heat shock 90kDa protein 1, alpha (HSPCA), mRNA /cds=(61,2259) /gb=Nm_005348 /gi=13129149 /ug=Hs.356531 /len=2259	NM_005348	Hs.356531	NP_005339
hfrc6509	NM_005397	podocalyxin-like (PODXL), mRNA /cds=(251,1837) /gb=Nm_005397 /gi=4885556 /ug=Hs.16426 /len=5869	NM_005397	Hs.16426	NP_005388
mioc6261	NM_005478	insulin-like 5 (INSL5), mRNA /cds=(48,455) /gb=Nm_005478 /gi=5729885 /ug=Hs.251380 /len=726	NM_005478	Hs.251380	NP_005469

fcr6551	NM_005606	legumain (LGMN), mRNA /cds=(142,1443) /gb=NM_005606 /gi=21914880 /ug=Hs.18069 /len=1981	NM_005606	Hs.18069	NP_005597
ncrc0292	NM_005687	phenylalanyl-tRNA synthetase beta-subunit (FRSB), mRNA /cds=(14,1783) /gb=NM_005687 /gi=19923332 /ug=Hs.9081 /len=3118	NM_005687	Hs.9081	NP_005678
fcr4738	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6 (ABCB6), nuclear gene encoding mitochondrial protein, mRNA /cds=(278,2806) /gb=NM_005689 /gi=9955962 /ug=Hs.107911 /len=2993	NM_005689	Hs.107911	NP_005680
ncr3434	NM_005699	interleukin 18 binding protein (IL18BP), transcript variant C, mRNA /cds=(929,1522) /gb=NM_005699 /gi=27502394 /ug=Hs.325978 /len=3630	NM_005699; NM_173042; NM_173043; NM_173044	Hs.325978	NP_766632
mioc6902	NM_005745	accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314	NM_005745	Hs.291904	NP_005736
seoa2652	NM_005780	lipoma HMGIC fusion partner (LHFP), mRNA /cds=(357,959) /gb=NM_005780 /gi=5031864 /ug=Hs.93765 /len=2012	NM_005780	Hs.93765	NP_005771
seoa2734	NM_005783	ATP binding protein associated with cell differentiation (APACD), mRNA /cds=(130,810) /gb=NM_005783 /gi=18104958 /ug=Hs.153884 /len=1494	NM_005783	Hs.153884	NP_005774
seoa1460	NM_005843	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 (STAM2), mRNA /cds=(351,1928) /gb=NM_005843 /gi=21265030 /ug=Hs.17200 /len=3928	NM_005843	Hs.17200	NP_005834
fcr0730	NM_005860	folistatin-like 3 (secreted glycoprotein) (FSTL3), mRNA /cds=(8,799) /gb=NM_005860 /gi=5031700 /ug=Hs.433827 /len=2500	NM_005860	Hs.433827	NP_005851
mioc4145	NM_005903	MAD, mothers against decapentaplegic 5 (Drosophila) (MADH5), mRNA /cds=(193,1590) /gb=NM_005903 /gi=20070216 /ug=Hs.37501 /len=2049	NM_005903	Hs.37501	NP_005894
seoc2589	NM_005904	MAD, mothers against decapentaplegic 7 (Drosophila) (MADH7), mRNA /cds=(296,1576) /gb=NM_005904 /gi=5174516 /ug=Hs.100602 /len=3111	NM_005904	Hs.100602	NP_005895
seoa5721	NM_005973	papillary renal cell carcinoma (translocation- associated) (PRCC), mRNA /cds=(219,1694) /gb=NM_005973 /gi=20070217 /ug=Hs.9629 /len=2075	NM_005973	Hs.9629	NP_005964

ncrb8056	NM_006013	ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=Nm_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
seoc2030	NM_006015	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1), transcript variant 1, mRNA /cds=(371,7228) /gb=Nm_006015 /gi=21264564 /ug=Hs.123090 /len=8595	NM_006015; NM_018450; NM_139135	Hs.123090	NP_624361
ncr3843	NM_006094	deleted in liver cancer 1 (DLC1), mRNA /cds=(296,3571) /gb=Nm_006094 /gi=6633799 /ug=Hs.8700 /len=3821	NM_006094	Hs.8700	NP_872584
seob0885	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(96,1049) /gb=Nm_006098 /gi=24475893 /ug=Hs.5662 /len=1093	NM_006098	Hs.5662	NP_006089
fcr3599	NM_006198	Purkinje cell protein 4 (PCP4), mRNA /cds=(59,247) /gb=Nm_006198 /gi=5453857 /ug=Hs.80296 /len=540	NM_006198	Hs.80296	NP_006189
seob3163	NM_006207	platelet-derived growth factor receptor-like (PDGFR), mRNA /cds=(62,1189) /gb=Nm_006207 /gi=5453871 /ug=Hs.170040 /len=1502	NM_006207	Hs.170040	NP_006198
fcr1068	NM_006265	RAD21 (S. pombe) (RAD21), mRNA /cds=(185,2080) /gb=Nm_006265 /gi=5453993 /ug=Hs.81848 /len=3647	NM_006265	Hs.81848	NP_006256
seob3378	NM_006356	ATP synthase, H transporting, mitochondrial F0 complex, subunit d (ATP5H), mRNA /cds=(46,531) /gb=Nm_006356 /gi=5453558 /ug=Hs.49018 /len=628	NM_006356	Hs.49018	NP_006347
seoa0099	NM_006357	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 yeast) (UBE2E3), mRNA /cds=(120,743) /gb=Nm_006357 /gi=5454145 /ug=Hs.4890 /len=1294	NM_006357	Hs.4890	NP_872619
seoa0860	NM_006472	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=Nm_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
fcr7102	NM_006472	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=Nm_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
miod4686	NM_006472	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=Nm_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
seob8204	NM_006475	osteoblast specific factor 2 (fascin I-like) (OSF-2), mRNA /cds=(12,2522) /gb=Nm_006475 /gi=5453833 /ug=Hs.136348 /len=3213	NM_006475	Hs.136348	NP_006466

fcrb2306	NM_006533	melanoma inhibitory activity (MIA), mRNA /cds=(72,467) /gb=Nm_006533 /gi=5729924 /ug=Hs.279651 /len=538	NM_006533	Hs.279651	NP_006524
hfc0618	NM_006571	likely ortholog of mouse dynactin 6 (DCTN6), mRNA /cds=(88,660) /gb=Nm_006571 /gi=18426895 /ug=Hs.39913 /len=1044	NM_006571	Hs.39913	NP_006562
mioa9179	NM_006585	chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA /cds=(29,1675) /gb=Nm_006585 /gi=6005726 /ug=Hs.15071 /len=1821	NM_006585	Hs.15071	NP_006576
fcrb3001	NM_006603	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=Nm_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
fcr2182	NM_006659	tubulin, gamma complex associated protein 2 (TUBGCP2), mRNA /cds=(64,2772) /gb=Nm_006659 /gi=5729839 /ug=Hs.13386 /len=2846	NM_006659	Hs.13386	NP_006650
mioa1603	NM_006701	similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=Nm_006701 /gi=20070233 /ug=Hs.433683 /len=1415	NM_006701	Hs.433683	NP_006692
ncr7952	NM_006734	immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=Nm_006734 /gi=19923373 /ug=Hs.75063 /len=9175	NM_006734	Hs.75063	NP_006725
miob3456	NM_006748	Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=Nm_006748 /gi=5803170 /ug=Hs.75367 /len=2665	NM_006748	Hs.75367	NP_006739
ncrc2839	NM_006793	peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=Nm_006793 /gi=5802973 /ug=Hs.75454 /len=1542	NM_006793	Hs.75454	NP_054817
seob9145	NM_006813	proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=Nm_006813 /gi=5802981 /ug=Hs.75969 /len=2061	NM_006813	Hs.75969	NP_006804
mioa7239	NM_006815	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=Nm_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
ncrc6981	NM_006815	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=Nm_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
seob6279	NM_006818	ALL1-fused gene from chromosome 1q (AF1Q), mRNA /cds=(353,625) /gb=Nm_006818 /gi=21626459 /ug=Hs.75823 /len=1653	NM_006818	Hs.75823	NP_006809



hfc0594	NM_006839	inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA /cds=(93,2369) /gb=NM_006839 /gi=5803114 /ug=Hs.78504 /len=2697	NM_006839	Hs.78504	NP_006830
mioc5772	NM_006873	stoned B-like factor (SBLF), mRNA /cds=(11,2218) /gb=NM_006873 /gi=26787992 /ug=Hs.54961 /len=5822	NM_006873	Hs.54961	NP_006864
ncrb6357	NM_006885	AT-binding transcription factor 1 (ATBF1), mRNA /cds=(674,11785) /gb=NM_006885 /gi=19923286 /ug=Hs.101842 /len=11893	NM_006885	Hs.101842	NP_008816
seob0133	NM_006886	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
seob1423	NM_006924	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA /cds=(36,782) /gb=NM_006924 /gi=19923382 /ug=Hs.73737 /len=2708	NM_006924	Hs.73737	NP_008855
seob0221	NM_006936	SMT3 suppressor of mif two 3 1 (yeast) (SMT3H1), mRNA /cds=(95,406) /gb=NM_006936 /gi=5902095 /ug=Hs.85119 /len=1733	NM_006936	Hs.85119	NP_008867
fcr7338	NM_006979	HLA class II region expressed gene KE4 (HKE4), mRNA /cds=(327,1616) /gb=NM_006979 /gi=5901935 /ug=Hs.278721 /len=2358	NM_006979	Hs.278721	NP_008910
fcrb2040	NM_006986	melanoma antigen, family D, 1 (MAGED1), mRNA /cds=(143,2479) /gb=NM_006986 /gi=14195633 /ug=Hs.5258 /len=2713	NM_006986	Hs.5258	NP_008917
fcrb3895	NM_007002	adhesion regulating molecule 1 (ADRM1), transcript variant 1, mRNA /cds=(81,1304) /gb=NM_007002 /gi=28373191 /ug=Hs.90107 /len=1410	NM_007002; NM_175573	Hs.90107	NP_783163
ncr0238	NM_007021	decidual protein induced by progesterone (DEPP), mRNA /cds=(219,857) /gb=NM_007021 /gi=5901937 /ug=Hs.93675 /len=2114	NM_007021	Hs.93675	NP_008952
miob8630	NM_007032	Tara-like protein (HRIHFB2122), transcript variant 1, mRNA /cds=(176,1957) /gb=NM_007032 /gi=20336765 /ug=Hs.40342 /len=2687	NM_007032; NM_138632	Hs.40342	NP_619538
fcrb1428	NM_007063	vascular Rab-GAP/TBC-containing (VRP), mRNA /cds=(1118,3811) /gb=NM_007063 /gi=5902153 /ug=Hs.164170 /len=4404	NM_007063	Hs.164170	NP_008994
fcr4695	NM_007104	ribosomal protein L10a (RPL10A), mRNA	NM_007104	Hs.425293	NP_009035

ncr8867	NM_007108	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B) (TCEB2), mRNA /cds=(1,357) /gb=NM_007108 /gi=6005889 /ug=Hs.172772 /len=357	NM_007108	Hs.172772	NP_009039
seoa6038	NM_007145	zinc finger protein 146 (ZNF146), mRNA /cds=(857,1735) /gb=NM_007145 /gi=6005965 /ug=Hs.301819 /len=3186	NM_007145	Hs.301819	NP_009076
mioc6898	NM_007194	CHK2 checkpoint (S. pombe) (CHEK2), transcript variant 1, mRNA /cds=(762,2393) /gb=NM_007194 /gi=22209010 /ug=Hs.146329 /len=2547	NM_007194; NM_145862	Hs.146329	NP_665861
fcrb3515	NM_007245	ataxin 2 related protein (A2LP), transcript variant A, mRNA /cds=(169,3396) /gb=NM_007245 /gi=27262646 /ug=Hs.43509 /len=4386	NM_007245; NM_017492; NM_145714; NM_148414; NM_148415; NM_148416	Hs.43509	NP_680782
miob7276	NM_007247	AP1 gamma subunit binding protein 1 (AP1GBP1), transcript variant 1, mRNA /cds=(44,2113) /gb=NM_007247 /gi=18105003 /ug=Hs.15384 /len=5115	NM_007247; NM_080550; NM_080551	Hs.15384	NP_542118
fcr3163	NM_007250	Kruppel-like factor 8 (KLF8), mRNA /cds=(439,1518) /gb=NM_007250 /gi=28376642 /ug=Hs.320861 /len=2208	NM_007250	Hs.320861	NP_009181
mioa4532	NM_007332	ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA /cds=(175,3534) /gb=NM_007332 /gi=6601589 /ug=Hs.137674 /len=5190	NM_007332	Hs.137674	NP_015628
fcrb5948	NM_007370	replication factor C (activator 1) 5, 36.5kDa (RFC5), mRNA /cds=(102,1124) /gb=NM_007370 /gi=19923788 /ug=Hs.171075 /len=2097	NM_007370	Hs.171075	NP_853556
seob3191	NM_012090	microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA /cds=(52,16344) /gb=NM_012090 /gi=15011903 /ug=Hs.108258 /len=17532	NM_012090; NM_033024; NM_033044	Hs.108258	NP_149033
ncrb5704	NM_012115	CASP8 associated protein 2 (CASP8AP2), mRNA /cds=(197,6145) /gb=NM_012115 /gi=16306505 /ug=Hs.122843 /len=6782	NM_012115	Hs.122843	NP_036247

fcrb7785	NM_012154	eukaryotic translation initiation factor 2C, 2 (EIF2C2), mRNA /cds=(111,1868) /gb=Nm_012154 /gi=24307940 /ug=Hs.193053 /len=2815	NM_012154	Hs.193053	NP_036286
ncrc0457	NM_012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=Nm_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333
mioc7662	NM_012218	interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 1, mRNA /cds=(267,2951) /gb=Nm_012218 /gi=24234749 /ug=Hs.256583 /len=6058	NM_004516; NM_012218; NM_153464	Hs.256583	NP_703194
fcr5211	NM_012286	mortality factor 4 like 2 (MORF4L2), mRNA /cds=(306,1172) /gb=Nm_012286 /gi=6912447 /ug=Hs.173714 /len=1826	NM_012286	Hs.173714	NP_036418
seob1001	NM_012334	myosin X (MYO10), mRNA /cds=(223,6399) /gb=Nm_012334 /gi=11037056 /ug=Hs.61638 /len=7787	NM_012334	Hs.61638	NP_036466
fcrb8239	NM_012369	olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA /cds=(1,954) /gb=Nm_012369 /gi=6912557 /ug=Hs.159898 /len=954	NM_012369	Hs.159898	NP_036501
ncrb7844	NM_012421	rearranged L-myc fusion sequence (RLF), mRNA /cds=(13,5757) /gb=Nm_012421 /gi=6912631 /ug=Hs.13321 /len=6229	NM_012421	Hs.13321	NP_036553
ncr3815	NM_012423	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=Nm_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
fcr5604	NM_012423	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=Nm_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
fcrb4470	NM_012423	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=Nm_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
seoa4571	NM_013252	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(198,764) /gb=Nm_013252 /gi=10281668 /ug=Hs.126355 /len=3510	NM_013252	Hs.126355	NP_037384
mioa8261	NM_013263	bromodomain containing 7 (BRD7), mRNA /cds=(6,1964) /gb=Nm_013263 /gi=7019344 /ug=Hs.279762 /len=2137	NM_013263	Hs.279762	NP_037395
fcr4067	NM_013265	chromosome 11 open reading frame2 (C11orf2), mRNA	NM_013265	Hs.5258	NP_037397
fcrb1969	NM_013292	myosin light chain 2 (HUMMLC2B), mRNA /cds=(60,569) /gb=Nm_013292 /gi=28372498 /ug=Hs.50889 /len=687	NM_013292	Hs.50889	NP_037424

seob0976	NM_013293	transformer-2 alpha (htra-2 alpha) (HSU53209), mRNA /cds=(158,1006) /gb=Nm_013293 /gi=9558732 /ug=Hs.130829 /len=1563	NM_013293	Hs.130829	NP_037425
seob5213	NM_013338	Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=Nm_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
fcrc4151	NM_013403	striatin, calmodulin binding protein 4 (STRN4), mRNA /cds=(1,2262) /gb=Nm_013403 /gi=7019572 /ug=Hs.108665 /len=3188	NM_013403	Hs.108665	NP_037535
fcrb8697	NM_013417	isoleucine-tRNA synthetase (IARS), transcript variant long, mRNA /cds=(256,4044) /gb=Nm_013417 /gi=7770071 /ug=Hs.172801 /len=4508	NM_002161; NM_013417	Hs.172801	NP_038203
seob9485	NM_014016	SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA /cds=(70,1833) /gb=Nm_014016 /gi=7662337 /ug=Hs.5867 /len=3572	NM_014016	Hs.5867	NP_054735
miob8425	NM_014018	mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, mRNA /cds=(24,587) /gb=Nm_014018 /gi=16579882 /ug=Hs.55097 /len=724	NM_014018	Hs.55097	NP_054737
seoc3469	NM_014034	anti-silencing function 1A (DKFZP547E2110), mRNA /cds=(193,807) /gb=Nm_014034 /gi=7661591 /ug=Hs.108110 /len=2367	NM_014034	Hs.108110	NP_054753
ncrc6047	NM_014056	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=Nm_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
miob9671	NM_014129	PRO0478 protein (PRO0478), mRNA	NM_014129	Hs.279558	NP_054848
miod4063	NM_014145	chromosome 20 open reading frame 30 (C20orf30), mRNA /cds=(114,476) /gb=Nm_014145 /gi=15559214 /ug=Hs.3576 /len=1440	NM_014145	Hs.3576	NP_054864
ncrb3317	NM_014166	HSPC126 protein (HSPC126), mRNA /cds=(26,838) /gb=Nm_014166 /gi=7661787 /ug=Hs.181112 /len=1424	NM_014166	Hs.181112	NP_054885
fc2102	NM_014300	signal peptidase complex (18kD) (SPC18), mRNA /cds=(78,617) /gb=Nm_014300 /gi=7657608 /ug=Hs.9534 /len=1105	NM_014300	Hs.9534	NP_055115
mioa3888	NM_014305	dTDP-D-glucose 4,6-dehydratase (TDPGD), mRNA /cds=(94,1146) /gb=Nm_014305 /gi=7657640 /ug=Hs.12393 /len=1889	NM_014305	Hs.12393	NP_055120

seoa0486	NM_014313	small membrane protein 1 (SMP1), mRNA /cds=(151,624) /gb=NM_014313 /gi=20357549 /ug=Hs.107979 /len=2284	NM_014313	Hs.107979	NP_055128
mioa2343	NM_014342	mitochondrial carrier 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(49,960) /gb=NM_014342 /gi=7657346 /ug=Hs.279609 /len=1104	NM_014342	Hs.279609	NP_055157
fcr5895	NM_014362	3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA /cds=(64,1209) /gb=NM_014362 /gi=7657159 /ug=Hs.236642 /len=1311	NM_014362	Hs.236642	NP_055177
seoc2595	NM_014386	polycystic kidney disease 2-like 2 (PKD2L2), mRNA /cds=(24,1853) /gb=NM_014386 /gi=7657458 /ug=Hs.272418 /len=2205	NM_014386	Hs.272418	NP_055201
miob4760	NM_014412	Siah-interacting protein (SIP), mRNA /cds=(118,804) /gb=NM_014412 /gi=7656951 /ug=Hs.27258 /len=2435	NM_014412	Hs.27258	NP_055227
ncr3284	NM_014454	p53 regulated PA26 nuclear protein (PA26), mRNA /cds=(12,1667) /gb=NM_014454 /gi=7657436 /ug=Hs.14125 /len=2785	NM_014454	Hs.14125	NP_055269
miod1613	NM_014462	Lsm1 protein (LSM1), mRNA /cds=(189,590) /gb=NM_014462 /gi=7657312 /ug=Hs.425311 /len=935	NM_014462	Hs.425311	NP_055277
fcrb3135	NM_014473	putative dimethyladenosine transferase (HSA9761), mRNA /cds=(79,1020) /gb=NM_014473 /gi=7657197 /ug=Hs.125819 /len=1505	NM_014473	Hs.125819	NP_055288
miod4895	NM_014584	ERO1-like (S. cerevisiae) (ERO1L), mRNA /cds=(227,1633) /gb=NM_014584 /gi=7657068 /ug=Hs.25740 /len=3334	NM_014584	Hs.25740	NP_055399
seob3322	NM_014585	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=NM_014585 /gi=19923794 /ug=Hs.5944 /len=3333	NM_014585	Hs.5944	NP_055400
miob1126	NM_014629	Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA /cds=(3732,7097) /gb=NM_014629 /gi=7662041 /ug=Hs.20695 /len=8467	NM_014629	Hs.20695	NP_055444
ncr1550	NM_014672	KIAA0391 gene product (KIAA0391), mRNA /cds=(360,2063) /gb=NM_014672 /gi=7662093 /ug=Hs.154668 /len=5677	NM_014672	Hs.154668	NP_055487
ncr4590	NM_014733	endosome-associated FYVE-domain protein (ENDOFIN), mRNA /cds=(249,4868) /gb=NM_014733 /gi=7662047 /ug=Hs.83790 /len=6632	NM_014733	Hs.83790	NP_055548

mioa3367	NM_014751	KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645	NM_014751	Hs.77694	NP_055566
seoa1992	NM_014814	KIAA0107 gene product (P44S10), mRNA /cds=(26,1195) /gb=NM_014814 /gi=7661913 /ug=Hs.23488 /len=1308	NM_014814	Hs.23488	NP_055629
seob2994	NM_014819	KIAA0438 gene product (KIAA0438), mRNA /cds=(118,2244) /gb=NM_014819 /gi=7662123 /ug=Hs.279849 /len=4765	NM_014819	Hs.279849	NP_055634
seoa0029	NM_014888	family with sequence similarity 3, member C (FAM3C), mRNA /cds=(168,851) /gb=NM_014888 /gi=7661713 /ug=Hs.29882 /len=2475	NM_014888	Hs.29882	NP_055703
seoc0034	NM_014899	Rho-related BTB domain containing 3 (RHOBTB3), mRNA /cds=(336,2171) /gb=NM_014899 /gi=7662355 /ug=Hs.10432 /len=4099	NM_014899	Hs.10432	NP_055714
mioa2073	NM_014915	KIAA1074 protein (KIAA1074), mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218	NP_055730
seoa9160	NM_015049	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA /cds=(382,3126) /gb=NM_015049 /gi=13027379 /ug=Hs.154248 /len=6470	NM_015049	Hs.154248	NP_055864
hfcr3011	NM_015079	KIAA1055 protein (KIAA1055), mRNA /cds=(428,1675) /gb=NM_015079 /gi=24307996 /ug=Hs.126084 /len=4863	NM_015079	Hs.126084	NP_055894
mioc6055	NM_015149	RalGDS-like gene (RGL), mRNA /cds=(450,2861) /gb=NM_015149 /gi=20127535 /ug=Hs.79219 /len=5111	NM_015149	Hs.79219	NP_055964
ncr7292	NM_015208	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023
seoa4647	NM_015216	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
mioa6442	NM_015254	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
mioc2928	NM_015254	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
mioc4232	NM_015271	tripartite motif-containing 2 (TRIM2), mRNA /cds=(147,2381) /gb=NM_015271 /gi=15011942 /ug=Hs.12372 /len=6734	NM_015271	Hs.12372	NP_056086
fcrb6160	NM_015278	KIAA0790 protein (KIAA0790), mRNA /cds=(10,3204) /gb=NM_015278 /gi=24308024 /ug=Hs.12002 /len=3711	NM_015278	Hs.12002	NP_056093

fcrb8257	NM_015319	tensin like C1 domain-containing phosphatase (TENC1), transcript variant 2, mRNA /cds=(196,4455) /gb=Nm_015319 /gi=23943863 /ug=Hs.6147 /len=4944	NM_015319; NM_170754	Hs.6147	NP_736610
fcrb5720	NM_015385	sorbin and SH3 domain containing 1 (SORBS1), mRNA /cds=(191,2641) /gb=Nm_015385 /gi=7661699 /ug=Hs.108924 /len=5943	NM_006434; NM_015385	Hs.108924	NP_056200
seoc2518	NM_015397	KIAA1892 protein (KIAA1892), mRNA /cds=(308,1669) /gb=Nm_015397 /gi=22218618 /ug=Hs.102669 /len=3636	NM_015397	Hs.102669	NP_056212
mioc5546	NM_015434	DKFZP434B168 protein (DKFZP434B168), mRNA /cds=(106,2994) /gb=Nm_015434 /gi=7661565 /ug=Hs.48604 /len=3463	NM_015434	Hs.48604	NP_056249
seoc1425	NM_015440	DKFZP586G1517 protein (DKFZP586G1517), mRNA /cds=(127,2328) /gb=Nm_015440 /gi=24308062 /ug=Hs.44155 /len=2749	NM_015440	Hs.44155	NP_056255
seoc1876	NM_015461	early hematopoietic zinc finger (EHZF), mRNA /cds=(150,4085) /gb=Nm_015461 /gi=24308068 /ug=Hs.26799 /len=4869	NM_015461	Hs.26799	NP_056276
fcrb1962	NM_015466	protein tyrosine phosphatase, non-receptor type 23 (PTPN23), mRNA /cds=(62,4972) /gb=Nm_015466 /gi=24308072 /ug=Hs.25524 /len=5248	NM_015466	Hs.25524	NP_056281
fcrb8674	NM_015466	protein tyrosine phosphatase, non-receptor type 23 (PTPN23), mRNA /cds=(62,4972) /gb=Nm_015466 /gi=24308072 /ug=Hs.25524 /len=5248	NM_015466	Hs.25524	NP_056281
fcrb2697	NM_015497	DKFZP564G2022 protein (DKFZP564G2022), mRNA /cds=(43,1710) /gb=Nm_015497 /gi=13794264 /ug=Hs.16492 /len=2286	NM_015497	Hs.16492	NP_056312
fcr5679	NM_015559	SET binding protein 1 (SETBP1), mRNA /cds=(6,4634) /gb=Nm_015559 /gi=7662121 /ug=Hs.151717 /len=5744	NM_015559	Hs.151717	NP_056374
ncrc4815	NM_015642	zinc finger protein 288 (ZNF288), mRNA /cds=(489,2495) /gb=Nm_015642 /gi=7661651 /ug=Hs.159456 /len=2829	NM_015642	Hs.159456	NP_056457
seoa8754	NM_015710	glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA /cds=(53,1489) /gb=Nm_015710 /gi=21359905 /ug=Hs.421907 /len=1610	NM_015710	Hs.421907	NP_056525
mioc2019	NM_015710	glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA /cds=(53,1489) /gb=Nm_015710 /gi=21359905 /ug=Hs.421907 /len=1610	NM_015710	Hs.421907	NP_056525

miob5491	NM_015938	CGI-07 protein (CGI-07), mRNA /cds=(124,1635) /gb=Nm_015938 /gi=19923795 /ug=Hs.181022 /len=2762	NM_015938	Hs.181022	NP_057022
hfcr0370	NM_015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=Nm_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
miod3946	NM_015969	mitochondrial ribosomal protein S17 (MRPS17), nuclear gene encoding mitochondrial protein, mRNA /cds=(31,423) /gb=Nm_015969 /gi=16554613 /ug=Hs.44298 /len=600	NM_015969	Hs.44298	NP_057053
ncrb8649	NM_016060	CGI-125 protein (CGI-125), mRNA /cds=(79,474) /gb=Nm_016060 /gi=7705591 /ug=Hs.27289 /len=1196	NM_016060	Hs.27289	NP_057144
seoa3392	NM_016081	palladin (KIAA0992), mRNA /cds=(212,3532) /gb=Nm_016081 /gi=21361584 /ug=Hs.194431 /len=5773	NM_016081	Hs.194431	NP_057165
mioc4331	NM_016105	FK506 binding protein 7 (FKBP7), mRNA /cds=(96,875) /gb=Nm_016105 /gi=23618828 /ug=Hs.344379 /len=1067	NM_016105	Hs.344379	NP_851939
ncr9487	NM_016125	PTD016 protein (LOC51136), mRNA /cds=(183,809) /gb=Nm_016125 /gi=21361528 /ug=Hs.30154 /len=1917	NM_016125	Hs.30154	NP_057209
hfcr6265	NM_016162	inhibitor of growth family, member 4 (ING4), mRNA /cds=(18,767) /gb=Nm_016162 /gi=7705860 /ug=Hs.108183 /len=1377	NM_016162	Hs.108183	NP_057246
seob0321	NM_016167	retinoic acid repressible protein (RARG-1), mRNA /cds=(33,806) /gb=Nm_016167 /gi=15743546 /ug=Hs.106346 /len=896	NM_016167	Hs.106346	NP_057251
ncrc0185	NM_016245	retinal short-chain dehydrogenase/reductase 2 (RetSDR2), mRNA /cds=(189,1091) /gb=Nm_016245 /gi=7705904 /ug=Hs.12150 /len=1760	NM_016245	Hs.12150	NP_057329
ncrb5940	NM_016252	baculoviral IAP repeat-containing 6 (apollon) (BIRC6), mRNA /cds=(1,14490) /gb=Nm_016252 /gi=10442821 /ug=Hs.250646 /len=14490	NM_016252	Hs.250646	NP_057336
mioc6391	NM_016271	STRIN protein (STRIN), mRNA /cds=(100,837) /gb=Nm_016271 /gi=21361538 /ug=Hs.180403 /len=3226	NM_016271	Hs.180403	NP_057355
mioc4842	NM_016277	RAB23, member RAS oncogene family (RAB23), mRNA /cds=(151,864) /gb=Nm_016277 /gi=19923480 /ug=Hs.94769 /len=2588	NM_016277	Hs.94769	NP_057361
ncrc4132	NM_016315	CED-6 protein (CED-6), mRNA /cds=(429,1343) /gb=Nm_016315 /gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056	NP_057399



mioc8694	NM_016316	REV1-like (yeast) (REV1L), mRNA /cds=(213,3968) /gb=Nm_016316 /gi=7706680 /ug=Hs.110347 /len=4276	NM_016316	Hs.110347	NP_057400
fcrc6174	NM_016397	TH1-like (Drosophila) (TH1L), mRNA /cds=(8,1429) /gb=Nm_016397 /gi=7705462 /ug=Hs.5184 /len=2130	NM_016397	Hs.5184	NP_057481
seoa4163	NM_016399	hypothetical protein HSPC132 (HSPC132), mRNA /cds=(4,234) /gb=Nm_016399 /gi=7705466 /ug=Hs.69499 /len=1171	NM_016399	Hs.69499	NP_057483
mioc2116	NM_016400	Huntingtin interacting protein K (HYPK), mRNA /cds=(177,566) /gb=Nm_016400 /gi=21361540 /ug=Hs.300954 /len=1349	NM_016400	Hs.300954	NP_057484
ncrb3226	NM_016468	chromosome 14 open reading frame 112 (C14orf112), mRNA /cds=(119,439) /gb=Nm_016468 /gi=21361531 /ug=Hs.433630 /len=933	NM_016468	Hs.433630	NP_057552
seob5886	NM_016530	RAB-8b protein (LOC51762), mRNA /cds=(92,715) /gb=Nm_016530 /gi=7706562 /ug=Hs.321245 /len=1265	NM_016530	Hs.321245	NP_057614
ncrb0074	NM_016547	calcium binding protein Cab45 precursor (Cab45), mRNA /cds=(294,1340) /gb=Nm_016547 /gi=7706572 /ug=Hs.42806 /len=2092	NM_016176; NM_016547	Hs.42806	NP_057631
miod6292	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=Nm_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
seoc7811	NM_016623	hypothetical protein BM-009 (BM-009), mRNA /cds=(386,1048) /gb=Nm_016623 /gi=7705303 /ug=Hs.92918 /len=1919	NM_016623	Hs.92918	NP_057707
seob5193	NM_016645	mesenchymal stem cell protein DSC92 (NEUGRIN), mRNA /cds=(632,1291) /gb=Nm_016645 /gi=7706195 /ug=Hs.323467 /len=1729	NM_016645	Hs.323467	NP_057729
hfcr2693	NM_016733	LIM domain kinase 2 (LIMK2), transcript variant 2b, mRNA /cds=(316,2169) /gb=Nm_016733 /gi=8051617 /ug=Hs.278027 /len=3806	NM_005569; NM_016733	Hs.278027	NP_057952
seob1783	NM_017423	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA /cds=(33,2006) /gb=Nm_017423 /gi=8393408 /ug=Hs.246315 /len=4266	NM_017423	Hs.246315	NP_059119
seoc1009	NM_017664	ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=Nm_017664 /gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134

mioc6251	NM_017845	hypothetical protein FLJ20502 (FLJ20502), mRNA /cds=(29,580) /gb=Nm_017845 /gi=8923457 /ug=Hs.23956 /len=1373	NM_017845	Hs.23956	NP_060315
miod0080	NM_017850	hypothetical protein FLJ20508 (FLJ20508), mRNA /cds=(191,802) /gb=Nm_017850 /gi=8923468 /ug=Hs.272673 /len=2376	NM_017850	Hs.272673	NP_060320
ncrc0304	NM_017869	BTG3 associated nuclear protein (BANP), transcript variant 1, mRNA /cds=(153,1562) /gb=Nm_017869 /gi=17986265 /ug=Hs.352397 /len=2136	NM_017869; NM_079837	Hs.352397	NP_524576
ncrc0324	NM_017903	hypothetical protein FLJ20618 (FLJ20618), mRNA /cds=(319,726) /gb=Nm_017903 /gi=8923570 /ug=Hs.52184 /len=2213	NM_017903	Hs.52184	NP_060373
fcrc6010	NM_017931	hypothetical protein FLJ20699 (FLJ20699), mRNA /cds=(33,1043) /gb=Nm_017931 /gi=8923627 /ug=Hs.15125 /len=2594	NM_017931	Hs.15125	NP_060401
miod4507	NM_017953	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=Nm_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
ncrc9187	NM_018004	hypothetical protein FLJ10134 (FLJ10134), mRNA /cds=(314,1141) /gb=Nm_018004 /gi=8922242 /ug=Hs.104800 /len=1564	NM_018004	Hs.104800	NP_060474
mioc4077	NM_018013	hypothetical protein FLJ10159 (FLJ10159), mRNA /cds=(1,807) /gb=Nm_018013 /gi=8922262 /ug=Hs.22505 /len=2070	NM_018013	Hs.22505	NP_060483
fcrc3808	NM_018090	hypothetical protein FLJ10420 (FLJ10420), mRNA /cds=(34,825) /gb=Nm_018090 /gi=20127581 /ug=Hs.289087 /len=2046	NM_018090	Hs.289087	NP_060560
ncr1221	NM_018121	chromosome 10 open reading frame 6 (C10orf6), mRNA /cds=(543,4064) /gb=Nm_018121 /gi=27532981 /ug=Hs.93581 /len=7284	NM_018121; NM_144592	Hs.93581	NP_653193
mioc2459	NM_018149	hypothetical protein FLJ10587 (FLJ10587), mRNA /cds=(16,2991) /gb=Nm_018149 /gi=21361713 /ug=Hs.7296 /len=3256	NM_018149	Hs.7296	NP_060619
miod4066	NM_018247	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=Nm_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
seob4676	NM_018845	stromal cell protein (LOC55974), mRNA /cds=(61,726) /gb=Nm_018845 /gi=10047123 /ug=Hs.292154 /len=1316	NM_018845	Hs.292154	NP_061333
mioa8919	NM_018947	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=Nm_018947 /gi=21361707 /ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820
ncr9956	NM_018997	mitochondrial ribosomal protein S21 (MRPS21), transcript variant 2, nuclear gene encoding mitochondrial protein, mRNA /cds=(519,782) /gb=Nm_018997 /gi=16950592 /ug=Hs.81281 /len=939	NM_018997; NM_031901	Hs.81281	NP_114107

miob0171	NM_019014	similar to DNA-directed RNA polymerase I (135 kDa) (Rpo1-2), mRNA /cds=(53,1063) /gb=Nm_019014 /gi=9506618 /ug=Hs.86337 /len=4684	NM_019014; NM_032212	Hs.86337	NP_061887
mioc4112	NM_019026	putative membrane protein (LOC54499), mRNA /cds=(139,705) /gb=Nm_019026 /gi=24308132 /ug=Hs.93832 /len=1186	NM_019026	Hs.93832	NP_061899
fcrc5164	NM_019035	protocadherin 18 (PCDH18), mRNA /cds=(388,3795) /gb=Nm_019035 /gi=14589928 /ug=Hs.97266 /len=5157	NM_019035	Hs.97266	NP_061908
miob5012	NM_019842	potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA /cds=(84,2882) /gb=Nm_019842 /gi=28373064 /ug=Hs.283644 /len=3325	NM_019842	Hs.283644	NP_062816
seob4002	NM_020159	likely ortholog of mouse enhancer trap locus 1 (ETL1), mRNA /cds=(79,3159) /gb=Nm_020159 /gi=14149729 /ug=Hs.21356 /len=4935	NM_020159	Hs.21356	NP_064544
ncr4332	NM_020186	DC11 protein (DC11), mRNA /cds=(21,398) /gb=Nm_020186 /gi=9910179 /ug=Hs.42785 /len=957	NM_020186	Hs.42785	NP_064571
ncr1545	NM_020313	hypothetical protein LOC57019 (LOC57019), mRNA /gb=Nm_020313 /gi=10092672 /ug=Hs.4900 /len=2105	NM_020313	Hs.4900	NP_064709
seob4539	NM_020365	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa (EIF2B3), mRNA /cds=(103,1461) /gb=Nm_020365 /gi=9966778 /ug=Hs.283627 /len=1602	NM_020365	Hs.283627	NP_065098
seob6853	NM_020414	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=Nm_020414 /gi=14251213 /ug=Hs.155986 /len=2967	NM_020414	Hs.155986	NP_065147
seob9406	NM_020432	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=Nm_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
fcrc5389	NM_020532	reticulon 4 (RTN4), mRNA /cds=(245,3823) /gb=Nm_020532 /gi=24638438 /ug=Hs.65450 /len=4166	NM_007008; NM_020532; NM_153828	Hs.65450	NP_722550
ncrc6756	NM_020548	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=Nm_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438

seob8031	NM_020548	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=Nm_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438
ncr9572	NM_020674	cytochrome P450 monooxygenase (CYP-M), mRNA /cds=(88,1395) /gb=Nm_020674 /gi=10257438 /ug=Hs.352566 /len=1755	NM_020674; NM_177538	Hs.352566	NP_803882
miob3986	NM_020749	AT2 receptor-interacting protein 1 (ATIP1), mRNA /cds=(1,1311) /gb=Nm_020749 /gi=21361871 /ug=Hs.7946 /len=3455	NM_020749	Hs.7946	NP_065800
ncr4020	NM_020824	Rho-GTPase activating protein 10 (ARHGAP10), mRNA /cds=(438,6311) /gb=Nm_020824 /gi=20977540 /ug=Hs.11611 /len=7130	NM_020824	Hs.11611	NP_065875
fcrb8855	NM_020839	WD repeat endosomal protein (KIAA1449), mRNA /cds=(11,2044) /gb=Nm_020839 /gi=21314694 /ug=Hs.109778 /len=3705	NM_020839	Hs.109778	NP_065890
ncrb8319	NM_021005	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(343,1587) /gb=Nm_021005 /gi=14149745 /ug=Hs.347991 /len=1740	NM_021005	Hs.347991	NP_066285
ncrc1999	NM_021034	interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=Nm_021034 /gi=11995467 /ug=Hs.381234 /len=808	NM_021034	Hs.381234	NP_066362
mioc5603	NM_021122	fatty-acid-Coenzyme A ligase, long-chain 2 (FACL2), mRNA /cds=(14,2110) /gb=Nm_021122 /gi=12669906 /ug=Hs.154890 /len=3635	NM_021122	Hs.154890	NP_066945
seob0046	NM_021145	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=Nm_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968
fcrb1580	NM_021145	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=Nm_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968
ncrc5760	NM_021222	TcD37 (HTCD37), mRNA /cds=(137,1498) /gb=Nm_021222 /gi=24308262 /ug=Hs.78524 /len=2995	NM_021222	Hs.78524	NP_067045
ncrc3161	NM_021626	likely of rat and mouse retinoid-inducible serine carboxypeptidase (RISC), mRNA /cds=(33,1391) /gb=Nm_021626 /gi=11055991 /ug=Hs.106747 /len=1921	NM_021626	Hs.106747	NP_067639
mioc0690	NM_021639	hypothetical protein SP192 (SP192), mRNA /cds=(445,1869) /gb=Nm_021639 /gi=21314695 /ug=Hs.169854 /len=2728	NM_021639	Hs.169854	NP_067652

miob8146	NM_021818	WW45 protein (WW45), mRNA /cds=(339,1490) /gb=NM_021818 /gi=18860913 /ug=Hs.288906 /len=3031	NM_021818	Hs.288906	NP_068590
mioa5594	NM_021914	cofilin 2 (muscle) (CFL2), mRNA	NM_021914	Hs.180141	NP_619579
fcrb1525	NM_021941	chromosome 21 open reading frame 97 (C21orf97), mRNA /cds=(665,1351) /gb=NM_021941 /gi=11345479 /ug=Hs.4746 /len=1819	NM_021941	Hs.4746	NP_068760
fcrc6826	NM_022073	egl nine 3 (C. elegans) (EGLN3), mRNA /cds=(327,1046) /gb=NM_022073 /gi=11545786 /ug=Hs.18878 /len=2770	NM_022073; NM_033344	Hs.18878	NP_071356
fcrb5709	NM_022130	golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655	NM_022130	Hs.18271	NP_071413
ncrb8142	NM_022130	golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655	NM_022130	Hs.18271	NP_071413
fcrb5687	NM_022464	endoplasmic reticulum chaperone SIL1, of yeast (SIL1), mRNA /cds=(97,1482) /gb=NM_022464 /gi=11968008 /ug=Hs.297875 /len=1702	NM_022464	Hs.297875	NP_071909
miod1792	NM_022495	hypothetical protein FLJ12799 (FLJ12799), mRNA /cds=(485,1324) /gb=NM_022495 /gi=22095362 /ug=Hs.22549 /len=1926	NM_022495	Hs.22549	NP_071940
ncrc2531	NM_022662	anaphase-promoting complex 1 (meiotic checkpoint regulator) (ANAPC1), mRNA /cds=(263,6097) /gb=NM_022662 /gi=12056970 /ug=Hs.40137 /len=6282	NM_022662	Hs.40137	NP_073153
ncrb8343	NM_022748	tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702	NM_022748	Hs.12210	NP_073585
ncrb6818	NM_022830	hypothetical protein FLJ22347 (FLJ22347), mRNA /cds=(60,2684) /gb=NM_022830 /gi=12383073 /ug=Hs.106004 /len=2747	NM_022830	Hs.106004	NP_073741
seoc8306	NM_022917	nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant alpha, mRNA /cds=(61,3501) /gb=NM_022917 /gi=22212928 /ug=Hs.183253 /len=4854	NM_022917; NM_130793; NM_139235	Hs.183253	NP_631981

fcrb7207	NM_023109	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1), transcript variant 7, mRNA /cds=(727,2715) /gb=NM_023109 /gi=13186244 /ug=Hs.748 /len=4066	NM_000604; NM_015850; NM_023105; NM_023106; NM_023107; NM_023108; NM_023109; NM_023110; NM_023111	Hs.748	NP_075599
fcr0076	NM_024047	nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), mRNA /cds=(326,1378) /gb=NM_024047 /gi=20127621 /ug=Hs.301789 /len=1718	NM_024047	Hs.301789	NP_076952
seob7224	NM_024077	SECIS binding protein 2 (SBP2), mRNA /cds=(58,2622) /gb=NM_024077 /gi=21359954 /ug=Hs.288141 /len=3457	NM_024077	Hs.288141	NP_076982
ncrb5227	NM_024292	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
seob4213	NM_024420	phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA /cds=(139,2388) /gb=NM_024420 /gi=23943919 /ug=Hs.211587 /len=2875	NM_024420	Hs.211587	NP_077734
seoa7249	NM_024430	proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2), mRNA	NM_024430	Hs.69149	NP_077748
miod1820	NM_024570	hypothetical protein FLJ11712 (FLJ11712), mRNA /cds=(287,1225) /gb=NM_024570 /gi=13375741 /ug=Hs.14920 /len=1515	NM_024570	Hs.14920	NP_078846
mioc4769	NM_024635	hypothetical protein FLJ22643 (FLJ22643), mRNA /cds=(15,650) /gb=NM_024635 /gi=13375865 /ug=Hs.43579 /len=997	NM_024635	Hs.43579	NP_078911
mioc3904	NM_024683	hypothetical protein FLJ22729 (FLJ22729), mRNA /cds=(603,1079) /gb=NM_024683 /gi=13375953 /ug=Hs.94891 /len=1278	NM_024683	Hs.94891	NP_078959
miob9901	NM_024697	hypothetical protein FLJ22419 (FLJ22419), mRNA /cds=(409,1596) /gb=NM_024697 /gi=13375980 /ug=Hs.99256 /len=1674	NM_024697	Hs.99256	NP_078973
seob8641	NM_024715	hypothetical protein FLJ22625 (FLJ22625), mRNA /cds=(694,1776) /gb=NM_024715 /gi=21362011 /ug=Hs.106534 /len=2747	NM_024715	Hs.106534	NP_078991

miob9714	NM_024769	hypothetical protein FLJ22415 (FLJ22415), mRNA /cds=(342,1463) /gb=NM_024769 /gi=13376114 /ug=Hs.135121 /len=2627	NM_024769	Hs.135121	NP_079045
fcrb2330	NM_024899	hypothetical protein FLJ12542 (FLJ12542), mRNA /cds=(157,2136) /gb=NM_024899 /gi=21314727 /ug=Hs.236940 /len=2884	NM_024899	Hs.236940	NP_079175
fcr7667	NM_025133	F-box only protein 11 (FBXO11), mRNA /cds=(319,2748) /gb=NM_025133 /gi=28316723 /ug=Hs.284289 /len=3960	NM_012167; NM_018693; NM_025133	Hs.284289	NP_079409
miod3341	NM_025137	hypothetical protein FLJ21439 (FLJ21439), mRNA /cds=(207,1484) /gb=NM_025137 /gi=13376718 /ug=Hs.288872 /len=2010	NM_025137	Hs.288872	NP_079413
mioc3565	NM_025191	chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467
mioc1596	NM_025202	likely ortholog of neuronally expressed calcium binding protein (FLJ13612), mRNA /cds=(101,820) /gb=NM_025202 /gi=20149495 /ug=Hs.24391 /len=1898	NM_025202	Hs.24391	NP_079478
miod1942	NM_030921	hypothetical protein DC42 (DC42), mRNA /cds=(463,771) /gb=NM_030921 /gi=24475707 /ug=Hs.72805 /len=1632	NM_030921	Hs.72805	NP_112183
ncrc1140	NM_031284	hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262	NM_031284	Hs.10748	NP_112574
ncr5149	NM_031305	hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593	NM_031305	Hs.93589	NP_112595
ncrc9060	NM_031370	heterogeneous nuclear ribonucleoprotein D (AU- rich element RNA binding protein 1, 37kDa) (HNRPD), transcript variant 1, mRNA /cds=(286,1353) /gb=NM_031370 /gi=14110419 /ug=Hs.406404 /len=2197	NM_002138; NM_031369; NM_031370	Hs.406404	NP_112738
mioc5636	NM_031458	B aggressive lymphoma gene (BAL), mRNA /cds=(229,2793) /gb=NM_031458 /gi=13899296 /ug=Hs.47783 /len=3243	NM_031458	Hs.47783	NP_113646
fcrb1560	NM_031484	hypothetical protein MGC4415 (MGC4415), mRNA /cds=(154,675) /gb=NM_031484 /gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672
fcrb3848	NM_031484	hypothetical protein MGC4415 (MGC4415), mRNA /cds=(154,675) /gb=NM_031484 /gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672

hfc3160	NM_031492	hypothetical protein similar to RNA-binding protein lark (MGC10871), mRNA /cds=(54,1133) /gb=Nm_031492 /gi=13899353 /ug=Hs.49994 /len=1821	NM_031492	Hs.49994	NP_113680
hfc2722	NM_031902	mitochondrial ribosomal protein S5 (MRPS5), nuclear gene encoding mitochondrial protein, mRNA /cds=(219,1511) /gb=Nm_031902 /gi=16554614 /ug=Hs.433117 /len=1678	NM_031902	Hs.433117	NP_114108
miob0670	NM_032042	hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA /cds=(22,1272) /gb=Nm_032042 /gi=21362017 /ug=Hs.25307 /len=4204	NM_032042	Hs.25307	NP_114431
ncr3971	NM_032102	Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA /cds=(283,1131) /gb=Nm_032102 /gi=15055542 /ug=Hs.155160 /len=2186	NM_032102	Hs.155160	NP_115285
mioc0214	NM_032151	dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (DCOHM), mRNA /cds=(21,413) /gb=Nm_032151 /gi=14149824 /ug=Hs.150186 /len=5641	NM_032151	Hs.150186	NP_115527
seoa0488	NM_032236	FLJ23277 protein (FLJ23277), mRNA /cds=(141,3089) /gb=Nm_032236 /gi=18860906 /ug=Hs.334477 /len=3911	NM_032236	Hs.334477	NP_115612
ncrb4101	NM_032297	hypothetical protein DKFZp761D112 (DKFZP761D112), mRNA /cds=(60,464) /gb=Nm_032297 /gi=14150051 /ug=Hs.103849 /len=2573	NM_032297	Hs.103849	NP_115673
ncrc1884	NM_032348	hypothetical protein MGC3047 (MGC3047), mRNA /cds=(41,1369) /gb=Nm_032348 /gi=14150144 /ug=Hs.59384 /len=2299	NM_032348	Hs.59384	NP_115724
fcrb5588	NM_032548	ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1), transcript variant 1, mRNA /cds=(526,1536) /gb=Nm_032548 /gi=25777622 /ug=Hs.107812 /len=2020	NM_032548; NM_172027; NM_172028	Hs.107812	NP_742025
seob0418	NM_032557	HP43.8KD protein (HP43.8KD), mRNA /cds=(507,3635) /gb=Nm_032557 /gi=27545312 /ug=Hs.332841 /len=4684	NM_032557	Hs.332841	NP_115946
ncr8111	NM_032601	methylmalonyl CoA epimerase (MCEE), mRNA /cds=(11,541) /gb=Nm_032601 /gi=21314761 /ug=Hs.94949 /len=850	NM_032601	Hs.94949	NP_115990
fcrb1539	NM_032704	tubulin alpha 6 (TUBA6), mRNA /cds=(1,1350) /gb=Nm_032704 /gi=14389308 /ug=Hs.406578 /len=1350	NM_032704	Hs.406578	NP_116093



ncr2507	NM_032772	hypothetical protein MGC2555 (MGC2555), mRNA /cds=(258,2198) /gb=Nm_032772 /gi=24432031 /ug=Hs.158210 /len=2807	NM_032772	Hs.158210	NP_116161
fcrb1697	NM_032801	junctional adhesion molecule 3 (JAM3), mRNA /cds=(25,1092) /gb=Nm_032801 /gi=21704285 /ug=Hs.334703 /len=3675	NM_032801	Hs.334703	NP_116190
fcrb4921	NM_032836	hypothetical protein FLJ14768 (FLJ14768), mRNA /cds=(91,1581) /gb=Nm_032836 /gi=14249547 /ug=Hs.129888 /len=2651	NM_032836	Hs.129888	NP_116225
seob1219	NM_032936	DC32 (DC32), mRNA /cds=(229,630) /gb=Nm_032936 /gi=24475725 /ug=Hs.19025 /len=883	NM_032936	Hs.19025	NP_116325
mioc0940	NM_032936	DC32 (DC32), mRNA /cds=(229,630) /gb=Nm_032936 /gi=24475725 /ug=Hs.19025 /len=883	NM_032936	Hs.19025	NP_116325
ncrc6455	NM_032961	protocadherin 10 (PCDH10), transcript variant 1, mRNA /cds=(827,3949) /gb=Nm_032961 /gi=14589915 /ug=Hs.146858 /len=5384	NM_020815; NM_032961	Hs.146858	NP_116586
ncr5890	NM_052860	kruppel-like zinc finger protein (ZNF300), mRNA /cds=(268,2082) /gb=Nm_052860 /gi=16604251 /ug=Hs.288928 /len=3104	NM_052860	Hs.288928	NP_443092
mioa2620	NM_054027	ankylosis, progressive (mouse) (ANKH), transcript variant 2, mRNA /cds=(265,1743) /gb=Nm_054027 /gi=21536394 /ug=Hs.168640 /len=4031	NM_019847; NM_054027	Hs.168640	NP_473368
seoa0799	NM_057180	vacuolar protein sorting 29 (yeast) (VPS29) transcript variant 2, mRNA /cds=(61,621) /gb=Nm_057180 /gi=17402911 /ug=Hs.69192 /len=1107	NM_016226; NM_057180	Hs.69192	NP_476528
mioa0908	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=Nm_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351
miob8191	NM_080597	oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, mRNA /cds=(175,3027) /gb=Nm_080597 /gi=19718740 /ug=Hs.252716 /len=4165	NM_018030; NM_080597; NM_133268	Hs.252716	NP_579802
miod4938	NM_080737	synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA /cds=(333,2348) /gb=Nm_080737 /gi=18152766 /ug=Hs.247525 /len=3914	NM_080737	Hs.247525	NP_542775

ncrc5536	NM_080748	chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(164,403) /gb=Nm_080748 /gi=18152784 /ug=Hs.401703 /len=602	NM_080748	Hs.401703	NP_542786
mioc4910	NM_080792	protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA /cds=(28,1542) /gb=Nm_080792 /gi=18426910 /ug=Hs.156114 /len=3872	NM_080792	Hs.156114	NP_542970
fcrb2460	NM_100264	WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA /cds=(332,2140) /gb=Nm_100264 /gi=18379329 /ug=Hs.70333 /len=3088	NM_016628; NM_100264; NM_100486	Hs.70333	NP_567823
fcrb4734	NM_133502	zinc finger protein 274 (ZNF274), transcript variant ZNF274c, mRNA /cds=(460,2421) /gb=Nm_133502 /gi=19743800 /ug=Hs.83761 /len=2839	NM_016324; NM_016325; NM_133502	Hs.83761	NP_598009
mioc5179	NM_134442	cAMP responsive element binding protein 1 (CREB1), transcript variant B, mRNA /cds=(182,1207) /gb=Nm_134442 /gi=22219460 /ug=Hs.79194 /len=3006	NM_004379; NM_134442	Hs.79194	NP_604391
seoc0317	NM_138459	hypothetical protein, MGC:7199 (LOC116150), mRNA /cds=(174,1055) /gb=Nm_138459 /gi=20270242 /ug=Hs.289008 /len=2645	NM_138459	Hs.289008	NP_612468
fcr4699	NM_139276	signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=Nm_139276 /gi=21618339 /ug=Hs.321677 /len=3455	NM_003150; NM_139276	Hs.321677	NP_644805
fcrb9684	NM_144582	hypothetical protein MGC32043 (MGC32043), mRNA /cds=(8,457) /gb=Nm_144582 /gi=21389354 /ug=Hs.226138 /len=3131	NM_144582	Hs.226138	NP_653183
miod1863	NM_144583	ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=Nm_144583 /gi=21389364 /ug=Hs.372429 /len=3033	NM_144583	Hs.372429	NP_653184
seob9772	NM_144629	hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=Nm_144629 /gi=21389456 /ug=Hs.350388 /len=3113	NM_144629	Hs.350388	NP_653230
mioc7352	NM_144664	hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=Nm_144664 /gi=21389552 /ug=Hs.288304 /len=1399	NM_144664	Hs.288304	NP_653265

miod6947	NM_144721	hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=Nm_144721 /gi=21389506 /ug=Hs.143692 /len=2260	NM_144721	Hs.143692	NP_653322
fcrb6676	NM_145056	thymus expressed gene 3-like (MGC15476), mRNA /cds=(441,1655) /gb=Nm_145056 /gi=21450823 /ug=Hs.134185 /len=2544	NM_145056	Hs.134185	NP_659493
seob0409	NM_145241	similar to spermatid WD-repeat protein (LOC114987), mRNA /cds=(238,1338) /gb=Nm_145241 /gi=21687047 /ug=Hs.133331 /len=3121	NM_145241	Hs.133331	NP_660284
mioa0582	NM_145297	similar to DNA-binding protein; zinc finger protein 253 (LOC199777), mRNA /cds=(130,408) /gb=Nm_145297 /gi=21699081 /ug=Hs.334568 /len=647	NM_145297	Hs.334568	NP_660340
ncr3163	NM_145645	Williams-Beuren Syndrome critical region protein 20 copy B (WBSCR20B), mRNA /cds=(984,1448) /gb=Nm_145645 /gi=21717802 /ug=Hs.406306 /len=1634	NM_145645	Hs.406306	NP_663620
mioa0891	NM_145693	lipin 1 (LPIN1), mRNA /cds=(68,2740) /gb=Nm_145693 /gi=22027647 /ug=Hs.81412 /len=5363	NM_145693	Hs.81412	NP_663731
seoa7943	NM_145728	desmuslin (DMN), transcript variant A, mRNA /cds=(121,4818) /gb=Nm_145728 /gi=22027637 /ug=Hs.10587 /len=7343	NM_015286; NM_145728	Hs.10587	NP_663780
miob6113	NM_145791	microsomal glutathione S-transferase 1 (MGST1), transcript variant 1c, mRNA /cds=(144,611) /gb=Nm_145791 /gi=22035635 /ug=Hs.389700 /len=987	NM_020300; NM_145764; NM_145791; NM_145792	Hs.389700	NP_665735
mioa3239	NM_145859	programmed cell death 10 (PDCD10), transcript variant 2, mRNA	NM_007217; NM_145859; NM_145860	Hs.28866	NP_665859
seob2717	NM_147166	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 4, mRNA /cds=(223,5190) /gb=Nm_147166 /gi=22538388 /ug=Hs.58103 /len=6058	NM_005751; NM_147166; NM_147171; NM_147185	Hs.58103	NP_671714

seoa4802	NM_148571	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_016504; NM_148570; NM_148571	Hs.7736	NP_683412
fcr6635	NM_152253	choline kinase-like (CHKL), transcript variant 2, mRNA /cds=(185,568) /gb=NM_152253 /gi=23238260 /ug=Hs.154886 /len=4914	NM_005198; NM_152253	Hs.154886	NP_689466
fcrb3776	NM_152282	hypothetical protein FLJ23751 (FLJ23751), mRNA /cds=(121,1563) /gb=NM_152282 /gi=22748648 /ug=Hs.37443 /len=2994	NM_152282	Hs.37443	NP_689495
seoc5833	NM_152380	T-box 15 (TBX15), mRNA /cds=(230,1093) /gb=NM_152380 /gi=23943887 /ug=Hs.164680 /len=2782	NM_152380	Hs.164680	NP_689593
fcr6748	NM_152436	hypothetical protein MGC39497 (MGC39497), mRNA /cds=(9,770) /gb=NM_152436 /gi=22748922 /ug=Hs.406728 /len=1745	NM_152436	Hs.406728	NP_689649
ncr3944	NM_152586	hypothetical protein FLJ37318 (FLJ37318), mRNA /cds=(226,2025) /gb=NM_152586 /gi=22749206 /ug=Hs.130184 /len=3114	NM_152586	Hs.130184	NP_689799
mioc7974	NM_152594	sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA /cds=(106,1440) /gb=NM_152594 /gi=22749220 /ug=Hs.302718 /len=3816	NM_152594	Hs.302718	NP_689807
ncr4545	NM_152608	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349	NM_152608	Hs.99210	NP_689821
ncrb7600	NM_152609	hypothetical protein FLJ32001 (FLJ32001), mRNA /cds=(212,2389) /gb=NM_152609 /gi=22749246 /ug=Hs.288742 /len=3608	NM_152609	Hs.288742	NP_689822
seob5859	NM_152731	hypothetical protein FLJ30162 (FLJ30162), mRNA /cds=(272,841) /gb=NM_152731 /gi=22749448 /ug=Hs.311163 /len=2278	NM_152731	Hs.311163	NP_689944
mioc0734	NM_152912	mitochondrial translational initiation factor 3 (MTIF3), mRNA /cds=(237,1073) /gb=NM_152912 /gi=24432096 /ug=Hs.406591 /len=1693	NM_152912	Hs.406591	NP_690876
seob0547	NM_152989	SRY (sex determining region Y)-box 5 (SOX5), transcript variant B, mRNA /cds=(373,2625) /gb=NM_152989 /gi=23308714 /ug=Hs.87224 /len=4492	NM_006940; NM_152989; NM_178010	Hs.87224	NP_821078
ncr8995	NM_153366	hypothetical protein FLJ90754 (FLJ90754), mRNA /cds=(677,5170) /gb=NM_153366 /gi=23503304 /ug=Hs.8963 /len=5421	NM_153366	Hs.8963	NP_699197

ncr6637	NM_153607	adult retina protein (LOC153222), mRNA /cds=(305,2224) /gb=Nm_153607 /gi=23957697 /ug=Hs.163725 /len=5446	NM_153607	Hs.163725	NP_705835
fcrb2483	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=Nm_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
fcr3575	NM_153822	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (PSMD4), transcript variant 2, mRNA /cds=(63,869) /gb=Nm_153822 /gi=25121957 /ug=Hs.148495 /len=1508	NM_002810; NM_153822	Hs.148495	NP_722544
seoc7373	NM_170601	cytosolic sialic acid 9-O-acetylerase (CSE-C), mRNA	NM_018978; NM_170601		NP_733746
seob7402	NM_170665	ATPase, Ca transporting, cardiac muscle, slow twitch 2 (ATP2A2), transcript variant 1, mRNA /cds=(164,3292) /gb=Nm_170665 /gi=27886537 /ug=Hs.1526 /len=4205	NM_001681; NM_170665	Hs.1526	NP_733765
ncr0377	NM_170695	TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 1, mRNA /cds=(388,1593) /gb=Nm_170695 /gi=28178842 /ug=Hs.90077 /len=2076	NM_003244; NM_170695; NM_173207; NM_173208; NM_173209; NM_173210; NM_173211; NM_174886	Hs.90077	NP_777480
mioa1015	NM_172178	mitochondrial ribosomal protein L42 (MRPL42), transcript variant 3, nuclear gene encoding mitochondrial protein, mRNA /cds=(179,607) /gb=Nm_172178 /gi=26667173 /ug=Hs.112110 /len=2093	NM_014050; NM_172177; NM_172178	Hs.112110	NP_751918
miob0746	NM_173639	hypothetical protein FLJ35976 (FLJ35976), mRNA /cds=(59,601) /gb=Nm_173639 /gi=27735030 /ug=Hs.131810 /len=1838	NM_173639	Hs.131810	NP_775910
seob3840	NM_173824	hypothetical protein MGC26717 (MGC26717), mRNA /cds=(107,1090) /gb=Nm_173824 /gi=28376661 /ug=Hs.406060 /len=1387	NM_173824	Hs.406060	NP_776185

fcr1994	NM_174856	isocitrate dehydrogenase 3 (NAD ) beta (IDH3B), transcript variant 3, nuclear gene encoding mitochondrial protein, mRNA /cds=(572,1273) /gb=NM_174856 /gi=28178818 /ug=Hs.155410 /len=1645	NM_006899; NM_174855; NM_174856	Hs.155410	NP_777281
seoc2232	NM_174928	hypothetical protein LOC221143 (LOC221143), mRNA /cds=(82,726) /gb=NM_174928 /gi=28372546 /ug=Hs.32450 /len=890	NM_174928	Hs.32450	NP_777588
seoc7006	U79258	clone 23732 mRNA, partial cds	NM_018997; NM_031901		NP_061870
seoa4670	U93051	putative protein tyrosine phosphatase (PTEN) mRNA, complete cds /cds=(1,1212) /gb=U93051 /gi=1916351 /ug=Hs.356062 /len=1212	NM_000314	Hs.356062	NP_000305
fcr7508	X56932	23 kD highly basic protein	NM_012423	Hs.389335	NP_036555
seob9187	X60459	IFNAR gene for interferon alpha/beta receptor			CAA42992
fcr4214	X63224	ubiquinone oxidoreductase complex CI-PDSW	NM_175818	Bt.70	NP_787012
mioc2561	XM_040708	KIAA1377 protein (KIAA1377), mRNA			XP_040708
ncrc4016	XM_046097	LOC92606 (LOC92606), mRNA			XP_046097
seob2938	XM_046827	nuclear factor I/A (NFIA), mRNA			NP_005586
ncrc5491	XM_046853	LOC92719 (LOC92719), mRNA			XP_046853
seoc0416	XM_058647	similar to mitochondrial ribosomal protein L52 CG1577-PA (LOC122704), mRNA			NP_851824
hfcr0412	XM_084654	LOC143914 (LOC143914), mRNA			XP_084654
seob3462	XM_088391	similar to Tropomyosin alpha 4 chain (Tropomyosin 4) (TM30p1) (LOC157784), mRNA			XP_088391
fcrb1763	XM_209913	similar to ring finger protein 5 (LOC286140), mRNA			NP_872402

**Table 6b:** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for moderate OA only

Clone Name	Genbank	Description	RefSeq	UniGene	Rep_prot
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fcrb0131	NM_000018	acyl-Coenzyme A dehydrogenase, very long chain (ACADVL), nuclear gene encoding mitochondrial protein, mRNA /cds=(86,2053) /gb=Nm_000018 /gi=4557234 /ug=Hs.82208 /len=2219	NM_000018	Hs.82208	NP_000009
seoa0045	NM_000060	biotinidase (BTD), mRNA /cds=(36,1667) /gb=Nm_000060 /gi=4557372 /ug=Hs.78885 /len=2016	NM_000060	Hs.78885	NP_000051
ncrc0644	NM_000063	complement component 2 (C2), mRNA /cds=(37,2295) /gb=Nm_000063 /gi=20631970 /ug=Hs.2253 /len=2609	NM_000063	Hs.2253	NP_000054
ncrb6394	NM_000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=Nm_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
seoa0032	NM_000089	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=Nm_000089 /gi=21536289 /ug=Hs.179573 /len=5084	NM_000089	Hs.179573	NP_000080

mioa1097	NM_000089	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=Nm_000089 /gi=21536289 /ug=Hs.179573 /len=5084	NM_000089	Hs.179573	NP_000080
miob4221	NM_000130	coagulation factor V (proaccelerin, labile factor) (F5), mRNA /cds=(98,6772) /gb=Nm_000130 /gi=10518500 /ug=Hs.30054 /len=6914	NM_000130	Hs.30054	NP_000121
seob0370	NM_000137	fumarylacetoaceta te hydrolase (fumarylacetoaceta se) (FAH), mRNA /cds=(57,1316) /gb=Nm_000137 /gi=4557586 /ug=Hs.73875 /len=1447	NM_000137	Hs.73875	NP_000128
seob0200	NM_000186	H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=Nm_000186 /gi=4504374 /ug=Hs.250651 /len=3926	NM_000186	Hs.250651	NP_000177
miob4975	NM_000204	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=Nm_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195



mioa1445	NM_000255	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=Nm_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246
miod0592	NM_000255	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=Nm_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246
seoa0054	NM_000269	non-metastatic cells 1, protein (NM23A) expressed in (NME1), mRNA /cds=(85,543) /gb=Nm_000269 /gi=4557796 /ug=Hs.118638 /len=732	NM_000269	Hs.118638	NP_000260
seoa8348	NM_000274	ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, mRNA /cds=(55,1374) /gb=Nm_000274 /gi=4557808 /ug=Hs.75485 /len=2013	NM_000274	Hs.75485	NP_000265

ncrb8539	NM_000319	peroxisome receptor 1 (PXR1), mRNA /cds=(52,1947) /gb=Nm_000319 /gi=21361203 /ug=Hs.158084 /len=3227	NM_000319	Hs.158084	NP_000310
seob3307	NM_000358	transforming growth factor, beta- induced, 68kDa (TGFB1), mRNA /cds=(48,2099) /gb=Nm_000358 /gi=4507466 /ug=Hs.118787 /len=2691	NM_000358	Hs.118787	NP_000349
miob9124	NM_000358	transforming growth factor, beta- induced, 68kDa (TGFB1), mRNA /cds=(48,2099) /gb=Nm_000358 /gi=4507466 /ug=Hs.118787 /len=2691	NM_000358	Hs.118787	NP_000349
seob4925	NM_000385	aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=Nm_000385 /gi=4755121 /ug=Hs.76152 /len=1662	NM_000385	Hs.76152	NP_000376
seoa4518	NM_000390	choroideremia (Rab escort protein 1) (CHM), transcript variant 2950156, mRNA /cds=(31,1992) /gb=Nm_000390 /gi=9966760 /ug=Hs.2010 /len=2115	NM_000390	Hs.2010	NP_000381

seoa4158	NM_000391	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA /cds=(30,1721) /gb=Nm_000391 /gi=5597012 /ug=Hs.20478 /len=3502	NM_000391	Hs.20478	NP_000382
seoc4960	NM_000405	GM2 ganglioside activator protein (GM2A), mRNA /cds=(96,677) /gb=Nm_000405 /gi=16507969 /ug=Hs.289082 /len=2478	NM_000405	Hs.289082	NP_000396
seoa8399	NM_000414	hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=Nm_000414 /gi=4504504 /ug=Hs.75441 /len=2593	NM_000414	Hs.75441	NP_000405
fcr4129	NM_000466	peroxisome biogenesis factor 1 (PEX1), mRNA /cds=(61,3912) /gb=Nm_000466 /gi=4505724 /ug=Hs.99847 /len=4343	NM_000466	Hs.99847	NP_000457
fcrb4266	NM_000500	cytochrome P450, family 21, subfamily A, polypeptide 2 (CYP21A2), mRNA /cds=(119,1606) /gb=Nm_000500 /gi=20522237 /ug=Hs.278430 /len=2112	NM_000500	Hs.278430	NP_000491

fcrb3298	NM_000581	glutathione peroxidase 1 (GPX1), mRNA /cds=(319,924) /gb=Nm_000581 /gi=10834975 /ug=Hs.76686 /len=1134	NM_000581	Hs.76686	NP_000572
miob2093	NM_000593	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(165,2591) /gb=Nm_000593 /gi=24797159 /ug=Hs.352018 /len=2960	NM_000593	Hs.352018	NP_000584
miob9285	NM_000596	insulin-like growth factor binding protein 1 (IGFBP1), mRNA /cds=(166,945) /gb=Nm_000596 /gi=4504614 /ug=Hs.102122 /len=1514	NM_000596	Hs.102122	NP_000587
ncr0212	NM_000599	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=Nm_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
ncr0429	NM_000624	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5 (SERPINA5), mRNA /cds=(140,1360) /gb=Nm_000624 /gi=21361194 /ug=Hs.76353 /len=2254	NM_000624	Hs.76353	NP_000615

miob3320	NM_000627	latent transforming growth factor beta binding protein 1 (LTBP1), mRNA /cds=(91,4275) /gb=Nm_000627 /gi=4557730 /ug=Hs.241257 /len=5075	NM_000627	Hs.241257	NP_000618
fcr6054	NM_000646	amylase, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 6, mRNA	NM_000028; NM_000642; NM_000643; NM_000644; NM_000645; NM_000646	Hs.904	NP_000637
ncrb6462	NM_000689	aldehyde dehydrogenase 1 family, member A1 (ALDH1A1), mRNA /cds=(54,1559) /gb=Nm_000689 /gi=25777722 /ug=Hs.76392 /len=2116	NM_000689	Hs.76392	NP_000680
seoa4739	NM_000690	aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(442,1995) /gb=Nm_000690 /gi=25777731 /ug=Hs.195432 /len=2445	NM_000690	Hs.195432	NP_000681
fcrc1311	NM_000696	aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA /cds=(378,1862) /gb=Nm_000696 /gi=25777738 /ug=Hs.2533 /len=2713	NM_000696	Hs.2533	NP_000687

miob3968	NM_000809	gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA /cds=(39,1703) /gb=Nm_000809 /gi=4557604 /ug=Hs.248112 /len=1703	NM_000809	Hs.248112	NP_000800
seoa9777	NM_000849	glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=Nm_000849 /gi=23065551 /ug=Hs.2006 /len=1572	NM_000849	Hs.2006	NP_000840
seoa9582	NM_000877	interleukin 1 receptor, type I (IL1R1), mRNA /cds=(83,1792) /gb=Nm_000877 /gi=27894331 /ug=Hs.82112 /len=4909	NM_000877	Hs.82112	NP_000868
ncrc6012	NM_000938	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA /cds=(44,3568) /gb=Nm_000938 /gi=4505940 /ug=Hs.296014 /len=3748	NM_000938	Hs.296014	NP_000929
fcrb4985	NM_000967	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=Nm_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958
mioc8766	NM_000969	ribosomal protein L5 (RPL5), mRNA /cds=(63,956) /gb=Nm_000969 /gi=14591908 /ug=Hs.180946 /len=1033	NM_000969	Hs.180946	NP_000960

mioa8076	NM_000982	ribosomal protein L21 (RPL21), mRNA /cds=(30,512) /gb=NM_000982 /gi=18104947 /ug=Hs.431927 /len=568	NM_000982	Hs.431927	NP_000973
seob9869	NM_000982	ribosomal protein L21 (RPL21), mRNA /cds=(30,512) /gb=NM_000982 /gi=18104947 /ug=Hs.431927 /len=568	NM_000982	Hs.431927	NP_000973
ncrc9749	BC032295	clone IMAGE:3921971, mRNA, partial cds		Hs.326249	NP_000974
seoa0429	NM_000984	ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546	NM_000984	Hs.419463	NP_000975
fcrb5472	NM_000991	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
fcrb3181	NM_000991	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
ncr3339	NM_000996	ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511	NM_000996	Hs.288544	NP_000987

seoa4202	NM_001001	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=Nm_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
ncrb8802	NM_001010	ribosomal protein S6 (RPS6), mRNA /cds=(43,792) /gb=Nm_001010 /gi=17158043 /ug=Hs.380843 /len=829	NM_001010	Hs.380843	NP_001001
mioa2156	NM_001010	ribosomal protein S6 (RPS6), mRNA /cds=(43,792) /gb=Nm_001010 /gi=17158043 /ug=Hs.380843 /len=829	NM_001010	Hs.380843	NP_001001
fcrb3841	NM_001012	ribosomal protein S8 (RPS8), mRNA /cds=(24,650) /gb=Nm_001012 /gi=4506742 /ug=Hs.399720 /len=705	NM_001012	Hs.399720	NP_001003
ncr2926	NM_001015	ribosomal protein S11 (RPS11), mRNA /cds=(34,510) /gb=Nm_001015 /gi=14277698 /ug=Hs.182740 /len=594	NM_001015	Hs.182740	NP_001006
mioa3693	NM_001019	ribosomal protein S15a (RPS15A), mRNA /cds=(84,476) /gb=Nm_001019 /gi=14165468 /ug=Hs.433406 /len=541	NM_001019	Hs.433406	NP_001010
seob4303	NM_001028	ribosomal protein S25 (RPS25), mRNA /cds=(64,441) /gb=Nm_001028 /gi=14591916 /ug=Hs.409158	NM_001028	Hs.409158	NP_001019



		/len=514			
mioa9792	NM_001067	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=Nm_001067 /gi=19913405 /ug=Hs.156346 /len=5698	NM_001067	Hs.156346	NP_001058
fcrb6740	NM_001084	procollagen-lysine, 2-oxoglutarate 5- dioxygenase 3 (PLOD3), mRNA /cds=(323,2539) /gb=Nm_001084 /gi=21361165 /ug=Hs.153357 /len=2852	NM_001084	Hs.153357	NP_001075
hfc2832	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=Nm_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
ncrc9637	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=Nm_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
mioc4888	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=Nm_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092

hfcf5970	NM_001103	actinin, alpha 2 (ACTN2), mRNA /cds=(174,2858) /gb=Nm_001103 /gi=4501892 /ug=Hs.83672 /len=4181	NM_001103	Hs.83672	NP_001094
ncr3442	NM_001124	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=Nm_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP_001115
ncrc4780	NM_001124	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=Nm_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP_001115
seoa4608	NM_001159	aldehyde oxidase 1 (AOX1), mRNA /cds=(299,4315) /gb=Nm_001159 /gi=6598319 /ug=Hs.406238 /len=5125	NM_001159	Hs.406238	NP_001150
ncrb4351	NM_001206	basic transcription element binding protein 1 (BTEB1), mRNA /cds=(1265,1999) /gb=Nm_001206 /gi=4557374 /ug=Hs.150557 /len=4859	NM_001206	Hs.150557	NP_001197
mioc3671	NM_001239	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=Nm_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP_001230

ncr6745	NM_001240	cyclin T1 (CCNT1), mRNA /cds=(324,2504) /gb=Nm_001240 /gi=17978465 /ug=Hs.279906 /len=2568	NM_001240	Hs.279906	NP_001231
miod6488	NM_001253	CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=Nm_001253 /gi=16357499 /ug=Hs.155174 /len=3012	NM_001253	Hs.155174	NP_001244
seoc2205	NM_001271	chromodomain helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=Nm_001271 /gi=4557448 /ug=Hs.36787 /len=7764	NM_001271	Hs.36787	NP_001262
mioa4818	NM_001310	cAMP responsive element binding protein-like 2 (CREBL2), mRNA /cds=(277,639) /gb=Nm_001310 /gi=21536277 /ug=Hs.13313 /len=3748	NM_001310	Hs.13313	NP_001301
mioc1580	NM_001354	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=Nm_001354 /gi=24497581 /ug=Hs.201967 /len=1290	NM_001354	Hs.201967	NP_001345

mioc3571	NM_001354	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=Nm_001354 /gi=24497581 /ug=Hs.201967 /len=1290	NM_001354	Hs.201967	NP_001345
seob4972	NM_001386	dihydropyrimidinase-like 2 (DPYSL2), mRNA /cds=(275,1993) /gb=Nm_001386 /gi=19923654 /ug=Hs.173381 /len=4459	NM_001386	Hs.173381	NP_001377
fcr0781	NM_001398	enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA /cds=(28,1014) /gb=Nm_001398 /gi=4503446 /ug=Hs.196176 /len=1196	NM_001398	Hs.196176	NP_001389
fcrb2346	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=Nm_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
fcr1115	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=Nm_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393

ncrb4025	NM_001439	exostoses (multiple)-like 2 (EXTL2), mRNA /cds=(288,1280) /gb=Nm_001439 /gi=14149608 /ug=Hs.61152 /len=2833	NM_001439	Hs.61152	NP_001430
miob6338	NM_001449	four and a half LIM domains 1 (FHL1), mRNA /cds=(218,1060) /gb=Nm_001449 /gi=21361121 /ug=Hs.239069 /len=2407	NM_001449	Hs.239069	NP_001440
mioc3648	BC028089	Similar to filamin A, alpha (actin binding protein 280), clone IMAGE:4156935, mRNA		Hs.195464	NP_001447
mioc4472	NM_001461	flavin containing monooxygenase 5 (FMO5), mRNA /cds=(82,1683) /gb=Nm_001461 /gi=4503760 /ug=Hs.14286 /len=2326	NM_001461	Hs.14286	NP_001452
ncrc4940	NM_001463	frizzled-related protein (FRZB), mRNA /cds=(209,1186) /gb=Nm_001463 /gi=4503788 /ug=Hs.153684 /len=1476	NM_001463	Hs.153684	NP_001454
mioa1165	NM_001514	general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=Nm_001514 /gi=13435384 /ug=Hs.258561 /len=1268	NM_001514	Hs.258561	NP_001505

seoc2192	NM_001514	general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=Nm_001514 /gi=13435384 /ug=Hs.258561 /len=1268	NM_001514	Hs.258561	NP_001505
ncrc6848	NM_001521	general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), mRNA /cds=(40,2775) /gb=Nm_001521 /gi=4504204 /ug=Hs.75782 /len=3594	NM_001521	Hs.75782	NP_001512
seob6492	NM_001540	heat shock 27kDa protein 1 (HSPB1), mRNA /cds=(108,725) /gb=Nm_001540 /gi=4996892 /ug=Hs.76067 /len=865	NM_001540	Hs.76067	NP_001531
seob6268	AB007935	mRNA for KIAA0466 protein, partial cds	NM_001542	Hs.81234	NP_001533
seoa6175	NM_001545	immature colon carcinoma transcript 1 (ICT1), mRNA /cds=(3,623) /gb=Nm_001545 /gi=4557656 /ug=Hs.9078 /len=888	NM_001545	Hs.9078	NP_001536
seob4945	NM_001560	interleukin 13 receptor, alpha 1 (IL13RA1), mRNA /cds=(44,1327) /gb=Nm_001560 /gi=26787975 /ug=Hs.285115 /len=4006	NM_001560	Hs.285115	NP_001551

ncrc1871	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=Nm_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
ncrb3585	NM_001613	actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA /cds=(48,1181) /gb=Nm_001613 /gi=4501882 /ug=Hs.195851 /len=1330	NM_001613	Hs.195851	NP_001604
seob7906	NM_001642	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(73,2364) /gb=Nm_001642 /gi=4502146 /ug=Hs.279518 /len=3727	NM_001642	Hs.279518	NP_001633
miob6615	NM_001685	ATP synthase, H transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial protein, mRNA /cds=(693,1019) /gb=Nm_001685 /gi=19913429 /ug=Hs.73851 /len=1178	NM_001685	Hs.73851	NP_001676
fcr4166	BC016512	Similar to ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide, clone MGC:5231 IMAGE:2900336, mRNA, complete cds	NM_001686	Hs.406510	NP_001677

fcr0591	NM_001686	ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(46,1665) /gb=Nm_001686 /gi=4502294 /ug=Hs.406510 /len=1807	NM_001686	Hs.406510	NP_001677
mioc4534	NM_001686	ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(46,1665) /gb=Nm_001686 /gi=4502294 /ug=Hs.406510 /len=1807	NM_001686	Hs.406510	NP_001677
seob6758	NM_001688	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=Nm_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
ncrc7127	NM_001688	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=Nm_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679



fcr6228	NM_001731	B-cell translocation gene 1, anti- proliferative (BTG1), mRNA /cds=(309,824) /gb=Nm_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001731	Hs.77054	NP_001722
ncr3165	NM_001743	calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=Nm_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734
ncr0496	NM_001748	calpain 2, (m/II) large subunit (CAPN2), mRNA /cds=(143,2245) /gb=Nm_001748 /gi=12408645 /ug=Hs.76288 /len=3419	NM_001748	Hs.76288	NP_001739
seo9627	NM_001762	chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), mRNA /cds=(56,1651) /gb=Nm_001762 /gi=22095341 /ug=Hs.82916 /len=2562	NM_001762	Hs.82916	NP_001753
mio4667	NM_001799	cyclin-dependent kinase 7 (MO15 Xenopus laevis, cdk-activating kinase) (CDK7), mRNA /cds=(89,1129) /gb=Nm_001799 /gi=16950659 /ug=Hs.184298 /len=1427	NM_001799	Hs.184298	NP_001790

seoa2004	NM_001826	CDC28 protein kinase regulatory subunit 1B (CKS1B), mRNA /cds=(10,249) /gb=Nm_001826 /gi=4502856 /ug=Hs.348669 /len=717	NM_001826	Hs.348669	NP_001817
fcrb7535	NM_001846	collagen, type IV, alpha 2 (COL4A2), mRNA /cds=(289,5427) /gb=Nm_001846 /gi=17986276 /ug=Hs.75617 /len=6276	NM_001846	Hs.75617	NP_001837
seoc2218	NM_001863	cytochrome c oxidase subunit VIb (COX6B), nuclear gene encoding mitochondrial protein, mRNA /cds=(163,423) /gb=Nm_001863 /gi=17999530 /ug=Hs.431668 /len=578	NM_001863	Hs.431668	NP_001854
seoa4708	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=Nm_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856

seob0876	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=Nm_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
miod1714	NM_001892	casein kinase 1, alpha 1 (CSNK1A1), mRNA /cds=(140,1153) /gb=Nm_001892 /gi=19923745 /ug=Hs.283738 /len=2080	NM_001892	Hs.283738	NP_001883
ncr0679	NM_001932	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA /cds=(337,2094) /gb=Nm_001932 /gi=21536463 /ug=Hs.423809 /len=3012	NM_001932	Hs.423809	NP_001923
ncrc4219	BC033736	dermatopontin, clone MGC:45278 IMAGE:5176855, mRNA, complete cds		Hs.80552	NP_001928
mioa2290	NM_001937	dermatopontin (DPT), mRNA /cds=(7,612) /gb=Nm_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928
miod1108	NM_001949	E2F transcription factor 3 (E2F3) mRNA, complete cds /cds=(67,1464) /gb=Nm_001949 /gi=12669913 /ug=Hs.1189 /len=4744	NM_001949	Hs.1189	NP_001940

seob6041	NM_001949	E2F transcription factor 3 (E2F3) mRNA, complete cds /cds=(67,1464) /gb=Nm_001949 /gi=12669913 /ug=Hs.1189 /len=4744	NM_001949	Hs.1189	NP_001940
fcrb2979	NM_001961	eukaryotic translation elongation factor 2 (EEF2), mRNA /cds=(69,2645) /gb=Nm_001961 /gi=25453476 /ug=Hs.75309 /len=3148	NM_001961	Hs.75309	NP_001952
fcrb8215	NM_001964	early growth response 1 (EGR1), mRNA /cds=(271,1902) /gb=Nm_001964 /gi=4503492 /ug=Hs.326035 /len=3132	NM_001964	Hs.326035	NP_001955
seoa6155	NM_002027	farnesyltransferase, CAAX box, alpha (FNTA), mRNA /cds=(7,1146) /gb=Nm_002027 /gi=4503770 /ug=Hs.356463 /len=1644	NM_002027	Hs.356463	NP_002018
fcrb1329	NM_002032	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=Nm_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
seob8333	NM_002032	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=Nm_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023

fcr1772	NM_002046	glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA /cds=(76,1083) /gb=Nm_002046 /gi=7669491 /ug=Hs.169476 /len=1283	NM_002046	Hs.169476	NP_002037
seob3131	NM_002056	glutamine-fructose-6-phosphate transaminase 1 (GFPT1), mRNA /cds=(123,2168) /gb=Nm_002056 /gi=4503980 /ug=Hs.1674 /len=3082	NM_002056	Hs.1674	NP_002047
mioc1135	BC017742	clone IMAGE:4391536, mRNA	NM_002076	Hs.334534	NP_002067
fcr1404	NM_002087	granulin (GRN), mRNA	NM_002087	Hs.180577	NP_002078
seob9946	NM_002113	H factor (complement)-like 1 (HFL1), mRNA /cds=(78,1070) /gb=Nm_002113 /gi=11321586 /ug=Hs.278568 /len=1266	NM_002113	Hs.278568	NP_002104
seob3370	NM_002124	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=Nm_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115
fcrb8915	NM_002129	high-mobility group box 2 (HMGB2), mRNA /cds=(191,820) /gb=Nm_002129 /gi=14141173 /ug=Hs.80684 /len=1277	NM_002129	Hs.80684	NP_002120

ncrc5738	NM_002157	heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=Nm_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
miob2087	NM_002157	heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=Nm_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
seoa5366	NM_002160	tenascin C (hexabrachion) (TNC), mRNA	NM_002160	Hs.289114	NP_002151
mioa0485	NM_002213	integrin, beta 5 (ITGB5), mRNA /cds=(307,2706) /gb=Nm_002213 /gi=20127445 /ug=Hs.149846 /len=3401	NM_002213	Hs.149846	NP_002204
seob4669	NM_002265	karyopherin (importin) beta 1 (KPNB1), mRNA /cds=(337,2967) /gb=Nm_002265 /gi=24797084 /ug=Hs.180446 /len=4205	NM_002265	Hs.180446	NP_002256
hfcr1716	NM_002290	laminin, alpha 4 (LAMA4), mRNA /cds=(284,5734) /gb=Nm_002290 /gi=9845494 /ug=Hs.78672 /len=6297	NM_002290	Hs.78672	NP_002281
ncrc5091	NM_002381	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=Nm_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372

miob8992	NM_002414	CD99 antigen (CD99), mRNA /cds=(184,741) /gb=Nm_002414 /gi=20149541 /ug=Hs.433387 /len=1264	NM_002414	Hs.433387	NP_002405
fcr2861	NM_002415	macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA /cds=(98,445) /gb=Nm_002415 /gi=4505184 /ug=Hs.407995 /len=561	NM_002415	Hs.407995	NP_002406
miob6562	NM_002416	chemokine (C-X-C motif) ligand 9 (CXCL9), mRNA /cds=(40,417) /gb=Nm_002416 /gi=4505186 /ug=Hs.77367 /len=2545	NM_002416	Hs.77367	NP_002407
seob6696	NM_002431	menage a trois 1 (CAK assembly factor) (MNAT1), mRNA /cds=(35,964) /gb=Nm_002431 /gi=4505224 /ug=Hs.433410 /len=1281	NM_002431	Hs.433410	NP_002422
ncr6878	NM_002439	mutS 3 (E. coli) (MSH3), mRNA /cds=(17,3403) /gb=Nm_002439 /gi=4505248 /ug=Hs.42674 /len=4374	NM_002439	Hs.42674	NP_002430
seoc2447	NM_002473	myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA /cds=(1,5883) /gb=Nm_002473 /gi=22507396 /ug=Hs.146550 /len=7274	NM_002473	Hs.146550	NP_002464

fcrb8605	NM_002488	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa (NDUFA2), mRNA /cds=(57,356) /gb=Nm_002488 /gi=4505354 /ug=Hs.163867 /len=590	NM_002488	Hs.163867	NP_002479
seoa8543	NM_002495	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=Nm_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
mioc1991	NM_002495	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=Nm_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
fcrb4294	NM_002496	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase) (NDUFS8), mRNA /cds=(93,725) /gb=Nm_002496 /gi=4505370 /ug=Hs.90443 /len=779	NM_002496	Hs.90443	NP_002487



seoa5578	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
ncrc9039	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
fcrb6301	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
miod4332	BC039158	Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:24867 IMAGE:4778360, mRNA, complete cds	NM_002610	Hs.61712	NP_002601
ncrc1633	NM_002687	pinin, desmosome associated protein (PNN), mRNA /cds=(31,2262) /gb=NM_002687 /gi=4505922 /ug=Hs.44499 /len=2617	NM_002687	Hs.44499	NP_002678

seoa8432	NM_002696	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=Nm_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
ncr3705	NM_002764	phosphoribosyl pyrophosphate synthetase 1 (PRPS1), mRNA /cds=(101,1057) /gb=Nm_002764 /gi=19923737 /ug=Hs.56 /len=2078	NM_002764	Hs.56	NP_002755
mioa1513	NM_002778	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=Nm_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
ncrc6875	NM_002793	proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA /cds=(48,773) /gb=Nm_002793 /gi=22538462 /ug=Hs.407981 /len=872	NM_002793	Hs.407981	NP_002784
seoc1203	NM_002794	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=Nm_002794 /gi=22538463 /ug=Hs.432607 /len=850	NM_002794	Hs.432607	NP_002785

seob2077	NM_002795	proteasome (prosome, macropain) subunit, beta type, 3 (PSMB3), mRNA /cds=(79,696) /gb=Nm_002795 /gi=22538464 /ug=Hs.82793 /len=784	NM_002795	Hs.82793	NP_002786
ncrc0427	NM_002805	proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(42,1262) /gb=Nm_002805 /gi=24497434 /ug=Hs.79387 /len=1332	NM_002805	Hs.79387	NP_002796
ncrc3030	NM_002806	proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6), mRNA /cds=(21,1190) /gb=Nm_002806 /gi=24430159 /ug=Hs.79357 /len=1590	NM_002806	Hs.79357	NP_002797
fcrb3702	NM_002823	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=Nm_002823 /gi=21359859 /ug=Hs.250655 /len=1233	NM_002823	Hs.250655	NP_002814
mioc7225	NM_002851	protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(148,7092) /gb=Nm_002851 /gi=4506328 /ug=Hs.78867 /len=7941	NM_002851	Hs.78867	NP_002842

ncr0223	NM_002865	RAB2, member RAS oncogene family (RAB2), mRNA /cds=(209,847) /gb=Nm_002865 /gi=4506364 /ug=Hs.78305 /len=1148	NM_002865	Hs.78305	NP_002856
ncrc4773	NM_002901	reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA /cds=(53,1048) /gb=Nm_002901 /gi=4506454 /ug=Hs.167791 /len=2104	NM_002901	Hs.167791	NP_002892
mioa1632	NM_002947	replication protein A3, 14kDa (RPA3), mRNA /cds=(1182,1547) /gb=Nm_002947 /gi=19923751 /ug=Hs.1608 /len=1622	NM_002947	Hs.1608	NP_002938
fcr7659	NM_002952	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=Nm_002952 /gi=15055538 /ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943
mioc6212	NM_002958	RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(104,1918) /gb=Nm_002958 /gi=11863158 /ug=Hs.79350 /len=3031	NM_002958	Hs.79350	NP_002949
ncrc9944	NM_002970	spermidine/spermin e N1- acetyltransferase (SAT), mRNA /cds=(166,681) /gb=Nm_002970 /gi=4506788 /ug=Hs.28491 /len=1060	NM_002970	Hs.28491	NP_002961

hfcr4645	NM_003012	secreted frizzled-related protein 1 (SFRP1), mRNA /cds=(303,1244) /gb=Nm_003012 /gi=8400731 /ug=Hs.7306 /len=4469	NM_003012	Hs.7306	NP_003003
seoa1065	NM_003017	splicing factor, arginine/serine-rich 3 (SFRS3), mRNA /cds=(106,600) /gb=Nm_003017 /gi=24025684 /ug=Hs.388623 /len=1403	NM_003017	Hs.388623	NP_003008
mioa4771	AF114488	intersectin short isoform (ITSN) mRNA, complete cds	NM_003024	Hs.66392	NP_003015
fcrc2089	NM_003040	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1) (SLC4A2), mRNA /cds=(175,3900) /gb=Nm_003040 /gi=21361550 /ug=Hs.79410 /len=4078	NM_003040	Hs.79410	NP_003031
seob4160	NM_003068	snail 2 (Drosophila) (SNAI2), mRNA /cds=(165,971) /gb=Nm_003068 /gi=24497625 /ug=Hs.93005 /len=2101	NM_003068	Hs.93005	NP_003059
seoa8486	NM_003096	small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA /cds=(89,319) /gb=Nm_003096 /gi=21359839 /ug=Hs.77496 /len=606	NM_003096	Hs.77496	NP_003087

seob5081	NM_003133	signal recognition particle 9kDa (SRP9), mRNA /cds=(107,367) /gb=Nm_003133 /gi=4507216 /ug=Hs.75975 /len=1466	NM_003133	Hs.75975	NP_003124
seoa3852	NM_003144	signal sequence receptor, alpha (translocon- associated protein alpha) (SSR1), mRNA /cds=(112,972) /gb=Nm_003144 /gi=6552340 /ug=Hs.250773 /len=3285	NM_003144	Hs.250773	NP_003135
seoa5258	NM_003203	chromosome 2 open reading frame 3 (C2orf3), mRNA /cds=(69,2414) /gb=Nm_003203 /gi=7108364 /ug=Hs.184175 /len=2661	NM_003203	Hs.184175	NP_003194
ncrc1631	NM_003217	testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=Nm_003217 /gi=4507432 /ug=Hs.74637 /len=2600	NM_003217	Hs.74637	NP_003208
miob3329	NM_003248	thrombospondin 4 (THBS4), mRNA /cds=(28,2913) /gb=Nm_003248 /gi=4507488 /ug=Hs.75774 /len=3074	NM_003248	Hs.75774	NP_003239
fcr4503	NM_003258	thymidine kinase 1, soluble (TK1), mRNA /cds=(58,762) /gb=Nm_003258 /gi=4507518 /ug=Hs.105097 /len=1421	NM_003258	Hs.105097	NP_003249

ncrc5162	NM_003270	transmembrane 4 superfamily member 6 (TM4SF6), mRNA /cds=(104,841) /gb=Nm_003270 /gi=21265115 /ug=Hs.121068 /len=2069	NM_003270	Hs.121068	NP_003261
fcrc6389	NM_003279	troponin C2, fast (TNNC2), mRNA /cds=(65,547) /gb=Nm_003279 /gi=4507616 /ug=Hs.182421 /len=677	NM_003279	Hs.182421	NP_003270
hfcr5905	NM_003286	topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=Nm_003286 /gi=19913404 /ug=Hs.317 /len=3734	NM_003286	Hs.317	NP_003277
seoa0044	NM_003295	tumor protein, translationally- controlled 1 (TPT1), mRNA /cds=(95,613) /gb=Nm_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
seob7500	NM_003295	tumor protein, translationally- controlled 1 (TPT1), mRNA /cds=(95,613) /gb=Nm_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
fcrc3795	NM_003302	thyroid hormone receptor interactor 6 (TRIP6), mRNA /cds=(76,1506) /gb=Nm_003302 /gi=23308730 /ug=Hs.380230 /len=1695	NM_003302	Hs.380230	NP_003293

seob7022	NM_003350	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=Nm_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
mioc0206	NM_003350	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=Nm_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
miod3079	NM_003377	vascular endothelial growth factor B (VEGFB), mRNA /cds=(50,673) /gb=Nm_003377 /gi=20070172 /ug=Hs.78781 /len=1181	NM_003377	Hs.78781	NP_003368
seoa0396	NM_003383	very low density lipoprotein receptor (VLDLR), mRNA /cds=(86,2707) /gb=Nm_003383 /gi=4507900 /ug=Hs.73729 /len=3355	NM_003383	Hs.73729	NP_003374
ncr9337	NM_003407	zinc finger protein 36, C3H type, (mouse) (ZFP36), mRNA /cds=(60,1040) /gb=Nm_003407 /gi=4507960 /ug=Hs.343586 /len=1746	NM_003407	Hs.343586	NP_003398



fcrb9843	NM_003407	zinc finger protein 36, C3H type, (mouse) (ZFP36), mRNA /cds=(60,1040) /gb=Nm_003407 /gi=4507960 /ug=Hs.343586 /len=1746	NM_003407	Hs.343586	NP_003398
seoa1749	NM_003418	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=Nm_003418 /gi=4827070 /ug=Hs.2110 /len=1500	NM_003418	Hs.2110	NP_003409
fcrb1311	NM_003442	zinc finger protein 143 (clone pHZ-1) (ZNF143), mRNA /cds=(155,2035) /gb=Nm_003442 /gi=24475652 /ug=Hs.374355 /len=2641	NM_003442	Hs.374355	NP_003433
ncrc6871	NM_003455	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=Nm_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
ncr8337	NM_003470	ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(200,3508) /gb=Nm_003470 /gi=4507856 /ug=Hs.78683 /len=4022	NM_003470	Hs.78683	NP_003461

fcr5138	NM_003504	CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA /cds=(71,1771) /gb=Nm_003504 /gi=16357475 /ug=Hs.114311 /len=1932	NM_003504	Hs.114311	NP_003495
ncrc5327	NM_003563	speckle-type POZ protein (SPOP), mRNA /cds=(158,1282) /gb=Nm_003563 /gi=4507182 /ug=Hs.129951 /len=1642	NM_003563	Hs.129951	NP_003554
ncrc4302	NM_003576	serine/threonine kinase 24 (STE20 yeast) (STK24), mRNA /cds=(146,1477) /gb=Nm_003576 /gi=20070157 /ug=Hs.168913 /len=2505	NM_003576	Hs.168913	NP_003567
mioa7544	NM_003580	neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA /cds=(13,2766) /gb=Nm_003580 /gi=4505464 /ug=Hs.78687 /len=3380	NM_003580	Hs.78687	NP_003571
mioa5540	NM_003596	tyrosylprotein sulfotransferase 1 (TPST1), mRNA /cds=(328,1440) /gb=Nm_003596 /gi=21361092 /ug=Hs.421194 /len=2033	NM_003596	Hs.421194	NP_003587

seoa2620	NM_003615	solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA /cds=(72,3716) /gb=Nm_003615 /gi=19923175 /ug=Hs.132904 /len=7785	NM_003615	Hs.132904	NP_003606
mioa1149	NM_003642	histone acetyltransferase 1 (HAT1), mRNA /cds=(37,1296) /gb=Nm_003642 /gi=4504340 /ug=Hs.13340 /len=1568	NM_003642	Hs.13340	NP_003633
miod4867	NM_003663	CGG triplet repeat binding protein 1 (CGGBP1), mRNA /cds=(357,863) /gb=Nm_003663 /gi=21361098 /ug=Hs.86041 /len=4279	NM_003663	Hs.86041	NP_003654
seoa8638	NM_003670	basic helix-loop- helix domain containing, class B, 2 (BHLHB2), mRNA /cds=(197,1435) /gb=Nm_003670 /gi=4503298 /ug=Hs.171825 /len=2922	NM_003670	Hs.171825	NP_003661
mioa3514	NM_003690	protein kinase, interferon-inducible double stranded RNA dependent activator (PRKRA), mRNA /cds=(108,1049) /gb=Nm_003690 /gi=20149526 /ug=Hs.18571 /len=1843	NM_003690	Hs.18571	NP_003681

mioc2681	NM_003739	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3), mRNA /cds=(70,1041) /gb=Nm_003739 /gi=24497582 /ug=Hs.78183 /len=1224	NM_003739	Hs.78183	NP_003730
miob8663	BC031264	clone MGC:39731 IMAGE:5275603, mRNA, complete cds		Hs.6651	NP_003753
seoa3989	NM_003798	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA /cds=(44,2248) /gb=Nm_003798 /gi=4503128 /ug=Hs.58488 /len=2446	NM_003798	Hs.58488	NP_003789
seoa6223	NM_003800	RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=Nm_003800 /gi=4506562 /ug=Hs.27345 /len=4546	NM_003800	Hs.27345	NP_003791
seoa0070	NM_003850	succinate-CoA ligase, ADP-forming, beta subunit (SUCLA2), mRNA /cds=(58,1449) /gb=Nm_003850 /gi=11321582 /ug=Hs.182217 /len=2178	NM_003850	Hs.182217	NP_003841

ncr1235	NM_003859	dolichyl-phosphate mannosyltransferas e polypeptide 1, catalytic subunit (DPM1), mRNA /cds=(1,783) /gb=Nm_003859 /gi=4503362 /ug=Hs.5085 /len=1047	NM_003859	Hs.5085	NP_003850
ncrc0829	NM_003870	IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(468,5441) /gb=Nm_003870 /gi=4506786 /ug=Hs.1742 /len=7573	NM_003870	Hs.1742	NP_003861
fcrb2160	NM_003878	gamma-glutamyl hydrolase (conjugase, folylpolygammaglut amyl hydrolase) (GGH), mRNA /cds=(60,1016) /gb=Nm_003878 /gi=4503986 /ug=Hs.78619 /len=1280	NM_003878	Hs.78619	NP_003869
ncrc8903	NM_003879	CASP8 and FADD- like apoptosis regulator (CFLAR), mRNA /cds=(482,1924) /gb=Nm_003879 /gi=21361768 /ug=Hs.195175 /len=2243	NM_003879	Hs.195175	NP_003870

hfc0045	NM_003932	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=Nm_003932 /gi=21237722 /ug=Hs.119222 /len=3214	NM_003932	Hs.119222	NP_003923
ncr0721	NM_003945	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=Nm_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936
seoa8960	NM_003945	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=Nm_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936
mioa9891	NM_003972	BTAF1 RNA polymerase II, B-TFIIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=Nm_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
ncr0733	NM_004048	beta-2-microglobulin (B2M), mRNA /cds=(14,373) /gb=Nm_004048 /gi=4757825 /ug=Hs.48516 /len=925	NM_004048	Hs.48516	NP_004039

ncrc1687	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=Nm_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM_004064	Hs.238990	NP_004055
miob8639	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=Nm_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM_004064	Hs.238990	NP_004055
ncrc0672	NM_004065	cerebellar degeneration- related protein 1, 34kDa (CDR1), mRNA /cds=(61,732) /gb=Nm_004065 /gi=4757963 /ug=Hs.278427 /len=1165	NM_004065	Hs.278427	NP_004056
ncrc2693	NM_004065	cerebellar degeneration- related protein 1, 34kDa (CDR1), mRNA /cds=(61,732) /gb=Nm_004065 /gi=4757963 /ug=Hs.278427 /len=1165	NM_004065	Hs.278427	NP_004056
ncrb8237	BC018148	delta sleep inducing peptide, immunoreactor, clone MGC:9719 IMAGE:3851403, mRNA, complete cds	NM_004089	Hs.75450	NP_004080

hfcr6515	NM_004102	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), mRNA /cds=(46,447) /gb=Nm_004102 /gi=10938020 /ug=Hs.49881 /len=679	NM_004102	Hs.49881	NP_004093
miod3591	NM_004117	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=Nm_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
mioc0090	NM_004117	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=Nm_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
seoa6364	NM_004124	glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=Nm_004124 /gi=4758441 /ug=Hs.151413 /len=4131	NM_004124	Hs.151413	NP_004115
seob6415	NM_004134	heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA /cds=(94,2133) /gb=Nm_004134 /gi=24234687 /ug=Hs.3069 /len=2852	NM_004134	Hs.3069	NP_004125



fcrb5259	NM_004147	developmentally regulated GTP binding protein 1 (DRG1), mRNA /cds=(66,1169) /gb=Nm_004147 /gi=4758795 /ug=Hs.115242 /len=1383	NM_004147	Hs.115242	NP_004138
seob6601	AK055927	cDNA FLJ31365 fis, clone NB9N41000135, highly similar to RAS-RELATED PROTEIN RAB-1A	NM_004161	Hs.227327	NP_004152
miod4518	NM_004215	estrogen receptor binding site associated, antigen, 9 (EBAG9), mRNA /cds=(362,1003) /gb=Nm_004215 /gi=14577926 /ug=Hs.9222 /len=1182	NM_004215	Hs.9222	NP_004206
ncrc5553	NM_004251	RAB9A, member RAS oncogene family (RAB9A), mRNA /cds=(192,797) /gb=Nm_004251 /gi=20070189 /ug=Hs.330994 /len=1106	NM_004251	Hs.330994	NP_004242
mioc1416	NM_004268	cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa (CRSP6), mRNA /cds=(196,2151) /gb=Nm_004268 /gi=10835074 /ug=Hs.22630 /len=2546	NM_004268	Hs.22630	NP_004259

mioa3361	NM_004309	Rho GDP dissociation inhibitor (GDI) alpha (ARHGDIA), mRNA /cds=(102,716) /gb=Nm_004309 /gi=20149550 /ug=Hs.159161 /len=1921	NM_004309	Hs.159161	NP_004300
seob5454	NM_004311	ADP-ribosylation factor-like 3 (ARL3), mRNA /cds=(16,564) /gb=Nm_004311 /gi=4757773 /ug=Hs.182215 /len=900	NM_004311	Hs.182215	NP_004302
seob5021	NM_004313	arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=Nm_004313 /gi=21626464 /ug=Hs.18142 /len=1941	NM_004313	Hs.18142	NP_004304
mioa0466	NM_004323	BCL2-associated athanogene (BAG1), mRNA /cds=(66,1103) /gb=Nm_004323 /gi=7549801 /ug=Hs.41714 /len=1311	NM_004323	Hs.41714	NP_004314
fcrc1957	NM_004338	chromosome 18 open reading frame 1 (C18orf1), mRNA /cds=(243,989) /gb=Nm_004338 /gi=4757883 /ug=Hs.153498 /len=8093	NM_004338	Hs.153498	NP_004329
hfcr2930	NM_004356	CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA /cds=(41,751) /gb=Nm_004356 /gi=21237760 /ug=Hs.54457 /len=1332	NM_004356	Hs.54457	NP_004347

seoa9874	NM_004373	cytochrome c oxidase subunit VIa polypeptide 1 (COX6A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(27,356) /gb=Nm_004373 /gi=17999527 /ug=Hs.180714 /len=548	NM_004373	Hs.180714	NP_004364
mioc2039	NM_004375	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=Nm_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
mioc3220	NM_004385	chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA /cds=(267,10457) /gb=Nm_004385 /gi=21361115 /ug=Hs.81800 /len=11185	NM_004385	Hs.81800	NP_004376
ncr0265	NM_004414	Down syndrome critical region gene 1 (DSCR1), mRNA /cds=(66,659) /gb=Nm_004414 /gi=20149552 /ug=Hs.184222 /len=2289	NM_004414	Hs.184222	NP_004405
ncrc0439	NM_004508	isopentenyl-diphosphate delta isomerase (IDI1), mRNA /cds=(51,737) /gb=Nm_004508 /gi=4758583 /ug=Hs.76038 /len=1807	NM_004508	Hs.76038	NP_004499

mioa9821	NM_004566	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=Nm_004566 /gi=4758899 /ug=Hs.195471 /len=4322	NM_004566	Hs.195471	NP_004557
miob2656	NM_004568	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=Nm_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
ncr0018	NM_004568	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=Nm_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
seoa9712	NM_004582	Rab geranylgeranyltransferase, beta subunit (RABGGTB), mRNA /cds=(72,1067) /gb=Nm_004582 /gi=21359853 /ug=Hs.78948 /len=1526	NM_004582	Hs.78948	NP_004573
hfcr2250	NM_004629	Fanconi anemia, complementation group G (FANCG), mRNA /cds=(493,2361) /gb=Nm_004629 /gi=4759335 /ug=Hs.8047 /len=2649	NM_004629	Hs.8047	NP_004620

mioa8028	AL137295	mRNA; cDNA DKFZp434M2216 (from clone DKFZp434M2216)	NM_004641	Hs.199429	NP_004632
miob3695	NM_004674	ash2 (absent, small, or homeotic)- like (Drosophila) (ASH2L), mRNA /cds=(5,1891) /gb=Nm_004674 /gi=4757789 /ug=Hs.6856 /len=2381	NM_004674	Hs.6856	NP_004665
mioa6102	NM_004713	serologically defined colon cancer antigen 1 (SDCCAG1), mRNA /cds=(183,1271) /gb=Nm_004713 /gi=4759077 /ug=Hs.388584 /len=2078	NM_004713	Hs.388584	NP_004704
seoa0729	NM_004718	cytochrome c oxidase subunit VIIa polypeptide 2 like (COX7A2L), nuclear gene encoding mitochondrial protein, mRNA /cds=(56,400) /gb=Nm_004718 /gi=18105036 /ug=Hs.30888 /len=1145	NM_004718	Hs.30888	NP_004709
mioc3593	NM_004728	DEAD/H (Asp-Glu- Ala-Asp/His) box polypeptide 21 (DDX21), mRNA /cds=(266,2413) /gb=Nm_004728 /gi=13787208 /ug=Hs.169531 /len=3319	NM_004728	Hs.169531	NP_004719

fcrb2849	NM_004730	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=Nm_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
seob9092	NM_004779	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=Nm_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
seob3139	NM_004832	glutathione-S-transferase like; glutathione transferase omega (GSTTLp28), mRNA /cds=(10,735) /gb=Nm_004832 /gi=4758483 /ug=Hs.11465 /len=793	NM_004832	Hs.11465	NP_004823
seoa1083	NM_004836	eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA /cds=(303,3650) /gb=Nm_004836 /gi=21361154 /ug=Hs.102506 /len=4662	NM_004836	Hs.102506	NP_004827
seob6856	NM_004850	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=Nm_004850 /gi=6633807 /ug=Hs.58617 /len=6409	NM_004850	Hs.58617	NP_004841

fcrb1787	NM_004859	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(173,5200) /gb=Nm_004859 /gi=4758011 /ug=Hs.178710 /len=6111	NM_004859	Hs.178710	NP_004850
seob3904	NM_004862	LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(234,920) /gb=Nm_004862 /gi=4758913 /ug=Hs.76507 /len=1773	NM_004862	Hs.76507	NP_004853
seoa4717	NM_004872	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=Nm_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863
seob3189	NM_004894	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=Nm_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
seob3226	NM_004896	vacuolar protein sorting 26 (yeast) (VPS26), mRNA /cds=(80,1063) /gb=Nm_004896 /gi=17978518 /ug=Hs.67052 /len=2652	NM_004896	Hs.67052	NP_004887
seob6015	NM_004902	RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=Nm_004902 /gi=4757925 /ug=Hs.145696 /len=2595	NM_004902	Hs.145696	NP_004893

mioc3867	NM_004902	RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=Nm_004902 /gi=4757925 /ug=Hs.145696 /len=2595	NM_004902	Hs.145696	NP_004893
mioc4190	NM_004912	cerebral cavernous malformations 1 (CCM1), mRNA /cds=(26,1615) /gb=Nm_004912 /gi=4758657 /ug=Hs.93810 /len=2004	NM_004912	Hs.93810	NP_004903
fcrb6939	NM_004926	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=Nm_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP_004917
ncr1122	NM_004958	FK506 binding protein 12-rapamycin associated protein 1 (FRAP1), mRNA /cds=(80,7729) /gb=Nm_004958 /gi=19924298 /ug=Hs.338207 /len=8680	NM_004958	Hs.338207	NP_004949
ncr0491	NM_004967	integrin-binding sialoprotein (bone sialoprotein, bone sialoprotein II) (IBSP), mRNA /cds=(143,1096) /gb=Nm_004967 /gi=13259536 /ug=Hs.49215 /len=1108	NM_004967	Hs.49215	NP_004958



mioa5511	NM_004992	methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA /cds=(168,1628) /gb=Nm_004992 /gi=7710148 /ug=Hs.3239 /len=10182	NM_004992	Hs.3239	NP_004983
seob4363	AJ401610	mRNA for 3'5' cyclic nucleotide phosphodiesterase (PDE1A5 gene)		Hs.41717	NP_005010
miob6688	NM_005025	serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPIN1), mRNA /cds=(82,1314) /gb=Nm_005025 /gi=4826903 /ug=Hs.78589 /len=1559	NM_005025	Hs.78589	NP_005016
fcrc5233	NM_005047	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5), mRNA /cds=(20,1534) /gb=Nm_005047 /gi=25777613 /ug=Hs.193725 /len=3411	NM_005047	Hs.193725	NP_005038
ncr9125	NM_005077	transducin-like enhancer of split 1 (E(sp1) Drosophila) (TLE1), mRNA /cds=(451,2763) /gb=Nm_005077 /gi=21541823 /ug=Hs.28935 /len=3292	NM_005077	Hs.28935	NP_005068

ncr2391	NM_005086	sarcospan (Kras oncogene-associated gene) (SSPN), mRNA /cds=(85,816) /gb=Nm_005086 /gi=16933560 /ug=Hs.183428 /len=2707	NM_005086	Hs.183428	NP_005077
ncr9881	BC045613	nuclear receptor subfamily 1, group D, member 2, clone MGC:33914 IMAGE:5274113, mRNA, complete cds		Hs.37288	NP_005117
mioa0707	NM_005175	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=Nm_005175 /gi=4885080 /ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
ncrc4994	NM_005175	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=Nm_005175 /gi=4885080 /ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
seoa4436	NM_005194	CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA	NM_005194	Hs.99029	NP_005185
mioa8857	NM_005245	FAT tumor suppressor 1 (Drosophila) (FAT), mRNA /cds=(187,13959) /gb=Nm_005245 /gi=4885228 /ug=Hs.166994 /len=14756	NM_005245	Hs.166994	NP_005236

ncr4009	NM_005313	glucose regulated protein, 58kDa (GRP58), mRNA /cds=(90,1607) /gb=Nm_005313 /gi=21361656 /ug=Hs.13751 /len=2074	NM_005313	Hs.13751	NP_005304
fcr3181	NM_005318	H1 histone family, member 0 (H1F0), mRNA	NM_005318	Hs.226117	NP_005309
miob2375	NM_005324	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=Nm_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
fcrb2926	NM_005324	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=Nm_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
ncr6137	NM_005340	histidine triad nucleotide binding protein 1 (HINT1), mRNA /cds=(108,488) /gb=Nm_005340 /gi=4885412 /ug=Hs.256697 /len=641	NM_005340	Hs.256697	NP_005331
seoa5429	NM_005347	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=Nm_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338

seob1191	NM_005347	heat shock 70kDa protein 5 (glucose- regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=Nm_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338
fcrb4788	NM_005347	heat shock 70kDa protein 5 (glucose- regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=Nm_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338
ncrc9729	NM_005360	v-maf musculoaponeuroti c fibrosarcoma oncogene (avian) (MAF), mRNA /cds=(808,2019) /gb=Nm_005360 /gi=5453735 /ug=Hs.30250 /len=2145	NM_005360	Hs.30250	NP_005351
mioa0311	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=Nm_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389
miod2007	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=Nm_005398 /gi=21314622 /ug=Hs.303090	NM_005398	Hs.303090	NP_005389

		/len=2524			
ncrc3541	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=Nm_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389
ncrc6881	NM_005445	chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA /cds=(92,3745) /gb=Nm_005445 /gi=24475891 /ug=Hs.24485 /len=4096	NM_005445	Hs.24485	NP_005436
mioc2219	NM_005455	zinc finger protein 265 (ZNF265), mRNA /gb=Nm_005455 /gi=19923317 /ug=Hs.194718 /len=2837	NM_005455	Hs.194718	NP_005446
mioa7069	NM_005484	ADP- ribosyltransferase (NAD ; poly(ADP- ribose) polymerase)-like 2 (ADPRTL2), mRNA /cds=(150,1754) /gb=Nm_005484 /gi=11496991 /ug=Hs.24284 /len=1887	NM_005484	Hs.24284	NP_005475

fcrc2775	NM_005537	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=Nm_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528
fcrb2218	NM_005594	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=Nm_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
ncrc0408	AK024964	cDNA: FLJ21311 fis, clone COL02167. /gb=AK024964 /gi=10437390 /ug=Hs.173933 /len=3216		Hs.173933	NP_005586
ncr5975	NM_005603	ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA /cds=(1,3756) /gb=Nm_005603 /gi=5031696 /ug=Hs.406187 /len=3756	NM_005603	Hs.406187	NP_005594
seob8483	NM_005605	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA /cds=(337,1875) /gb=Nm_005605 /gi=21361289 /ug=Hs.75206 /len=2230	NM_005605	Hs.75206	NP_005596

seob1538	NM_005611	retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=Nm_005611 /gi=21361291 /ug=Hs.79362 /len=4853	NM_005611	Hs.79362	NP_005602
ncrc0907	NM_005623	chemokine (C-C motif) ligand 8 (CCL8), mRNA /cds=(456,755) /gb=Nm_005623 /gi=22538815 /ug=Hs.271387 /len=1351	NM_005623	Hs.271387	NP_005614
mioc3045	NM_005627	serum/glucocorticoid regulated kinase (SGK), mRNA /cds=(58,1353) /gb=Nm_005627 /gi=25168262 /ug=Hs.296323 /len=2386	NM_005627	Hs.296323	NP_005618
miob6290	NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=Nm_005642 /gi=14717406 /ug=Hs.155188 /len=2310	NM_005642	Hs.155188	NP_005633
miod4084	NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=Nm_005642 /gi=14717406 /ug=Hs.155188 /len=2310	NM_005642	Hs.155188	NP_005633

ncrb3329	NM_005655	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=Nm_005655 /gi=5032176 /ug=Hs.82173 /len=2899	NM_005655	Hs.82173	NP_005646
mioc4204	NM_005655	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=Nm_005655 /gi=5032176 /ug=Hs.82173 /len=2899	NM_005655	Hs.82173	NP_005646
miod1044	NM_005724	tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=Nm_005724 /gi=21264581 /ug=Hs.100090 /len=1842	NM_005724	Hs.100090	NP_005715
seoc1034	T66132	yc77a06.s1 Soares infant brain 1NIB cDNA clone IMAGE:21844 3', mRNA sequence /clone=IMAGE:218 44 /clone_end=3' /gb=T66132 /gi=675177 /ug=Hs.332583 /len=246		Hs.332583	NP_005728
seob9818	NM_005738	ADP-ribosylation factor-like 4 (ARL4), mRNA /cds=(154,756) /gb=Nm_005738 /gi=5031602 /ug=Hs.245540 /len=1077	NM_005738	Hs.245540	NP_005729
seob5726	NM_005749	transducer of ERBB2, 1 (TOB1), mRNA /cds=(36,1073) /gb=Nm_005749 /gi=22035666 /ug=Hs.178137 /len=1830	NM_005749	Hs.178137	NP_005740



seoc6745	NM_005752	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECSF1), mRNA /cds=(80,673) /gb=Nm_005752 /gi=5031636 /ug=Hs.287364 /len=673	NM_005752	Hs.287364	NP_005743
ncr0791	NM_005759	abl-interactor 2 (ABI-2), mRNA /cds=(35,1462) /gb=Nm_005759 /gi=20127476 /ug=Hs.343575 /len=1735	NM_005759	Hs.343575	NP_005750
seob6291	NM_005760	CCAAT-box-binding transcription factor (CBF2), mRNA /cds=(12,3008) /gb=Nm_005760 /gi=5031624 /ug=Hs.184760 /len=3216	NM_005760	Hs.184760	NP_005751
fcr0707	NM_005770	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=Nm_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761
miob6029	NM_005770	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=Nm_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761

ncrc1537	NM_005783	ATP binding protein associated with cell differentiation (APACD), mRNA /cds=(130,810) /gb=Nm_005783 /gi=18104958 /ug=Hs.153884 /len=1494	NM_005783	Hs.153884	NP_005774
mioa1343	AK056862	cDNA FLJ32300 fis, clone PROST2002227, highly similar to M- PHASE PHOSPHOPROTEI N 10. /gb=AK056862 /gi=16552379 /ug=Hs.201676 /len=2334		Hs.201676	NP_005782
seob8627	X91648	mRNA for pur alpha extended 3'untranslated region		Hs.29117	NP_005850
ncrb8396	NM_005863	neuroepithelial cell transforming gene 1 (NET1), mRNA /cds=(147,1775) /gb=Nm_005863 /gi=19923326 /ug=Hs.25155 /len=3236	NM_005863	Hs.25155	NP_005854
ncrc9004	NM_005863	neuroepithelial cell transforming gene 1 (NET1), mRNA /cds=(147,1775) /gb=Nm_005863 /gi=19923326 /ug=Hs.25155 /len=3236	NM_005863	Hs.25155	NP_005854
seoc1218	NM_005892	formin-like (FMNL), mRNA /cds=(635,2026) /gb=Nm_005892 /gi=21735573 /ug=Hs.100217 /len=2384	NM_005892	Hs.100217	NP_005883

seoa9931	NM_005981	sarcoma amplified sequence (SAS), mRNA /cds=(155,787) /gb=Nm_005981 /gi=21264346 /ug=Hs.50984 /len=1809	NM_005981	Hs.50984	NP_005972
seob3090	NM_006002	ubiquitin carboxyl- terminal esterase L3 (ubiquitin thiolesterase) (UCLH3), mRNA /cds=(43,735) /gb=Nm_006002 /gi=20149578 /ug=Hs.77917 /len=911	NM_006002	Hs.77917	NP_005993
seoa4395	NM_006004	ubiquinol- cytochrome c reductase hinge protein (UQCRH), mRNA /cds=(37,312) /gb=Nm_006004 /gi=5174744 /ug=Hs.73818 /len=515	NM_006004	Hs.73818	NP_005995
fcrb4252	NM_006009	tubulin, alpha 3 (TUBA3), mRNA /cds=(100,1455) /gb=Nm_006009 /gi=17986282 /ug=Hs.433394 /len=1677	NM_006009	Hs.433394	NP_006000
ncrc9709	NM_006013	ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=Nm_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
ncr0634	NM_006029	paraneoplastic antigen MA1 (PNMA1), mRNA /cds=(665,1726) /gb=Nm_006029 /gi=14719429 /ug=Hs.194709 /len=2530	NM_006029	Hs.194709	NP_006020

seob1617	NM_006055	LanC lantibiotic synthetase component C-like 1 (bacterial) (LANCL1), mRNA /cds=(105,1304) /gb=Nm_006055 /gi=5174444 /ug=Hs.13351 /len=4544	NM_006055	Hs.13351	NP_006046
fcrb1618	NM_006082	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(68,1423) /gb=Nm_006082 /gi=5174476 /ug=Hs.334842 /len=1596	NM_006082	Hs.334842	NP_006073
seob4726	NM_006096	N-myc downstream regulated gene 1 (NDRG1), mRNA /cds=(111,1295) /gb=Nm_006096 /gi=5174656 /ug=Hs.75789 /len=3020	NM_006096	Hs.75789	NP_006087
miob9902	NM_000202	iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA /cds=(332,1984) /gb=Nm_000202 /gi=5360215 /ug=Hs.172458 /len=2504	NM_000202; NM_006123	Hs.172458	NP_006114
mioa4674	NM_006134	chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=Nm_006134 /gi=8659558 /ug=Hs.284142 /len=750	NM_006134	Hs.284142	NP_006125

seoa5784	NM_006148	LIM and SH3 protein 1 (LASP1), mRNA /cds=(76,861) /gb=Nm_006148 /gi=5453709 /ug=Hs.334851 /len=3846	NM_006148	Hs.334851	NP_006139
seoa4587	NM_006153	NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=Nm_006153 /gi=20070226 /ug=Hs.54589 /len=1947	NM_006153	Hs.54589	NP_006144
mioc7559	NM_006166	nuclear transcription factor Y, beta (NFYB), mRNA /cds=(101,724) /gb=Nm_006166 /gi=11496976 /ug=Hs.84928 /len=734	NM_006166	Hs.84928	NP_006157
fcrb0265	NM_006196	poly(rC) binding protein 1 (PCBP1), mRNA /cds=(178,1248) /gb=Nm_006196 /gi=14141164 /ug=Hs.2853 /len=1634	NM_006196	Hs.2853	NP_006187
seob7082	NM_006196	poly(rC) binding protein 1 (PCBP1), mRNA /cds=(178,1248) /gb=Nm_006196 /gi=14141164 /ug=Hs.2853 /len=1634	NM_006196	Hs.2853	NP_006187
ncrc9910	NM_006206	platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA /cds=(395,3664) /gb=Nm_006206 /gi=15451787 /ug=Hs.74615 /len=6633	NM_006206	Hs.74615	NP_006197

ncr4793	D30036	mRNA for phosphatidylinositol transfer protein (PI- TPalpha), complete cds	NM_006224	Hs.433429	NP_006215
seoc1906	NM_006241	protein phosphatase 1, regulatory (inhibitor) subunit 2 (PPP1R2), mRNA /cds=(235,852) /gb=Nm_006241 /gi=19923357 /ug=Hs.267819 /len=3355	NM_006241	Hs.267819	NP_006232
ncr0766	NM_006286	transcription factor Dp-2 (E2F dimerization partner 2) (TFDP2), mRNA /cds=(141,1301) /gb=Nm_006286 /gi=5454111 /ug=Hs.379018 /len=2320	NM_006286	Hs.379018	NP_006277
seoa1132	NM_006294	ubiquinol- cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=Nm_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
seob6535	NM_006317	brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=Nm_006317 /gi=5453749 /ug=Hs.79516 /len=1486	NM_006317	Hs.79516	NP_006308

fcrc4669	NM_006317	brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=Nm_006317 /gi=5453749 /ug=Hs.79516 /len=1486	NM_006317	Hs.79516	NP_006308
miob4238	NM_006335	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=Nm_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
seoc2504	NM_006335	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=Nm_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
ncrc0327	NM_006356	ATP synthase, H transporting, mitochondrial F0 complex, subunit d (ATP5H), mRNA /cds=(46,531) /gb=Nm_006356 /gi=5453558 /ug=Hs.49018 /len=628	NM_006356	Hs.49018	NP_006347
seoa5986	NM_006367	adenylyl cyclase- associated protein (CAP), mRNA /cds=(63,1490) /gb=Nm_006367 /gi=10938021 /ug=Hs.104125 /len=2614	NM_006367	Hs.104125	NP_006358

seob1420	NM_006369	MUF1 protein (MUF1), mRNA /cds=(1,1854) /gb=NM_006369 /gi=5453747 /ug=Hs.172210 /len=2165	NM_006369	Hs.172210	NP_006360
fcr4128	NM_006371	cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307	NM_006371	Hs.155481	NP_006362
miod2696	NM_006380	amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA /cds=(289,2046) /gb=NM_006380 /gi=18104961 /ug=Hs.84084 /len=6468	NM_006380	Hs.84084	NP_006371
seob4036	NM_006394	regulated in glioma (RIG), mRNA /cds=(26,358) /gb=NM_006394 /gi=5454007 /ug=Hs.278503 /len=2569	NM_006394	Hs.278503	NP_006385
mioa3945	NM_006402	hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605	NM_006402	Hs.433355	NP_006393
mioc4174	NM_006404	protein C receptor, endothelial (EPCR) (PROCR), mRNA /cds=(83,799) /gb=NM_006404 /gi=21361313 /ug=Hs.82353 /len=1381	NM_006404	Hs.82353	NP_006395



ncrc6712	NM_006407	vitamin A responsive; cytoskeleton related (JWA), mRNA /cds=(90,656) /gb=Nm_006407 /gi=7669496 /ug=Hs.92384 /len=2088	NM_006407	Hs.92384	NP_006398
miob4322	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=Nm_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
fcr2099	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=Nm_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
ncr8420	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=Nm_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
fcr6039	NM_006482	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA	NM_003583; NM_006482	Hs.173135	NP_006473
seoc4132	NM_006515	SET domain and mariner transposase fusion gene (SETMAR), mRNA	NM_006515	Hs.265855	NP_006506

miob0178	NM_006519	t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=Nm_006519 /gi=5730084 /ug=Hs.266940 /len=713	NM_006519	Hs.266940	NP_006510
fcr3322	NM_006533	melanoma inhibitory activity (MIA), mRNA /cds=(72,467) /gb=Nm_006533 /gi=5729924 /ug=Hs.279651 /len=538	NM_006533	Hs.279651	NP_006524
fcrb1633	NM_006559	KH domain containing, RNA binding, signal transduction associated 1 (KHDRBS1), mRNA /cds=(107,1438) /gb=Nm_006559 /gi=5730026 /ug=Hs.119537 /len=2685	NM_006559	Hs.119537	NP_006550
mioa6734	NM_006590	SnRNP assembly defective 1 (SAD1), mRNA /cds=(493,1467) /gb=Nm_006590 /gi=5730024 /ug=Hs.12820 /len=2166	NM_006590	Hs.12820	NP_006581
seob3303	NM_006603	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=Nm_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
mioc6925	NM_006603	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=Nm_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594

mioa5085	NM_006620	HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=Nm_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
miob9228	NM_006621	hydrolase-like 1 (AHCYL1), mRNA /cds=(369,1961) /gb=Nm_006621 /gi=21361646 /ug=Hs.4113 /len=2677	NM_006621	Hs.4113	NP_006612
seoa3514	NM_006628	cyclic AMP phosphoprotein, 19 kD (ARPP-19), mRNA /cds=(125,463) /gb=Nm_006628 /gi=19923363 /ug=Hs.7351 /len=5171	NM_006628	Hs.7351	NP_006619
seoa9709	NM_006636	methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydro folate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=Nm_006636 /gi=13699869 /ug=Hs.154672 /len=2154	NM_006636	Hs.154672	NP_006627
mioc3011	NM_006646	WAS protein family, member 3 (WASF3), mRNA /cds=(179,1687) /gb=Nm_006646 /gi=21237780 /ug=Hs.82318 /len=4768	NM_006646	Hs.82318	NP_006637

fcr2619	NM_006649	serologically defined colon cancer antigen 16 (SDCCAG16), mRNA /cds=(29,2344) /gb=Nm_006649 /gi=21361347 /ug=Hs.271926 /len=2509	NM_006649	Hs.271926	NP_006640
fcr2090	NM_006700	FLN29 gene product (FLN29), mRNA /cds=(55,1803) /gb=Nm_006700 /gi=5729827 /ug=Hs.5148 /len=2618	NM_006700	Hs.5148	NP_006691
seob1586	NM_006718	pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=Nm_006718 /gi=27894292 /ug=Hs.75825 /len=4816	NM_002656; NM_006718	Hs.75825	NP_006709
seob7015	NM_006734	immunodeficiency virus type I enhancer binding protein 2 (HIVBP2), mRNA /cds=(16,7518) /gb=Nm_006734 /gi=19923373 /ug=Hs.75063 /len=9175	NM_006734	Hs.75063	NP_006725
ncr7792	NM_006744	retinol binding protein 4, plasma (RBP4), mRNA /cds=(89,688) /gb=Nm_006744 /gi=8400727 /ug=Hs.418083 /len=919	NM_006744	Hs.418083	NP_006735
fcr2607	NM_006758	U2(RNU2) small nuclear RNA auxiliary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=Nm_006758 /gi=5803206 /ug=Hs.271687 /len=904	NM_006758	Hs.271687	NP_006749

fcrb8901	NM_006758	U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=Nm_006758 /gi=5803206 /ug=Hs.271687 /len=904	NM_006758	Hs.271687	NP_006749
fcrb7528	NM_006796	AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, mRNA /cds=(114,2507) /gb=Nm_006796 /gi=5802969 /ug=Hs.29385 /len=2963	NM_006796	Hs.29385	NP_006787
seoc2221	NM_006806	BTG family, member 3 (BTG3), mRNA /cds=(155,1045) /gb=Nm_006806 /gi=21361363 /ug=Hs.77311 /len=1511	NM_006806	Hs.77311	NP_006797
miob6087	NM_006810	for protein disulfide isomerase-related (PDIR), mRNA /cds=(57,1616) /gb=Nm_006810 /gi=5803120 /ug=Hs.76901 /len=1693	NM_006810	Hs.76901	NP_006801
ncrc5877	NM_006822	RAB40B, member RAS oncogene family (RAB40B), mRNA /cds=(46,882) /gb=Nm_006822 /gi=5803162 /ug=Hs.302498 /len=1673	NM_006822	Hs.302498	NP_006813

hfcr6370	NM_006825	cytoskeleton-associated protein 4 (CKAP4), mRNA /cds=(85,1893) /gb=Nm_006825 /gi=19920316 /ug=Hs.74368 /len=2913	NM_006825	Hs.74368	NP_006816
seoa5520	NM_006826	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(120,857) /gb=Nm_006826 /gi=21464103 /ug=Hs.74405 /len=2166	NM_006826	Hs.74405	NP_006817
seoa2819	NM_006827	transmembrane trafficking protein (TMP21), mRNA	NM_006827	Hs.74137	NP_006818
mioa3668	NM_006828	RNA helicase family (RNAH), mRNA /cds=(39,6647) /gb=Nm_006828 /gi=24307916 /ug=Hs.48295 /len=7315	NM_006828	Hs.48295	NP_006819
seoa6732	Z24725	mitogen inducible gene mig-2, complete CDS. /cds=(1,2165) /gb=Z24725 /gi=505032 /ug=Hs.75260 /len=3270	NM_006832	Hs.75260	NP_006823
ncr0144	NM_006860	RAB, member of RAS oncogene family-like 4 (RABL4), mRNA /cds=(364,921) /gb=Nm_006860 /gi=9257237 /ug=Hs.50267 /len=1021	NM_006860	Hs.50267	NP_006851

mioa0192	NM_006870	destrin (actin depolymerizing factor) (DSTN), mRNA /cds=(73,570) /gb=Nm_006870 /gi=6466447 /ug=Hs.408576 /len=1439	NM_006870	Hs.408576	NP_006861
seoa9016	NM_006918	sterol-C5-desaturase (ERG3 delta-5-desaturase fungal)-like (SC5DL), mRNA /cds=(49,948) /gb=Nm_006918 /gi=10800413 /ug=Hs.288031 /len=2092	NM_006918	Hs.288031	NP_008849
ncrc9428	NM_006925	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=Nm_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856
hfcr1964	NM_006985	nuclear pore complex interacting protein (NPIP), mRNA /cds=(1,1053) /gb=Nm_006985 /gi=5902013 /ug=Hs.251928 /len=1070	NM_006985	Hs.251928	NP_008916
hfcr0292	NM_007015	chondromodulin I precursor (CHM-I), mRNA /cds=(1,1005) /gb=Nm_007015 /gi=5901931 /ug=Hs.97932 /len=1328	NM_007015	Hs.97932	NP_008946
ncr4194	NM_007043	HIV-1 rev binding protein 2 (HRB2), mRNA /cds=(30,1175) /gb=Nm_007043 /gi=21359979 /ug=Hs.154762 /len=1527	NM_007043	Hs.154762	NP_008974

hfc3615	NM_007097	clathrin, light polypeptide (Lcb) (CLTB), transcript variant brain, mRNA /cds=(173,862) /gb=Nm_007097 /gi=6005994 /ug=Hs.380749 /len=1134	NM_001834; NM_007097	Hs.380749	NP_009028
seob7622	NM_007100	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) /gb=Nm_007100 /gi=6005716 /ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
ncrc4047	NM_007106	ubiquitin-like 3 (UBL3), mRNA /cds=(110,463) /gb=Nm_007106 /gi=6005927 /ug=Hs.173091 /len=3323	NM_007106	Hs.173091	NP_009037
seoc2696	NM_007111	transcription factor Dp-1 (TFDP1), mRNA /cds=(222,1454) /gb=Nm_007111 /gi=21361419 /ug=Hs.79353 /len=2394	NM_007111	Hs.79353	NP_009042
miob6103	AK022561	cDNA FLJ12499 fis, clone NT2RM2001671, highly similar to Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA	NM_007159	Hs.4007	NP_009090



mioc1122	NM_007266	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=Nm_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
seoa7212	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=Nm_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
seoc0056	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=Nm_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
fcrc2457	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=Nm_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
seob2081	NM_007278	GABA(A) receptor-associated protein (GABARAP), mRNA /cds=(105,458) /gb=Nm_007278 /gi=6005763 /ug=Hs.7719 /len=924	NM_007278	Hs.7719	NP_009209

mioa9648	NM_000345	synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA /cds=(47,469) /gb=Nm_000345 /gi=6806896 /ug=Hs.76930 /len=1543	NM_000345; NM_007308	Hs.76930	NP_009292
ncrc1653	NM_004799	MAD, mothers against decapentaplegic (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA /cds=(439,4410) /gb=Nm_004799 /gi=4759059 /ug=Hs.194716 /len=4839	NM_004799; NM_007323; NM_007324	Hs.194716	NP_015563
mioa3572	NM_007361	nidogen 2 (osteonidogen) (NID2), mRNA /cds=(1,4131) /gb=Nm_007361 /gi=6679055 /ug=Hs.82733 /len=4829	NM_007361	Hs.82733	NP_031387
seoa8993	NM_007362	nuclear cap binding protein subunit 2, 20kDa (NCBP2), mRNA /cds=(27,497) /gb=Nm_007362 /gi=19923386 /ug=Hs.240770 /len=2120	NM_007362	Hs.240770	NP_031388
ncrb6261	NM_007366	phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=Nm_007366 /gi=19923388 /ug=Hs.171945 /len=5633	NM_007366	Hs.171945	NP_031392

miod1707	J04806	Mus musculus osteopontin precursor, mRNA, complete cds	NM_009263	Mm.260317	NP_033289
seob5431	NM_009405	Mus musculus troponin I, skeletal, fast 2 (Tnni2), mRNA	NM_009405	Mm.39469	NP_033431
miob4574	NM_012086	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=Nm_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
seob6064	NM_012096	adaptor protein containing pH domain, PTB domain and leucine zipper motif (APPL), mRNA /cds=(59,2188) /gb=Nm_012096 /gi=6912241 /ug=Hs.27413 /len=5970	NM_012096	Hs.27413	NP_036228
seob5223	NM_012098	angiopoietin-like 2 (ANGPTL2), mRNA /cds=(22,1503) /gb=Nm_012098 /gi=6912235 /ug=Hs.8025 /len=1518	NM_012098	Hs.8025	NP_036230
miod0992	NM_012124	cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1), mRNA /cds=(85,1083) /gb=Nm_012124 /gi=6912303 /ug=Hs.22857 /len=2058	NM_012124	Hs.22857	NP_036256

miob3591	NM_012141	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26 (DDX26), mRNA /cds=(477,3140) /gb=Nm_012141 /gi=11024693 /ug=Hs.58570 /len=3690	NM_012141	Hs.58570	NP_036273
fcrb2622	NM_012158	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=Nm_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
ncr8538	NM_012158	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=Nm_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
ncrc9959	AF307332	meningioma-expressed antigen 5s splice variant mRNA, complete cds	NM_012215	Hs.5734	NP_036347
fcr6631	NM_012245	SKI-interacting protein (SNW1), mRNA /cds=(28,1638) /gb=Nm_012245 /gi=18860912 /ug=Hs.79008 /len=2146	NM_012245	Hs.79008	NP_036377
fcr0706	NM_012268	phospholipase D3 (PLD3), mRNA /cds=(488,1801) /gb=Nm_012268 /gi=7110640 /ug=Hs.74573 /len=2131	NM_012268	Hs.74573	NP_036400
mioc2868	AB023204	mRNA for KIAA0987 protein, partial cds	NM_012307	Hs.103839	NP_036439

miob8341	NM_012308	F-box and leucine-rich repeat protein 11 (FBXL11), mRNA /cds=(107,3595) /gb=Nm_012308 /gi=16306579 /ug=Hs.219614 /len=6210	NM_012308	Hs.219614	NP_036440
mioa6583	NM_012322	U6 snRNA-associated Sm-like protein (LSM5), mRNA /cds=(1,276) /gb=Nm_012322 /gi=6912487 /ug=Hs.227280 /len=749	NM_012322	Hs.227280	NP_036454
seoa4246	NM_012341	G protein-binding protein CRFG (CRFG), mRNA /cds=(24,1925) /gb=Nm_012341 /gi=6912531 /ug=Hs.215766 /len=2414	NM_012341	Hs.215766	NP_036473
mioa3092	NM_012414	rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA /cds=(74,4255) /gb=Nm_012414 /gi=19923789 /ug=Hs.197289 /len=5129	NM_012414	Hs.197289	NP_036546
ncrc6817	NM_013285	nucleolar GTPase (HUMAQUANTIG), mRNA /cds=(80,2275) /gb=Nm_013285 /gi=7019418 /ug=Hs.75528 /len=2331	NM_013285	Hs.75528	NP_037417
mioa8380	NM_013330	NME7 (NME7), mRNA /cds=(93,1223) /gb=Nm_013330 /gi=7242158 /ug=Hs.274479 /len=1475	NM_013330	Hs.274479	NP_037462

miob9336	NM_013386	hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA /cds=(25,315) /gb=Nm_013386 /gi=9558726 /ug=Hs.24713 /len=1294	NM_013386	Hs.24713	NP_037518
ncrc3049	NM_013989	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=Nm_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_000793; NM_013989	Hs.154424	NP_054644
seob1268	NM_013989	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=Nm_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_000793; NM_013989	Hs.154424	NP_054644
seoa3164	NM_014028	HSPC019 protein (HSPC019), mRNA /cds=(58,444) /gb=Nm_014028 /gi=7661737 /ug=Hs.163724 /len=2411	NM_014028	Hs.163724	NP_054747
ncrc0838	NM_014033	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=Nm_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752

seob5528	NM_014056	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=Nm_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
seoa7223	NM_014065	HT001 protein (HT001), mRNA /cds=(242,1204) /gb=Nm_014065 /gi=7661837 /ug=Hs.279040 /len=1402	NM_014065	Hs.279040	NP_054784
seoa9997	NM_014071	nuclear receptor coactivator 6 (NCOA6), mRNA /cds=(2755,8760) /gb=Nm_014071 /gi=7661975 /ug=Hs.159613 /len=9301	NM_014071	Hs.159613	NP_054790
seob4057	NM_014112	trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=Nm_014112 /gi=7657658 /ug=Hs.26102 /len=10011	NM_014112	Hs.26102	NP_054831
seob2148	NM_014153	zinc-finger protein AY163807 (HSPC055), mRNA /cds=(199,3114) /gb=Nm_014153 /gi=27414496 /ug=Hs.179898 /len=3859	NM_014153	Hs.179898	NP_054872
seob6386	NM_014168	HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=Nm_014168 /gi=7661791 /ug=Hs.273063 /len=963	NM_014168	Hs.273063	NP_054887

ncr3751	NM_014206	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=Nm_014206 /gi=7656933 /ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
miod3500	NM_014206	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=Nm_014206 /gi=7656933 /ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
fcrb3963	NM_014220	transmembrane 4 superfamily member 1 (TM4SF1), mRNA /cds=(102,710) /gb=Nm_014220 /gi=21265100 /ug=Hs.351316 /len=1583	NM_014220	Hs.351316	NP_055035
fcr2601	NM_014220	transmembrane 4 superfamily member 1 (TM4SF1), mRNA /cds=(102,710) /gb=Nm_014220 /gi=21265100 /ug=Hs.351316 /len=1583	NM_014220	Hs.351316	NP_055035
mioa0461	NM_014251	solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA /cds=(138,2165) /gb=Nm_014251 /gi=7657580 /ug=Hs.9599 /len=3150	NM_014251	Hs.9599	NP_055066
seob1187	NM_014280	DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=Nm_014280 /gi=7657610 /ug=Hs.433540 /len=1525	NM_014280	Hs.433540	NP_055095



mioa2478	NM_014300	signal peptidase complex (18kD) (SPC18), mRNA /cds=(78,617) /gb=Nm_014300 /gi=7657608 /ug=Hs.9534 /len=1105	NM_014300	Hs.9534	NP_055115
seoa1844	NM_014302	Sec61 gamma (SEC61G), mRNA /cds=(91,297) /gb=Nm_014302 /gi=14591933 /ug=Hs.9950 /len=482	NM_014302	Hs.9950	NP_055117
seob5054	NM_014306	hypothetical protein (HSPC117), mRNA /cds=(76,1593) /gb=Nm_014306 /gi=7657014 /ug=Hs.10729 /len=2005	NM_014306	Hs.10729	NP_055121
seob5562	NM_014315	kelch domain containing 2 (KLHDC2), mRNA /cds=(317,1537) /gb=Nm_014315 /gi=7657300 /ug=Hs.20597 /len=1721	NM_014315	Hs.20597	NP_055130
ncr3404	NM_014319	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=Nm_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014319	Hs.7256	NP_055134
seoa6620	NM_014325	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=Nm_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140

ncr0340	NM_014325	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=Nm_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
miod6781	NM_014367	hypothetical protein, estradiol-induced (E2IG5), mRNA /cds=(71,643) /gb=Nm_014367 /gi=21361426 /ug=Hs.5243 /len=1215	NM_014367	Hs.5243	NP_055182
miob3953	NM_014372	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=Nm_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
miob6713	NM_014415	zinc finger protein (ZNF-U69274), mRNA /cds=(162,3323) /gb=Nm_014415 /gi=7657702 /ug=Hs.301956 /len=5052	NM_014415	Hs.301956	NP_055230
seob1008	NM_014445	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 (SERP1), mRNA /cds=(316,516) /gb=Nm_014445 /gi=19923408 /ug=Hs.76698 /len=2488	NM_014445	Hs.76698	NP_055260
hfcr2378	AK093929	cDNA FLJ36610 fis, clone TRACH2015987		Hs.76698	NP_055260

seob4145	NM_014497	NP220 nuclear protein (NP220), mRNA /cds=(315,6251) /gb=Nm_014497 /gi=21626467 /ug=Hs.169984 /len=6570	NM_014497	Hs.169984	NP_055312
ncr2035	NM_014497	NP220 nuclear protein (NP220), mRNA /cds=(315,6251) /gb=Nm_014497 /gi=21626467 /ug=Hs.169984 /len=6570	NM_014497	Hs.169984	NP_055312
seoc0535	AL137543	mRNA; cDNA DKFZp434P2119 (from clone DKFZp434P2119); partial cds	NM_014547	Hs.22826	NP_055362
ncrc3313	NM_014572	LATS, large tumor suppressor, 2 (Drosophila) (LATS2), mRNA /cds=(375,3641) /gb=Nm_014572 /gi=18959199 /ug=Hs.432314 /len=4098	NM_014572	Hs.432314	NP_055387
ncrc3011	NM_014585	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=Nm_014585 /gi=19923794 /ug=Hs.5944 /len=3333	NM_014585	Hs.5944	NP_055400
ncr1712	NM_014606	hect domain and RLD 3 (HERC3), mRNA /cds=(167,3319) /gb=Nm_014606 /gi=7657151 /ug=Hs.35804 /len=4894	NM_014606	Hs.35804	NP_055421

ncrc5149	NM_014670	basic leucine zipper and W2 domains 1 (BZW1), mRNA /cds=(81,1340) /gb=Nm_014670 /gi=7661849 /ug=Hs.155291 /len=2998	NM_014670	Hs.155291	NP_055485
ncrc4597	NM_014685	endoplasmic reticulum stress- inducible, ubiquitin- like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=Nm_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
hfcr6501	NM_014718	calsyntenin 3 (CLSTN3), mRNA /cds=(539,3445) /gb=Nm_014718 /gi=7662267 /ug=Hs.107809 /len=4300	NM_014718	Hs.107809	NP_055533
fcrc0857	NM_014726	ProSAPiP2 protein (ProSAPiP2), mRNA /cds=(850,2697) /gb=Nm_014726 /gi=7662301 /ug=Hs.94790 /len=4121	NM_014726	Hs.94790	NP_055541
seoa1857	NM_014739	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=Nm_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554
mioa4552	NM_014752	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=Nm_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567

fcr0609	NM_014758	KIAA0254 gene product (KIAA0254), mRNA /cds=(529,3507) /gb=Nm_014758 /gi=7662025 /ug=Hs.76906 /len=6049	NM_014758	Hs.76906	NP_055573
seoa7078	NM_014765	translocase of outer mitochondrial membrane 20 (yeast) (KIAA0016), mRNA /cds=(102,539) /gb=Nm_014765 /gi=7657256 /ug=Hs.75187 /len=3259	NM_014765	Hs.75187	NP_055580
fcrb1714	NM_014765	translocase of outer mitochondrial membrane 20 (yeast) (KIAA0016), mRNA /cds=(102,539) /gb=Nm_014765 /gi=7657256 /ug=Hs.75187 /len=3259	NM_014765	Hs.75187	NP_055580
seoa1080	NM_014797	KIAA0441 gene product (KIAA0441), mRNA /cds=(169,2262) /gb=Nm_014797 /gi=7662127 /ug=Hs.32511 /len=5597	NM_014797	Hs.32511	NP_055612
ncrc5072	NM_014820	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=Nm_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635

ncr0046	NM_014820	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=Nm_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635
seob8660	NM_014886	hypothetical protein YR-29 (YR-29), mRNA /cds=(85,867) /gb=Nm_014886 /gi=21359901 /ug=Hs.8170 /len=1105	NM_014886	Hs.8170	NP_055701
ncrc6382	NM_014929	KIAA0971 protein (KIAA0971), mRNA /cds=(59,2005) /gb=Nm_014929 /gi=7662421 /ug=Hs.84429 /len=4999	NM_014929	Hs.84429	NP_055744
ncr1640	NM_014944	calsyntenin 1 (CLSTN1), mRNA /cds=(794,3739) /gb=Nm_014944 /gi=7662373 /ug=Hs.29665 /len=5219	NM_014944	Hs.29665	NP_055759
seob1385	NM_014949	KIAA0907 protein (KIAA0907), mRNA /cds=(27,1721) /gb=Nm_014949 /gi=7662371 /ug=Hs.24656 /len=4500	NM_014949	Hs.24656	NP_055764
mioc7444	NM_014992	dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=Nm_014992 /gi=21071076 /ug=Hs.197751 /len=4256	NM_014992	Hs.197751	NP_055807

ncr3237	NM_015001	SMART/HDAC1 associated repressor protein (SHARP), mRNA /cds=(205,11199) /gb=Nm_015001 /gi=14790189 /ug=Hs.184245 /len=12227	NM_015001	Hs.184245	NP_055816
ncr2484	NM_015017	pVHL-interacting deubiquitinating enzyme 1 (VDU1), mRNA /cds=(262,2997) /gb=Nm_015017 /gi=21489974 /ug=Hs.173694 /len=4323	NM_015017	Hs.173694	NP_055832
mioc2529	H09059	yl96f11.s1 Soares infant brain 1NIB cDNA clone IMAGE:45943 3' similar to contains Alu repetitive element; mRNA sequence /clone=IMAGE:45943 /clone_end=3' /gb=H09059 /gi=873881 /ug=Hs.438854 /len=494		Hs.438854	NP_055833
seob8501	NM_015023	KIAA1037 protein (KIAA1037), mRNA /cds=(399,2429) /gb=Nm_015023 /gi=22095348 /ug=Hs.172825 /len=4305	NM_015023	Hs.172825	NP_055838
ncrb4439	AB014540	mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824		Hs.153026	NP_055870

fcrc3760	AB020671	mRNA for KIAA0864 protein, partial cds. /cds=(1,4210) /gb=AB020671 /gi=20521679 /ug=Hs.433523 /len=4872		Hs.433523	NP_055949
miod7225	NM_015153	PHD finger protein 3 (PHF3), mRNA /cds=(28,6147) /gb=NK_015153 /gi=7662017 /ug=Hs.78893 /len=6948	NM_015153	Hs.78893	NP_055968
seoc2506	AF545571	sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699	NM_015170	Hs.70823	NP_055985
miob2947	NM_015208	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NK_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023
ncrc2472	NM_015216	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NK_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
miob0589	NM_015254	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NK_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069



miod5505	NM_015310	ADP-ribosylation factor guanine nucleotide factor 6 (EFA6R), mRNA /cds=(53,1657) /gb=Nm_015310 /gi=7662395 /ug=Hs.6763 /len=6722	NM_015310	Hs.6763	NP_056125
seoa1483	NM_015355	joined to JAZF1 (JJAZ1), mRNA /cds=(195,2414) /gb=Nm_015355 /gi=15149469 /ug=Hs.197803 /len=4441	NM_015355	Hs.197803	NP_056170
miod3254	NM_015383	hypothetical protein DJ328E19.C1.1 (DJ328E19.C1.1), mRNA /cds=(18,2783) /gb=Nm_015383 /gi=7657016 /ug=Hs.218329 /len=3689	NM_015383	Hs.218329	NP_056198
ncrb6680	NM_015387	preimplantation protein 3 (PREI3), mRNA /cds=(14,598) /gb=Nm_015387 /gi=7661623 /ug=Hs.107942 /len=2686	NM_015387	Hs.107942	NP_056202
miod7478	AB058721	mRNA for KIAA1818 protein, partial cds	NM_015409	Hs.306094	NP_056224
mioc6320	NM_015436	zinc finger protein 363 (ZNF363), mRNA /cds=(27,812) /gb=Nm_015436 /gi=24308060 /ug=Hs.48297 /len=1543	NM_015436	Hs.48297	NP_056251
seob4545	NM_015470	KIAA0857 protein (KIAA0857), mRNA /cds=(241,2202) /gb=Nm_015470 /gi=24308074 /ug=Hs.24557 /len=4340	NM_015470	Hs.24557	NP_056285

miob2968	NM_015497	DKFZP564G2022 protein (DKFZP564G2022) , mRNA /cds=(43,1710) /gb=Nm_015497 /gi=13794264 /ug=Hs.16492 /len=2286	NM_015497	Hs.16492	NP_056312
fcrb1575	NM_015507	EGF-like-domain, multiple 6 (EGFL6), mRNA /cds=(241,1902) /gb=Nm_015507 /gi=13124887 /ug=Hs.12844 /len=2398	NM_015507	Hs.12844	NP_056322
miob6485	NM_015555	coactivator for steroid receptors (COASTER), mRNA /cds=(226,3267) /gb=Nm_015555 /gi=20127147 /ug=Hs.172329 /len=4999	NM_015555	Hs.172329	NP_056370
seob7039	NM_015556	signal-induced proliferation- associated 1 like 1 (KIAA0440), mRNA /cds=(349,5763) /gb=Nm_015556 /gi=7662125 /ug=Hs.172180 /len=6028	NM_015556	Hs.172180	NP_056371
seob5319	NM_015577	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=Nm_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392

miod5894	NM_015578	DKFZP434D1335 protein (DKFZP434D1335) , mRNA /cds=(78,1469) /gb=Nm_015578 /gi=24308092 /ug=Hs.8258 /len=3389	NM_015578	Hs.8258	NP_056393
fcrb7234	AL117478	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	NM_015597	Hs.239370	NP_056412
fcrb6382	AL117478	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	NM_015597	Hs.239370	NP_056412
mioa8192	NM_015602	DKFZP586G011 protein (LAP1B), mRNA /cds=(56,1444) /gb=Nm_015602 /gi=24308098 /ug=Hs.234265 /len=3275	NM_015602	Hs.234265	NP_056417
seob7419	BC028715	erythroid differentiation- related factor 1, mRNA (cDNA clone IMAGE:4838997), partial cds		Hs.227209	NP_056423

seoa9792	AB036063	p53R2 mRNA for ribonucleotide reductase, complete cds. /cds=(245,1300) /gb=AB036063 /gi=7229085 /ug=Hs.94262 /len=4955		Hs.94262	NP_056528
seoa3108	NM_015933	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=Nm_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017
miob8825	NM_015933	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=Nm_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017
mioc8917	NM_015934	nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA /cds=(1,1590) /gb=Nm_015934 /gi=7706253 /ug=Hs.119908 /len=1590	NM_015934	Hs.119908	NP_057018
ncrc0336	NM_015938	CGI-07 protein (CGI-07), mRNA /cds=(124,1635) /gb=Nm_015938 /gi=19923795 /ug=Hs.181022 /len=2762	NM_015938	Hs.181022	NP_057022
fcrb8225	AK023560	cDNA FLJ13498 fis, clone PLACE1004550, highly similar to CGI-20 protein mRNA	NM_015949	Hs.107387	NP_057033
seoa5685	NM_015952	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=Nm_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036

seoc1402	NM_015960	CGI-32 protein (CGI-32), mRNA /cds=(103,924) /gb=Nm_015960 /gi=7705727 /ug=Hs.16606 /len=1323	NM_015960	Hs.16606	NP_057044
ncrc2484	NM_015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=Nm_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
ncrb8063	NM_015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=Nm_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
ncrc2600	NM_004830	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa (CRSP3), mRNA /cds=(120,4226) /gb=Nm_004830 /gi=7019352 /ug=Hs.29679 /len=5176	NM_004830; NM_015979	Hs.29679	NP_057063
mioa6739	NM_015984	ubiquitin carboxyl- terminal hydrolase L5 (UCHL5), mRNA /cds=(132,1121) /gb=Nm_015984 /gi=7706752 /ug=Hs.171581 /len=1728	NM_015984	Hs.171581	NP_057068

hfcr2708	NM_016001	CGI-48 protein (CGI-48), mRNA /cds=(108,1673) /gb=Nm_016001 /gi=7705764 /ug=Hs.6153 /len=1873	NM_016001	Hs.6153	NP_057085
seob1526	NM_016019	CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=Nm_016019 /gi=7706309 /ug=Hs.7194 /len=2296	NM_016019	Hs.7194	NP_057103
seoa3847	NM_016026	retinol dehydrogenase 11 (all-trans and 9-cis) (RDH11), mRNA /cds=(41,997) /gb=Nm_016026 /gi=20070271 /ug=Hs.179817 /len=2538	NM_016026	Hs.179817	NP_057110
hfcr4007	NM_016041	CGI-101 protein (F- LAN-1), mRNA /cds=(7,636) /gb=Nm_016041 /gi=7705603 /ug=Hs.286131 /len=1123	NM_016041	Hs.286131	NP_057125
seoa6226	NM_016045	chromosome 20 open reading frame 45 (C20orf45), mRNA /cds=(85,720) /gb=Nm_016045 /gi=7705609 /ug=Hs.3945 /len=2535	NM_016045	Hs.3945	NP_057129
miod5080	NM_016076	CGI-146 protein (PNAS-4), mRNA /cds=(59,640) /gb=Nm_016076 /gi=7705641 /ug=Hs.42409 /len=1108	NM_016076	Hs.42409	NP_057160

miod2996	NM_016077	CGI-147 protein (CGI-147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806	NM_016077	Hs.12677	NP_057161
mioc8153	NM_016077	CGI-147 protein (CGI-147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806	NM_016077	Hs.12677	NP_057161
mioa6580	NM_016078	CGI-148 protein (CGI-148), mRNA /cds=(300,845) /gb=NM_016078 /gi=7705643 /ug=Hs.87295 /len=2070	NM_016078	Hs.87295	NP_057162
ncr9044	AF125100	HSPC039 protein mRNA, complete cds /cds=(81,329) /gb=AF125100 /gi=5106995 /ug=Hs.406542 /len=1583	NM_016097	Hs.406542	NP_057181
ncrc9159	NM_016098	brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988	NM_016098	Hs.108725	NP_057182
miob6228	NM_016123	interleukin-1 receptor-associated kinase 4 (IRAK4), mRNA /cds=(50,1432) /gb=NM_016123 /gi=7705840 /ug=Hs.142295 /len=2817	NM_016123	Hs.142295	NP_057207
ncrc1623	AF527632	INSIG-2 membrane protein mRNA, complete cds	NM_016133	Hs.7089	NP_057217

seob6872	NM_016147	protein phosphatase methylesterase-1 (PME-1), mRNA /cds=(100,1260) /gb=Nm_016147 /gi=7706644 /ug=Hs.63304 /len=2484	NM_016147	Hs.63304	NP_057231
ncr5760	NM_016183	chromosome 1 open reading frame 33 (C1orf33), mRNA /cds=(32,751) /gb=Nm_016183 /gi=18490986 /ug=Hs.274201 /len=1185	NM_016183	Hs.274201	NP_057267
fcr2860	NM_016207	cleavage and polyadenylation specific factor 3, 73kDa (CPSF3), mRNA /cds=(36,2090) /gb=Nm_016207 /gi=21314666 /ug=Hs.16251 /len=2286	NM_016207	Hs.16251	NP_057291
ncr0438	NM_014933	yeast Sec31p (KIAA0905), mRNA /cds=(54,3716) /gb=Nm_014933 /gi=7662369 /ug=Hs.70266 /len=4129	NM_014933; NM_016211	Hs.70266	NP_057295
seob6000	NM_016217	hHDC for of Drosophila headcase (HDCL), mRNA /cds=(286,1917) /gb=Nm_016217 /gi=7706434 /ug=Hs.6679 /len=5634	NM_016217	Hs.6679	NP_057301
ncr9061	NM_016224	sorting nexin 9 (SNX9), mRNA /cds=(174,1961) /gb=Nm_016224 /gi=23111056 /ug=Hs.7905 /len=4200	NM_016224	Hs.7905	NP_057308



ncrb2053	NM_016227	chromosome 1 open reading frame 9 (C1orf9), mRNA /cds=(125,4342) /gb=Nm_016227 /gi=7705321 /ug=Hs.108636 /len=5919	NM_014283; NM_016227	Hs.108636	NP_057311
fcrc3826	NM_016274	CK2 interacting protein 1; HQ0024c protein (CKIP-1), mRNA /cds=(285,1514) /gb=Nm_016274 /gi=21361610 /ug=Hs.173380 /len=1633	NM_016274	Hs.173380	NP_057358
seoa5121	NM_016304	chromosome 15 open reading frame 15 (C15orf15), mRNA /cds=(144,635) /gb=Nm_016304 /gi=18491027 /ug=Hs.284162 /len=1487	NM_016304	Hs.284162	NP_057388
mioc6997	NM_016306	DnaJ (Hsp40) subfamily B, member 11 (DNAJB11), mRNA /cds=(160,1236) /gb=Nm_016306 /gi=25014110 /ug=Hs.278605 /len=1621	NM_016306	Hs.278605	NP_057390
miob4333	NM_016316	REV1-like (yeast) (REV1L), mRNA /cds=(213,3968) /gb=Nm_016316 /gi=7706680 /ug=Hs.110347 /len=4276	NM_016316	Hs.110347	NP_057400
seob0096	NM_016322	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=Nm_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406

fcrb1457	NM_016322	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=Nm_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406
ncrc2172	AW292456	UI-H-BI2-agp-f-12- 0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:272 5031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745		Hs.437793	NP_057446
miod4184	NM_016403	hypothetical protein HSPC148 (HSPC148), mRNA /cds=(64,753) /gb=Nm_016403 /gi=7705474 /ug=Hs.42743 /len=1046	NM_016403	Hs.42743	NP_057487
seob4928	NM_016441	cysteine-rich motor neuron 1 (CRIM1), mRNA /cds=(40,3150) /gb=Nm_016441 /gi=10092638 /ug=Hs.19280 /len=5601	NM_016441	Hs.19280	NP_057525
miod1377	NM_016441	cysteine-rich motor neuron 1 (CRIM1), mRNA /cds=(40,3150) /gb=Nm_016441 /gi=10092638 /ug=Hs.19280 /len=5601	NM_016441	Hs.19280	NP_057525

miob0167	NM_016474	hypothetical protein LOC51244 (LOC51244), mRNA /cds=(340,1233) /gb=Nm_016474 /gi=24475969 /ug=Hs.158006 /len=1614	NM_016474	Hs.158006	NP_057558
miod7486	BC025306	clone IMAGE:4893383, mRNA, partial cds	NM_016488	Hs.281428	NP_057572
ncr3968	NM_016505	putative S1 RNA binding domain protein (PS1D), mRNA /cds=(137,862) /gb=Nm_016505 /gi=21361575 /ug=Hs.54971 /len=1602	NM_016505	Hs.54971	NP_057589
hfcr5220	NM_016581	ECSIT (LOC51295), mRNA /cds=(78,1373) /gb=Nm_016581 /gi=20149632 /ug=Hs.22199 /len=1668	NM_016581	Hs.22199	NP_057665
seoa9729	NM_016587	chromobox 3 (HP1 gamma Drosophila) (CBX3), transcript variant 2, mRNA /cds=(152,703) /gb=Nm_016587 /gi=20544150 /ug=Hs.406384 /len=1851	NM_007276; NM_016587	Hs.406384	NP_057671
fcrb7340	NM_016594	FK506 binding protein 11, 19 kDa (FKBP11), mRNA /cds=(73,678) /gb=Nm_016594 /gi=7706130 /ug=Hs.24048 /len=727	NM_016594	Hs.24048	NP_057678

miob1134	NM_016608	ALEX1 protein (ALEX1), mRNA /cds=(372,1733) /gb=Nm_016608 /gi=7706142 /ug=Hs.9728 /len=2141	NM_016608	Hs.9728	NP_057692
ncrc6332	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=Nm_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
miob3354	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=Nm_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
miod1323	NM_016627	hypothetical protein LOC51321 (LOC51321), mRNA /cds=(635,1195) /gb=Nm_016627 /gi=7706167 /ug=Hs.268122 /len=1304	NM_016627	Hs.268122	NP_057711
ncr3148	NM_016632	ARF protein (LOC51326), mRNA /cds=(88,489) /gb=Nm_016632 /gi=7706177 /ug=Hs.264509 /len=826	NM_016632	Hs.264509	NP_057716
seoa9724	NM_016640	mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=Nm_016640 /gi=16950598 /ug=Hs.28555 /len=1482	NM_016640	Hs.28555	NP_057724

ncrc8873	NM_006855	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA /cds=(157,801) /gb=Nm_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855; NM_016657	Hs.250696	NP_057839
ncrb4022	NM_017444	chromatin accessibility complex 1 (CHRA1), mRNA /cds=(196,591) /gb=Nm_017444 /gi=24432041 /ug=Hs.279704 /len=2496	NM_017444	Hs.279704	NP_059140
fcr5316	NM_017510	gp25L2 protein (HSGP25L2G), mRNA	NM_017510	Hs.279929	NP_059980
ncrb2085	NM_017548	hypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=Nm_017548 /gi=24475997 /ug=Hs.283690 /len=3346	NM_017548	Hs.283690	NP_060018
miod4614	NM_017599	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=Nm_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
mioc5198	NM_017606	hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA /cds=(191,580) /gb=Nm_017606 /gi=8922146 /ug=Hs.32352 /len=2133	NM_017606	Hs.32352	NP_060076

mioc5210	NM_017615	hypothetical protein FLJ20003 (FLJ20003), mRNA /cds=(31,1188) /gb=Nm_017615 /gi=8923008 /ug=Hs.258798 /len=1387	NM_017615	Hs.258798	NP_060085
miob9370	AF246705	putative serine-rich protein mRNA, partial cds	NM_017632	Hs.32922	NP_060102
ncrb4435	NM_017691	hypothetical protein FLJ20156 (FLJ20156), mRNA /cds=(248,2305) /gb=Nm_017691 /gi=8923153 /ug=Hs.12692 /len=2780	NM_017691	Hs.12692	NP_060161
miod4629	NM_017755	hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=Nm_017755 /gi=8923284 /ug=Hs.17138 /len=2427	NM_017755	Hs.17138	NP_060225
ncrc0217	NM_017761	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=Nm_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
ncrb2272	NM_017791	chromosome 14 open reading frame 58 (C14orf58), mRNA /cds=(325,1905) /gb=Nm_017791 /gi=8923349 /ug=Hs.267566 /len=3614	NM_017791	Hs.267566	NP_060261

ncrc4373	NM_017830	ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=Nm_017830 /gi=8923426 /ug=Hs.132071 /len=1434	NM_017830	Hs.132071	NP_060300
seoa4167	NM_017849	hypothetical protein FLJ20507 (FLJ20507), mRNA /cds=(258,974) /gb=Nm_017849 /gi=8923465 /ug=Hs.202955 /len=4223	NM_017849	Hs.202955	NP_060319
seoc0957	NM_017910	hypothetical protein FLJ20628 (FLJ20628), mRNA /cds=(23,1456) /gb=Nm_017910 /gi=13435382 /ug=Hs.32356 /len=1846	NM_017910	Hs.32356	NP_060380
miod3325	NM_017913	Hsp90-associating relative of Cdc37 (HARC), mRNA /cds=(100,1113) /gb=Nm_017913 /gi=8923591 /ug=Hs.128646 /len=1542	NM_017913	Hs.128646	NP_060383
seob5880	AL834521	mRNA; cDNA DKFZp667F0310 (from clone DKFZp667F0310)	NM_017925	Hs.29032	NP_060395
mioc4782	NM_017943	F-box only protein 34 (FBXO34), mRNA /cds=(7,924) /gb=Nm_017943 /gi=8923650 /ug=Hs.15467 /len=2006	NM_017943	Hs.15467	NP_060413
miob8286	AL832991	mRNA; cDNA DKFZp666K033 (from clone DKFZp666K033)	NM_017944	Hs.300700	NP_060414

miod1030	NM_017971	mitochondrial ribosomal protein L20 (MRPL20), nuclear gene encoding mitochondrial protein, mRNA /cds=(65,514) /gb=Nm_017971 /gi=26638656 /ug=Hs.182698 /len=705	NM_017971	Hs.182698	NP_060441
ncrc0178	BC043393	Similar to hypothetical protein LOC208146, clone IMAGE:5498791, mRNA		Hs.318127	NP_060493
ncrc4402	NM_018032	LUC7-like (S. cerevisiae) (LUC7L), mRNA /cds=(89,1066) /gb=Nm_018032 /gi=21359922 /ug=Hs.16803 /len=1542	NM_018032	Hs.16803	NP_060502
ncrc7169	NM_018047	hypothetical protein FLJ10290 (FLJ10290), mRNA /cds=(78,1340) /gb=Nm_018047 /gi=8922327 /ug=Hs.25516 /len=2297	NM_018047	Hs.25516	NP_060517
fcrb4270	NM_018049	likely ortholog of mouse guanine nucleotide releasing protein x (GNRPX), mRNA /cds=(82,531) /gb=Nm_018049 /gi=8922332 /ug=Hs.173739 /len=1215	NM_018049	Hs.173739	NP_060519
seob7682	NM_018058	cartilage acidic protein 1 (CRTAC1), mRNA /cds=(319,1575) /gb=Nm_018058 /gi=8922351 /ug=Hs.326444 /len=2178	NM_018058	Hs.326444	NP_060528



seoa3761	NM_018061	hypothetical protein FLJ10330 (FLJ10330), mRNA /cds=(77,1717) /gb=Nm_018061 /gi=8922357 /ug=Hs.342307 /len=3239	NM_018061	Hs.342307	NP_060531
fcrb8465	NM_018077	hypothetical protein FLJ10377 (FLJ10377), mRNA /cds=(116,2395) /gb=Nm_018077 /gi=8922387 /ug=Hs.274263 /len=2809	NM_018077	Hs.274263	NP_060547
mioc8471	NM_018115	hypothetical protein FLJ10498 (FLJ10498), mRNA /cds=(37,1920) /gb=Nm_018115 /gi=8922466 /ug=Hs.109045 /len=2755	NM_018115	Hs.109045	NP_060585
fcrb3896	NM_018184	hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=Nm_018184 /gi=8922600 /ug=Hs.104222 /len=2944	NM_018184	Hs.104222	NP_060654
mioc3079	NM_018255	elongator protein 2 (ELP2), mRNA /cds=(11,2491) /gb=Nm_018255 /gi=8922734 /ug=Hs.8739 /len=2494	NM_018255	Hs.8739	NP_060725
ncr2908	NM_018259	hypothetical protein FLJ10890 (FLJ10890), mRNA /cds=(29,3454) /gb=Nm_018259 /gi=21361786 /ug=Hs.17283 /len=3533	NM_018259	Hs.17283	NP_060729

mioc3139	NM_018285	chromosome 15 open reading frame 12 (C15orf12), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,602) /gb=Nm_018285 /gi=8922793 /ug=Hs.6118 /len=1115	NM_018285	Hs.6118	NP_060755
miob7267	AB067490	mRNA for KIAA1903 protein, partial cds	NM_018353	Hs.89278	NP_060823
ncrb0364	NM_018382	hypothetical protein FLJ11292 (FLJ11292), mRNA /cds=(151,615) /gb=Nm_018382 /gi=8922980 /ug=Hs.272246 /len=1948	NM_018382	Hs.272246	NP_060852
fcrb9959	NM_018462	uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=Nm_018462 /gi=27544938 /ug=Hs.421654 /len=888	NM_018462	Hs.421654	NP_060932
miod0807	NM_018464	uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=Nm_018464 /gi=8923929 /ug=Hs.43549 /len=636	NM_018464	Hs.43549	NP_060934

miob3308	NM_018471	uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=Nm_018471 /gi=8923807 /ug=Hs.6375 /len=2140	NM_018471	Hs.6375	NP_060941
ncr2695	NM_018480	uncharacterized hypothalamus protein HT007 (HT007), mRNA /cds=(228,887) /gb=Nm_018480 /gi=8923801 /ug=Hs.24371 /len=1172	NM_018480	Hs.24371	NP_060950
ncrb4182	NM_018590	chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=Nm_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
mioc2290	NM_018638	ethanolamine kinase (EKI1), mRNA /cds=(90,1448) /gb=Nm_018638 /gi=21071078 /ug=Hs.120439 /len=2221	NM_018638	Hs.120439	NP_061108
seob3220	AB033073	mRNA for KIAA1247 protein, partial cds. /cds=(286,2943) /gb=AB033073 /gi=14133244 /ug=Hs.43857 /len=4397	NM_018837	Hs.43857	NP_061325
seoc1318	BC005940	Similar to G-protein gamma-12 subunit, clone MGC:14561 IMAGE:4049838, mRNA, complete cds		Hs.8107	NP_061329

mioa5409	NM_004105	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA /cds=(150,1631) /gb=Nm_004105 /gi=9665261 /ug=Hs.76224 /len=2742	NM_004105; NM_018894	Hs.76224	NP_061489
mioa0626	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=Nm_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
mioa6811	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=Nm_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
miob7831	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=Nm_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
mioc5197	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=Nm_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
mioc7372	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=Nm_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821

miob4933	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=Nm_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
seob4766	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=Nm_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
seoc2050	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=Nm_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
mioc1425	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=Nm_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
ncr3604	BC013629	clone IMAGE:3445410, mRNA, partial cds		Hs.432900	NP_061852
miob7155	AB002342	mRNA for KIAA0344 gene, partial cds	NM_018979	Hs.432900	NP_061852
seoc0775	BC034698	Similar to RAB5 interacting protein 2, clone IMAGE:4508733, mRNA		Hs.62349	NP_061866
mioa0791	BC034698	Similar to RAB5 interacting protein 2, clone IMAGE:4508733, mRNA		Hs.62349	NP_061866

ncrb4000	XM_033181	strand-exchange protein 1 (SEP1), mRNA			NP_061874
mioa0535	NM_019026	putative membrane protein (LOC54499), mRNA /cds=(139,705) /gb=Nm_019026 /gi=24308132 /ug=Hs.93832 /len=1186	NM_019026	Hs.93832	NP_061899
ncrc4247	NM_019043	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), mRNA /cds=(88,2085) /gb=Nm_019043 /gi=26665876 /ug=Hs.98874 /len=2423	NM_019043	Hs.98874	NP_061916
mioa4177	NM_019059	of Tom7 (S. cerevisiae) (TOM7), mRNA /cds=(94,261) /gb=Nm_019059 /gi=9506858 /ug=Hs.112318 /len=487	NM_019059	Hs.112318	NP_061932
mioc2255	AK001149	cDNA FLJ10287 fis, clone HEMBB1001387	NM_019083	Hs.40337	NP_061956
miob2671	NM_019088	hypothetical protein F23149_1 (PD2), mRNA /cds=(229,1824) /gb=Nm_019088 /gi=9506582 /ug=Hs.152894 /len=1966	NM_019088	Hs.152894	NP_061961

ncrc9469	NM_002961	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental (S100A4), transcript variant 1, mRNA /cds=(70,375) /gb=Nm_002961 /gi=9845514 /ug=Hs.81256 /len=512	NM_002961; NM_019554	Hs.81256	NP_062427
mioc2961	NM_019591	zinc finger protein 26 (KOX 20) (ZNF26), mRNA /cds=(699,1298) /gb=Nm_019591 /gi=11034838 /ug=Hs.26432 /len=2385	NM_019591	Hs.26432	NP_062537
miod5008	BC000819	Similar to CG6950 gene product, clone MGC:5114 IMAGE:3453829, mRNA, complete cds		Hs.180378	NP_062556
seoc4093	NM_020123	SM-11044 binding protein (SMBP), mRNA /cds=(20,1780) /gb=Nm_020123 /gi=10047129 /ug=Hs.8203 /len=3389	NM_020123	Hs.8203	NP_064508
ncrb6453	NM_020133	lysophosphatidic acid acyltransferase-delta (LPAAT-delta), mRNA /cds=(158,1294) /gb=Nm_020133 /gi=9910391 /ug=Hs.353175 /len=1774	NM_020133	Hs.353175	NP_064518

ncrb8224	NM_020153	hypothetical protein FLJ21827 (FLJ21827), mRNA /cds=(379,1446) /gb=NM_020153 /gi=21361819 /ug=Hs.334360 /len=1834	NM_020153	Hs.334360	NP_064538
fcr4433	NM_020154	chromosome 11 hypothetical protein ORF3 (LOC56851), mRNA /cds=(14,742) /gb=NM_020154 /gi=9910345 /ug=Hs.4245 /len=1072	NM_020154	Hs.4245	NP_064539
ncrc3856	NM_020192	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901	NM_020192	Hs.83313	NP_064577
seob6229	NM_020192	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901	NM_020192	Hs.83313	NP_064577
ncr6344	NM_020199	HTGN29 protein (HTGN29), mRNA /cds=(205,1002) /gb=NM_020199 /gi=9910277 /ug=Hs.283437 /len=2371	NM_020199	Hs.283437	NP_064584
ncrb3424	NM_020213	hypothetical protein from EUROIMAGE 1977056 (LOC56965), mRNA /cds=(609,1358) /gb=NM_020213 /gi=9910373 /ug=Hs.8694 /len=2359	NM_020213; NM_020214	Hs.8694	NP_064599



seoc2923	NM_020215	hypothetical protein DKFZp761F2014 (DKFZp761F2014), mRNA /cds=(117,638) /gb=Nm_020215 /gi=9910205 /ug=Hs.6434 /len=3477	NM_020215	Hs.6434	NP_064600
ncrc3397	NM_020232	hepatocellular carcinoma susceptibility protein (HCCA3), mRNA /cds=(53,847) /gb=Nm_020232 /gi=22726188 /ug=Hs.3726 /len=1073	NM_020232	Hs.3726	NP_064617
ncrc9591	NM_020234	x 009 protein (MDS009), mRNA /cds=(127,534) /gb=Nm_020234 /gi=9910425 /ug=Hs.64641 /len=1133	NM_020234	Hs.64641	NP_064619
miob7274	NM_020250	MOST2 protein (MOST2), mRNA /cds=(3461,3952) /gb=Nm_020250 /gi=9910449 /ug=Hs.193920 /len=4750	NM_020250	Hs.193920	NP_064635
ncrc3587	NM_020345	I-kappa-B- interacting Ras-like protein 1 (KBRAS1), mRNA /cds=(1,579) /gb=Nm_020345 /gi=9966808 /ug=Hs.173202 /len=579	NM_020345	Hs.173202	NP_065078
miod0956	BC012145	Similar to I-kappa- B-interacting Ras- like protein 1, clone MGC:20358 IMAGE:4549097, mRNA, complete cds		Hs.173202	NP_065078
miob5873	AF165191	BPAG1n3 (BPAG1) mRNA, partial cds	NM_001723; NM_015548; NM_020388	Hs.198689	NP_065121

mioc5308	AF165191	BPAG1n3 (BPAG1) mRNA, partial cds	NM_001723; NM_015548; NM_020388	Hs.198689	NP_065121
miod6773	NM_020405	tumor endothelial marker 7 precursor (TEM7), mRNA /cds=(83,1585) /gb=Nm_020405 /gi=21361852 /ug=Hs.125036 /len=6140	NM_020405	Hs.125036	NP_065138
ncr5971	NM_020422	hypothetical protein from clone 24796 (LOC57146), mRNA /cds=(113,598) /gb=Nm_020422 /gi=21361853 /ug=Hs.27191 /len=1683	NM_020422	Hs.27191	NP_065155
fcrb4974	BC040556	CTL2 gene, clone MGC:41799 IMAGE:5268313, mRNA, complete cds	NM_020428	Hs.105509	NP_065161
fcrc0106	AL133060	mRNA; cDNA DKFZp434M2315 (from clone DKFZp434M2315) (=BC012766.1)		Hs.180428	NP_065195
ncrb3445	NM_020466	hypothetical protein dJ122O8.2 (DJ122O8.2), mRNA /cds=(34,300) /gb=Nm_020466 /gi=20070310 /ug=Hs.268115 /len=902	NM_020466	Hs.268115	NP_065199
ncrc3995	NM_020474	UDP-N-acetyl- alpha-D- galactosamine:poly peptide N- acetylgalactosamin yltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(32,1711) /gb=Nm_020474 /gi=13124890 /ug=Hs.80120 /len=3778	NM_020474	Hs.80120	NP_065207

mioc3042	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=Nm_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
seoa6654	NM_020648	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=Nm_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
mioc6341	NM_020665	kidney-specific membrane protein (NX17), mRNA /cds=(261,929) /gb=Nm_020665 /gi=21361864 /ug=Hs.129614 /len=1605	NM_020665	Hs.129614	NP_065716
fcrb6167	NM_020680	SCY1-like 1 (S. cerevisiae) (SCYL1), mRNA /cds=(40,2400) /gb=Nm_020680 /gi=19923565 /ug=Hs.238839 /len=2580	NM_020680	Hs.238839	NP_065731
seob4734	NM_020685	HT021 (HT021), mRNA /cds=(145,531) /gb=Nm_020685 /gi=10190735 /ug=Hs.47166 /len=797	NM_020685	Hs.47166	NP_065736

seoc5815	NM_020749	AT2 receptor-interacting protein 1 (ATIP1), mRNA /cds=(1,1311) /gb=Nm_020749 /gi=21361871 /ug=Hs.7946 /len=3455	NM_020749	Hs.7946	NP_065800
miob2941	NM_020755	likely ortholog of mouse tumor differentially expressed 1, like (TDE1L), mRNA /cds=(76,1437) /gb=Nm_020755 /gi=24308212 /ug=Hs.146668 /len=3149	NM_020755	Hs.146668	NP_065806
miod5775	AK023639	cDNA FLJ13577 fis, clone PLACE1008748		Hs.107287	NP_065870
mioa9709	NM_020843	zinc finger protein 291 (ZNF291), mRNA /cds=(38,4237) /gb=Nm_020843 /gi=16507197 /ug=Hs.285848 /len=4703	NM_020843	Hs.285848	NP_065894
seoa3701	NM_020904	pleckstrin domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA /cds=(526,2865) /gb=Nm_020904 /gi=10190743 /ug=Hs.9469 /len=3056	NM_020904	Hs.9469	NP_065955
fcrb1328	AB046829	mRNA for KIAA1609 protein, partial cds. /cds=(1,1423) /gb=AB046829 /gi=15425661 /ug=Hs.14449 /len=4683		Hs.14449	NP_065998

ncrc2827	NM_020948	mesoderm induction early response 1 (MI-ER1), mRNA /cds=(234,1844) /gb=Nm_020948 /gi=24308260 /ug=Hs.222746 /len=4972	NM_020948	Hs.222746	NP_065999
ncrc3596	NM_021009	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=Nm_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
fcrb1731	NM_021075	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa (NDUFV3), mRNA /cds=(575,1945) /gb=Nm_021075 /gi=21361323 /ug=Hs.59745 /len=2023	NM_021075	Hs.59745	NP_066553
fcrb4409	NM_021102	serine protease inhibitor, Kunitz type, 2 (SPINT2), mRNA /cds=(301,1059) /gb=Nm_021102 /gi=10863908 /ug=Hs.31439 /len=1544	NM_021102	Hs.31439	NP_066925
ncr2700	BC035161	clone IMAGE:5265444, mRNA /gb=BC035161 /gi=23242943 /ug=Hs.7278 /len=4402		Hs.7278	NP_066940

seob7649	NM_001959	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=Nm_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959; NM_021121	Hs.421608	NP_066944
hfc1189	NM_001959	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=Nm_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959; NM_021121	Hs.421608	NP_066944
seob4076	NM_021129	pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,947) /gb=Nm_021129 /gi=11056043 /ug=Hs.184011 /len=1282	NM_021129	Hs.184011	NP_066952
ncrc1421	NM_021130	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=Nm_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787	NP_066953

miob0636	NM_021132	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) (PPP3CB), mRNA /cds=(117,1691) /gb=Nm_021132 /gi=11036639 /ug=Hs.151531 /len=3079	NM_021132	Hs.151531	NP_066955
ncrc1203	NM_021137	tumor necrosis factor, alpha-induced protein 1 (endothelial) (TNFAIP1), mRNA /cds=(212,1162) /gb=Nm_021137 /gi=26051238 /ug=Hs.76090 /len=3571	NM_021137	Hs.76090	NP_066960
ncrc6774	NM_021188	likely ortholog of mouse another partner for ARF 1 (APA1), mRNA /cds=(183,1619) /gb=Nm_021188 /gi=10863994 /ug=Hs.405945 /len=2207	NM_021188	Hs.405945	NP_067011
miod3743	NM_021215	chromosome 20 open reading frame 77 (C20orf77), mRNA /cds=(298,1278) /gb=Nm_021215 /gi=22507393 /ug=Hs.27192 /len=4219	NM_021215	Hs.27192	NP_067038
fcrb5964	NM_021227	DC2 protein (DC2), mRNA /cds=(60,509) /gb=Nm_021227 /gi=24308270 /ug=Hs.103180 /len=1090	NM_021227	Hs.103180	NP_067050

mioa9649	NM_021645	KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=Nm_021645 /gi=11063982 /ug=Hs.127376 /len=5585	NM_021645	Hs.127376	NP_067677
seoc2477	AB014526	mRNA for KIAA0626 protein, complete cds	NM_021647	Hs.178121	NP_067679
fcrb1733	NM_021809	TGFB-induced factor 2 (TALE family homeobox) (TGIF2), mRNA /cds=(170,883) /gb=Nm_021809 /gi=19923576 /ug=Hs.94785 /len=3433	NM_021809	Hs.94785	NP_068581
seob1197	NM_021814	of yeast long chain polyunsaturated fatty acid elongation enzyme 2 (HELO1), mRNA /cds=(345,1244) /gb=Nm_021814 /gi=21361903 /ug=Hs.250175 /len=3011	NM_021814	Hs.250175	NP_068586
ncrb8203	NM_021826	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=Nm_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598
seob7739	NM_021831	hypothetical protein FLJ21839 (FLJ21839), mRNA /cds=(445,2619) /gb=Nm_021831 /gi=19923577 /ug=Hs.433334 /len=3252	NM_021831	Hs.433334	NP_068603



seob9285	NM_021831	hypothetical protein FLJ21839 (FLJ21839), mRNA /cds=(445,2619) /gb=Nm_021831 /gi=19923577 /ug=Hs.433334 /len=3252	NM_021831	Hs.433334	NP_068603
fcrb4383	NM_021939	FK506 binding protein 10, 65 kDa (FKBP10), mRNA /cds=(87,1835) /gb=Nm_021939 /gi=21361894 /ug=Hs.3849 /len=2641	NM_021939	Hs.3849	NP_068758
seoa2679	NM_021945	hypothetical protein FLJ22174 (FLJ22174), mRNA /cds=(1712,2173) /gb=Nm_021945 /gi=24431990 /ug=Hs.7734 /len=3326	NM_021945	Hs.7734	NP_068764
mioc0567	NM_021967	small EDRK-rich factor 1A (telomeric) (SERF1A), mRNA /cds=(184,516) /gb=Nm_021967 /gi=11415045 /ug=Hs.32567 /len=1912	NM_021967	Hs.32567	NP_068802
miod6058	NM_021970	mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA /cds=(250,624) /gb=Nm_021970 /gi=21614526 /ug=Hs.6361 /len=1416	NM_021970	Hs.6361	NP_068805

ncrc0632	NM_021999	integral membrane protein 2B (ITM2B), mRNA /cds=(171,971) /gb=Nm_021999 /gi=11527401 /ug=Hs.239625 /len=1843	NM_021999	Hs.239625	NP_068839
fcrb9802	AJ310543	mRNA for EGLN1 protein	NM_022051	Hs.6523	NP_071334
seob0569	NM_022333	TIA1 cytotoxic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(158,955) /gb=Nm_022333 /gi=13435393 /ug=Hs.182741 /len=1760	NM_003252; NM_022333	Hs.182741	NP_071728
fcrb1320	NM_022333	TIA1 cytotoxic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(158,955) /gb=Nm_022333 /gi=13435393 /ug=Hs.182741 /len=1760	NM_003252; NM_022333	Hs.182741	NP_071728
seob6198	NM_003349	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=Nm_003349 /gi=15718757 /ug=Hs.75875 /len=2394	NM_003349; NM_021988; NM_022442	Hs.75875	NP_071887

seob3313	NM_003349	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=Nm_003349 /gi=15718757 /ug=Hs.75875 /len=2394	NM_003349; NM_021988; NM_022442	Hs.75875	NP_071887
mioc7763	NM_022488	autophagy Apg3p/Aut1p-like (APG3), mRNA /cds=(120,1064) /gb=Nm_022488 /gi=19526772 /ug=Hs.26367 /len=1381	NM_022488	Hs.26367	NP_071933
seob5044	NM_022551	ribosomal protein S18 (RPS18), mRNA /cds=(46,504) /gb=Nm_022551 /gi=14165467 /ug=Hs.275865 /len=549	NM_022551	Hs.275865	NP_072045
fcrc6570	NM_002890	RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA /cds=(119,3262) /gb=Nm_002890 /gi=4506430 /ug=Hs.758 /len=4307	NM_002890; NM_022650	Hs.758	NP_072179
miod0355	NM_022735	golgi complex associated protein 1, 60kDa (GOCAP1), mRNA /cds=(56,1642) /gb=Nm_022735 /gi=15826851 /ug=Hs.6831 /len=3598	NM_022735	Hs.6831	NP_073572

fcrb1729	NM_022735	golgi complex associated protein 1, 60kDa (GOCAP1), mRNA /cds=(56,1642) /gb=Nm_022735 /gi=15826851 /ug=Hs.6831 /len=3598	NM_022735	Hs.6831	NP_073572
seob1955	AK091247	cDNA FLJ33928 fis, clone CTONG2017444		Hs.16603	NP_073592
fcrb9909	NM_022757	hypothetical protein FLJ12892 (FLJ12892), mRNA /cds=(145,1929) /gb=Nm_022757 /gi=24308284 /ug=Hs.17731 /len=2987	NM_022757	Hs.17731	NP_073594
ncrc4267	NM_022763	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=Nm_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600
fcrc5134	NM_017411	survival of motor neuron 2, centromeric (SMN2), transcript variant d, mRNA /cds=(164,1048) /gb=Nm_017411 /gi=13259525 /ug=Hs.367729 /len=1623	NM_017411; NM_022875; NM_022876; NM_022877	Hs.367729	NP_075015
seoa0114	X70326	MacMarcks mRNA	NM_023009	Hs.75061	NP_075385
fcrc5169	NM_023012	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=Nm_023012 /gi=20127619 /ug=Hs.81648 /len=1878	NM_023012	Hs.81648	NP_075388

ncrb8607	NM_023080	hypothetical protein FLJ20989 (FLJ20989), mRNA /cds=(53,742) /gb=Nm_023080 /gi=12751496 /ug=Hs.169615 /len=2643	NM_023080	Hs.169615	NP_075568
ncrb8239	NM_023928	hypothetical protein FLJ12389 similar to acetoacetyl-CoA synthetase (FLJ12389), mRNA /cds=(149,2167) /gb=Nm_023928 /gi=12965198 /ug=Hs.239758 /len=3253	NM_023928	Hs.239758	NP_076417
miob7156	NM_001356	DEAD/H (Asp-Glu- Ala-Asp/His) box polypeptide 3 (DDX3), transcript variant 2, mRNA /cds=(857,2845) /gb=Nm_001356 /gi=13514812 /ug=Hs.380774 /len=5322	NM_001356; NM_024005	Hs.380774	NP_076829
mioa1473	NM_024010	methyltransferase reductase (MTRR), transcript variant 2, mRNA /cds=(31,2208) /gb=Nm_024010 /gi=13325067 /ug=Hs.153792 /len=3291	NM_002454; NM_024010	Hs.153792	NP_076915
fcrc0835	NM_024038	hypothetical protein MGC2803 (MGC2803), mRNA /cds=(68,598) /gb=Nm_024038 /gi=13128991 /ug=Hs.239894 /len=954	NM_024038	Hs.239894	NP_076943

mioc3206	NM_024041	hypothetical protein MGC3180 (MGC3180), mRNA /cds=(76,768) /gb=Nm_024041 /gi=13128997 /ug=Hs.250570 /len=846	NM_024041	Hs.250570	NP_076946
mioc3316	NM_024045	nucleolar protein GU2 (GU2), mRNA /cds=(108,2321) /gb=Nm_024045 /gi=13129005 /ug=Hs.7392 /len=2575	NM_024045	Hs.7392	NP_076950
seoc0619	NM_022902	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=Nm_022902 /gi=20070322 /ug=Hs.129445 /len=2952	NM_022902; NM_024055	Hs.129445	NP_076960
mioa9033	NM_024292	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=Nm_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
seoc7547	BC042615	Similar to v-maf musculoaponeuroti c fibrosarcoma oncogene family, protein B (avian), clone IMAGE:4470615, mRNA, partial cds		Hs.7041	NP_077288
seob1513	NM_024332	c6.1A (C6.1A), mRNA /cds=(3,953) /gb=Nm_024332 /gi=13236582 /ug=Hs.301927 /len=2846	NM_024332	Hs.301927	NP_077308
mioa0890	AK097314	cDNA FLJ39995 fis, clone STOMA2002141		Hs.102548	NP_077318

seoa7517	NM_024408	Notch 2 (Drosophila) (NOTCH2), mRNA /cds=(257,7672) /gb=Nm_024408 /gi=24041034 /ug=Hs.8121 /len=11433	NM_024408	Hs.8121	NP_077719
seoa3245	NM_024491	p10-binding protein (BITE), mRNA /cds=(149,1942) /gb=Nm_024491 /gi=13346499 /ug=Hs.42315 /len=2628	NM_024491	Hs.42315	NP_077817
ncrc4757	AB058768	mRNA for KIAA1865 protein, partial cds. /cds=(622,2793) /gb=AB058768 /gi=14017946 /ug=Hs.179260 /len=3641		Hs.179260	NP_078772
seoc0778	NM_024511	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=Nm_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787
mioc2828	NM_024524	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(1758,3863) /gb=Nm_024524 /gi=21362055 /ug=Hs.324507 /len=5226	NM_024524	Hs.324507	NP_078800
fcrb3258	NM_024536	hypothetical protein FLJ22678 (FLJ22678), mRNA /cds=(188,2515) /gb=Nm_024536 /gi=27545322 /ug=Hs.7718 /len=2965	NM_024536	Hs.7718	NP_078812
ncr6426	AK074267	cDNA FLJ23687 fis, clone HEP10109		Hs.13222	NP_078836

ncrc5054	NM_024592	hypothetical protein FLJ13352 (FLJ13352), mRNA /cds=(97,1053) /gb=Nm_024592 /gi=13375784 /ug=Hs.22972 /len=2271	NM_024592	Hs.22972	NP_078868
ncrc6825	NM_024635	hypothetical protein FLJ22643 (FLJ22643), mRNA /cds=(15,650) /gb=Nm_024635 /gi=13375865 /ug=Hs.43579 /len=997	NM_024635	Hs.43579	NP_078911
fcrb6715	NM_024656	hypothetical protein FLJ22329 (FLJ22329), mRNA /cds=(36,767) /gb=Nm_024656 /gi=13375904 /ug=Hs.367653 /len=2501	NM_024656	Hs.367653	NP_078932
seoa9494	NM_024713	hypothetical protein FLJ22557 (FLJ22557), mRNA /cds=(87,1001) /gb=Nm_024713 /gi=13376012 /ug=Hs.106101 /len=2676	NM_024713	Hs.106101	NP_078989
mioa8275	NM_024793	KIAA0643 protein (KIAA0643), mRNA /cds=(80,823) /gb=Nm_024793 /gi=13435144 /ug=Hs.155995 /len=2221	NM_024793	Hs.155995	NP_079069
mioc1226	NM_024818	hypothetical protein FLJ23251 (FLJ23251), mRNA /cds=(235,1449) /gb=Nm_024818 /gi=13376211 /ug=Hs.170737 /len=2132	NM_024818	Hs.170737	NP_079094



seoc1175	NM_024829	hypothetical protein FLJ22662 (FLJ22662), mRNA /cds=(66,1586) /gb=Nm_024829 /gi=13376231 /ug=Hs.178470 /len=1707	NM_024829	Hs.178470	NP_079105
ncrc7151	NM_024843	duodenal cytochrome b (FLJ23462), mRNA /cds=(74,934) /gb=Nm_024843 /gi=19923602 /ug=Hs.31297 /len=4254	NM_024843	Hs.31297	NP_079119
seoc0212	NM_025027	hypothetical protein FLJ14260 (FLJ14260), mRNA /cds=(431,1219) /gb=Nm_025027 /gi=13430885 /ug=Hs.287629 /len=2441	NM_025027	Hs.287629	NP_079303
seoc2201	AB002306	mRNA for KIAA0308 gene, partial cds	NM_025134	Hs.8182	NP_079410
seoc0369	NM_025146	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=Nm_025146 /gi=13376734 /ug=Hs.288932 /len=3576	NM_025146	Hs.288932	NP_079422
miob7518	NM_025180	hypothetical protein FLJ13386 (FLJ13386), mRNA /cds=(428,2539) /gb=Nm_025180 /gi=22095366 /ug=Hs.300876 /len=2770	NM_025180	Hs.300876	NP_079456

ncrc0747	NM_025184	hypothetical protein FLJ22843 (FLJ22843), mRNA /cds=(532,1287) /gb=Nm_025184 /gi=13376775 /ug=Hs.301143 /len=2291	NM_025184	Hs.301143	NP_079460
seoc0577	AL832422	mRNA; cDNA DKFZp762K012 (from clone DKFZp762K012)		Hs.301651	NP_079465
ncrc9517	NM_025190	KIAA1641 protein (KIAA1641), mRNA /cds=(41,454) /gb=Nm_025190 /gi=13449272 /ug=Hs.44566 /len=2418	NM_025190	Hs.44566	NP_079466
seoc4078	NM_025198	transcription termination factor- like protein (LOC80298), mRNA /cds=(341,1498) /gb=Nm_025198 /gi=21314735 /ug=Hs.5009 /len=1792	NM_025198	Hs.5009	NP_079474
fcrb9018	NM_025222	hypothetical protein PRO2730 (PRO2730), mRNA /cds=(1346,1759) /gb=Nm_025222 /gi=21361950 /ug=Hs.194110 /len=2990	NM_025222	Hs.194110	NP_079498
ncrc4663	NM_025234	recombination protein REC14 (REC14), mRNA /cds=(77,994) /gb=Nm_025234 /gi=13376839 /ug=Hs.296242 /len=1205	NM_025234	Hs.296242	NP_079510

seoa2428	NM_001357	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) (DDX9), transcript variant 1, mRNA /cds=(81,3920) /gb=Nm_001357 /gi=13514819 /ug=Hs.74578 /len=4199	NM_001357; NM_030588	Hs.74578	NP_085077
seoa6432	AB051481	mRNA for KIAA1694 protein, partial cds. /cds=(1,2275) /gb=AB051481 /gi=12697932 /ug=Hs.19597 /len=4235	NM_030629	Hs.19597	NP_085132
fcr1020	NM_030662	mitogen-activated protein kinase kinase 2 (MAP2K2), mRNA /cds=(255,1457) /gb=Nm_030662 /gi=21614527 /ug=Hs.72241 /len=1759	NM_030662	Hs.72241	NP_109587
seob0949	NM_030752	t-complex 1 (TCP1), mRNA /cds=(22,1692) /gb=Nm_030752 /gi=13540472 /ug=Hs.4112 /len=2019	NM_030752	Hs.4112	NP_110379
fcrb4413	NM_030755	thioredoxin domain-containing (TXNDC), mRNA /cds=(118,960) /gb=Nm_030755 /gi=13559515 /ug=Hs.24766 /len=1112	NM_030755	Hs.24766	NP_110382

miob4684	NM_030762	basic helix-loop-helix domain containing, class B, 3 (BHLHB3), mRNA /cds=(135,1583) /gb=Nm_030762 /gi=13540520 /ug=Hs.33829 /len=3641	NM_030762	Hs.33829	NP_110389
ncrb4385	AW298400	UI-H-BW0-ajj-h-09-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732033 3', mRNA sequence /clone=IMAGE:2732033 /clone_end=3' /gb=AW298400 /gi=6704960 /ug=Hs.438172 /len=635		Hs.438172	NP_110435
ncrc9877	NM_030917	hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA /cds=(168,1730) /gb=Nm_030917 /gi=13569873 /ug=Hs.334812 /len=1914	NM_030917	Hs.334812	NP_112179
miob8080	NM_030920	leucine-rich acidic nuclear protein like (LANPL), mRNA /cds=(332,1138) /gb=Nm_030920 /gi=23463320 /ug=Hs.71331 /len=3273	NM_030920	Hs.71331	NP_112182
seoa2135	NM_030971	similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA /cds=(75,1040) /gb=Nm_030971 /gi=13569945 /ug=Hs.283844 /len=2735	NM_030971	Hs.283844	NP_112233

fcrb4271	NM_030981	RAB1B, member RAS oncogene family (RAB1B), mRNA /cds=(48,653) /gb=Nm_030981 /gi=13569961 /ug=Hs.300816 /len=1985	NM_030981	Hs.300816	NP_112243
hfc2390	NM_005968	heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 1, mRNA /cds=(231,2423) /gb=Nm_005968 /gi=14141151 /ug=Hs.79024 /len=2703	NM_005968; NM_031203	Hs.79024	NP_112480
mioa3018	NM_031210	hypothetical protein DC50 (DC50), mRNA /cds=(37,366) /gb=Nm_031210 /gi=24475712 /ug=Hs.324521 /len=442	NM_031210	Hs.324521	NP_112487
ncrb3702	NM_031229	chromosome 20 open reading frame 18 (C20orf18), transcript variant 2, mRNA /cds=(677,2179) /gb=Nm_031229 /gi=14043035 /ug=Hs.247280 /len=2715	NM_006462; NM_031227; NM_031228; NM_031229	Hs.247280	NP_112506
ncrc1740	NM_031243	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(170,1231) /gb=Nm_031243 /gi=14043071 /ug=Hs.232400 /len=1780	NM_002137; NM_031243	Hs.232400	NP_112533

fcrb7098	NM_031298	hypothetical protein MGC2963 (MGC2963), mRNA /cds=(135,467) /gb=Nm_031298 /gi=13775219 /ug=Hs.30011 /len=673	NM_031298	Hs.30011	NP_112588
fcrb1604	NM_031302	glycosyltransferase (LOC83468), mRNA /cds=(408,1457) /gb=Nm_031302 /gi=21314737 /ug=Hs.159993 /len=1908	NM_031302	Hs.159993	NP_112592
ncrc5845	NM_031370	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD), transcript variant 1, mRNA /cds=(286,1353) /gb=Nm_031370 /gi=14110419 /ug=Hs.406404 /len=2197	NM_002138; NM_031369; NM_031370	Hs.406404	NP_112738
miob2192	NM_032174	hypothetical protein FLJ12770 (FLJ12770), mRNA /cds=(187,1113) /gb=Nm_032174 /gi=21362029 /ug=Hs.321653 /len=2670	NM_032174	Hs.321653	NP_115550
ncrc2780	NM_032231	hypothetical protein FLJ22875 (FLJ22875), mRNA /cds=(152,634) /gb=Nm_032231 /gi=15638951 /ug=Hs.406548 /len=1019	NM_032231	Hs.406548	NP_115607

seob8807	NM_032245	hypothetical protein DKFZp434I1916 (DKFZp434I1916), mRNA /cds=(144,563) /gb=Nm_032245 /gi=14149959 /ug=Hs.334641 /len=800	NM_032245	Hs.334641	NP_115621
miod5190	NM_032280	hypothetical protein DKFZp761J139 (DKFZp761J139), mRNA /cds=(3155,3970) /gb=Nm_032280 /gi=14150026 /ug=Hs.15536 /len=4635	NM_032280	Hs.15536	NP_115656
ncr8893	NM_032320	hypothetical protein MGC13007 (MGC13007), mRNA /cds=(1099,1653) /gb=Nm_032320 /gi=14150091 /ug=Hs.332382 /len=2479	NM_032320	Hs.332382	NP_115696
mioa4782	NM_032328	hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=Nm_032328 /gi=14150107 /ug=Hs.330664 /len=1026	NM_032328	Hs.330664	NP_115704
seoc4609	NM_032328	hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=Nm_032328 /gi=14150107 /ug=Hs.330664 /len=1026	NM_032328	Hs.330664	NP_115704

ncrb0653	NM_032357	hypothetical protein MGC12981 (MGC12981), mRNA /cds=(225,767) /gb=Nm_032357 /gi=21362049 /ug=Hs.104203 /len=1644	NM_032357	Hs.104203	NP_115733
fcrb4892	NM_018929	protocadherin gamma subfamily C, 5 (PCDHGC5), transcript variant 1, mRNA /cds=(1,2835) /gb=Nm_018929 /gi=14277683 /ug=Hs.335001 /len=4641	NM_018929; NM_032407	Hs.335001	NP_115783
seob2337	NM_032549	inner mitochondrial membrane peptidase 2 like (IMMP2L), mRNA /cds=(444,971) /gb=Nm_032549 /gi=14211844 /ug=Hs.89576 /len=1540	NM_032549	Hs.89576	NP_115938
ncrc4371	NM_032560	hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=Nm_032560 /gi=19923643 /ug=Hs.334657 /len=2794	NM_017936; NM_032560	Hs.334657	NP_115949
fcrb1381	NM_032560	hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=Nm_032560 /gi=19923643 /ug=Hs.334657 /len=2794	NM_017936; NM_032560	Hs.334657	NP_115949
fcrb5914	NM_032603	lysyl oxidase-like 3 (LOXL3), mRNA /cds=(73,2334) /gb=Nm_032603 /gi=22095373 /ug=Hs.334702 /len=3121	NM_032603	Hs.334702	NP_115992



mioc8750	NM_032622	ligand of numb- protein X (LNX), mRNA /cds=(236,2134) /gb=Nm_032622 /gi=14249127 /ug=Hs.66295 /len=3737	NM_032622	Hs.66295	NP_116011
hfcr2658	NM_006411	1-acylglycerol-3- phosphate O- acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1), transcript variant 1, mRNA /cds=(319,1170) /gb=Nm_006411 /gi=26787964 /ug=Hs.240534 /len=2242	NM_006411; NM_032741	Hs.240534	NP_116130
fcrb9134	NM_032840	hypothetical protein FLJ14800 (FLJ14800), mRNA /cds=(22,1350) /gb=Nm_032840 /gi=14249553 /ug=Hs.62119 /len=2568	NM_032840	Hs.62119	NP_116229
fcrb4231	NM_032849	hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=Nm_032849 /gi=21361885 /ug=Hs.62905 /len=2342	NM_032849	Hs.62905	NP_116238
ncrc4384	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=Nm_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259

mioc8479	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=Nm_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
mioc2997	NM_032927	hypothetical protein MGC13159 (MGC13159), mRNA /cds=(592,1017) /gb=Nm_032927 /gi=14249719 /ug=Hs.12845 /len=1759	NM_032927	Hs.12845	NP_116316
miob7627	NM_033111	CG016 (LOC88523), mRNA /cds=(323,2230) /gb=Nm_033111 /gi=14916464 /ug=Hs.112434 /len=2431	NM_033111	Hs.112434	NP_149102
fcrb8060	BC040354	Similar to caldesmon 1, clone MGC:21352 IMAGE:4753285, mRNA, complete cds (=OK/SW-cl.14 mRNA, complete cds, AB062484.1)	NM_004342; NM_033138; NM_033139; NM_033140; NM_033157	Hs.325474	NP_149347
mioc3127	NM_033138	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=Nm_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_004342; NM_033138; NM_033139; NM_033140; NM_033157	Hs.325474	NP_149347
seob7404	NM_001656	ADP-ribosylation factor domain protein 1, 64kDa (ARFD1), transcript variant alpha, mRNA /cds=(23,1747) /gb=Nm_001656 /gi=15208639 /ug=Hs.792 /len=3565	NM_001656; NM_033227; NM_033228	Hs.792	NP_150231

mioa9492	NM_033264	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1C (Ppp1r1c), mRNA	NM_033264	Mm.29963	NP_150289
seoa7296	NM_012142	cyclin D-type binding-protein 1 (CCNDBP1), transcript variant 1, mRNA /cds=(158,1240) /gb=Nm_012142 /gi=16554565 /ug=Hs.36794 /len=1615	NM_012142; NM_037370	Hs.36794	NP_411241
miob6226	NM_052815	immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=Nm_052815 /gi=16554596 /ug=Hs.76095 /len=1345	NM_003897; NM_052815	Hs.76095	NP_434702
hfc2789	NM_052871	hypothetical protein MGC4677 (MGC4677), mRNA /cds=(1337,1495) /gb=Nm_052871 /gi=16418372 /ug=Hs.432419 /len=1607	NM_052871	Hs.432419	NP_443103
fcr2821	NM_000075	cyclin-dependent kinase 4 (CDK4), transcript variant 1, mRNA /cds=(228,1139) /gb=Nm_000075 /gi=16936531 /ug=Hs.95577 /len=1474	NM_000075; NM_052984	Hs.95577	NP_443710

seoa1104	NM_016071	mitochondrial ribosomal protein S33 (MRPS33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(139,459) /gb=Nm_016071 /gi=16950595 /ug=Hs.83006 /len=727	NM_016071; NM_053035	Hs.83006	NP_444263
ncrc3526	NM_006625	FUS interacting protein (serine-arginine rich) 1 (FUSIP1), transcript variant 1, mRNA	NM_006625; NM_054016	Hs.3530	NP_473357
fcrb6890	NM_013354	CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA /cds=(340,1128) /gb=Nm_013354 /gi=17978498 /ug=Hs.380963 /len=2653	NM_013354; NM_054026	Hs.380963	NP_473367
fcr2952	NM_058246	DnaJ (Hsp40) subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA /cds=(156,1136) /gb=Nm_058246 /gi=24234717 /ug=Hs.181195 /len=2495	NM_005494; NM_058246	Hs.181195	NP_490647
seob2974	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 2, mRNA /cds=(236,730) /gb=Nm_078467 /gi=17978494 /ug=Hs.179665 /len=2281	NM_000389; NM_078467	Hs.179665	NP_510867

seob1801	NM_078469	BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant C, mRNA /cds=(13,891) /gb=Nm_078469 /gi=17402872 /ug=Hs.279862 /len=2338	NM_016567; NM_078468; NM_078469	Hs.279862	NP_510869
fcrb1834	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=Nm_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
fcrb2208	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=Nm_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
ncrc4135	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=Nm_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149

ncrc0097	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=Nm_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
fcr3053	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=Nm_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351
miob2855	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=Nm_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351
fcr1745	BQ066467	AGENCOURT_686 1057 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:593 1113 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029		Hs.446485	NP_536351
hfcr5865	NM_080599	UPF2 regulator of nonsense transcripts (yeast) (UPF2), transcript variant 1, mRNA /cds=(130,3948) /gb=Nm_080599 /gi=18375675 /ug=Hs.3862 /len=5223	NM_015542; NM_080599	Hs.3862	NP_542166

mioc5103	NM_080655	similar to RIKEN cDNA 5730528L13 gene (MGC17337), mRNA /cds=(68,895) /gb=Nm_080655 /gi=18087818 /ug=Hs.78531 /len=1175	NM_080655	Hs.78531	NP_542386
miod4449	NM_080821	chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=Nm_080821 /gi=18201877 /ug=Hs.352413 /len=3026	NM_080821	Hs.352413	NP_543011
mioa9189	NM_030781	collectin sub-family member 12 (COLEC12), transcript variant II, mRNA /cds=(172,2040) /gb=Nm_030781 /gi=18641357 /ug=Hs.29423 /len=4685	NM_030781; NM_130386	Hs.29423	NP_569057
mioa6147	NM_133370	KIAA1966 protein (KIAA1966), mRNA /cds=(492,2468) /gb=Nm_133370 /gi=21166354 /ug=Hs.158184 /len=3248	NM_133370	Hs.158184	NP_588611
ncrc1811	NM_005732	RAD50 (S. cerevisiae) (RAD50), transcript variant 1, mRNA /cds=(388,4326) /gb=Nm_005732 /gi=19924128 /ug=Hs.41587 /len=5891	NM_005732; NM_133482	Hs.41587	NP_597816
seob4451	NM_133493	CD109 (CD109), mRNA /cds=(113,4450) /gb=Nm_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964	NP_598000

ncrc2119	NM_001920	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=Nm_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920; NM_133503; NM_133504; NM_133505; NM_133506; NM_133507	Hs.433989	NP_598014
seoa2654	BC000626	clone MGC:3081 IMAGE:3347416, mRNA, complete cds	NM_015227	Hs.22982	NP_598368
mioa6731	NM_134264	SOCS box- containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=Nm_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_015626; NM_134264; NM_134265	Hs.187991	NP_599027
seob5379	NM_134408	Rattus norvegicus calcium- independent alpha- latrotoxin receptor 2 (Cirl2), mRNA	NM_134408	Rn.12089	NP_599235
ncrb8585	NM_138363	hypothetical protein BC009518 (LOC90799), mRNA /cds=(59,2524) /gb=Nm_138363 /gi=19923898 /ug=Hs.135265 /len=2705	NM_138363	Hs.135265	NP_612372
fcrc2852	AK094179	cDNA FLJ36860 fis, clone ASTRO2015295. /gb=AK094179 /gi=21753186 /ug=Hs.352406 /len=2882		Hs.352406	NP_612398



fcr2220	NM_138619	golgi associated, gamma adaptin ear containing, ARF binding protein 3 (GGA3), transcript variant long, mRNA /cds=(10,2181) /gb=Nm_138619 /gi=20336266 /ug=Hs.87726 /len=3860	NM_014001; NM_138619	Hs.87726	NP_619525
ncrb5060	NM_012104	beta-site APP-cleaving enzyme (BACE), transcript variant a, mRNA /cds=(447,1952) /gb=Nm_012104 /gi=21040369 /ug=Hs.49349 /len=5832	NM_012104; NM_138971; NM_138972; NM_138973	Hs.49349	NP_620429
mioc9262	AJ345030	mRNA for presenilin-like protein 4 (PSL4 gene)	NM_139015	Hs.21143	NP_620584
ncr2717	NM_139078	mitogen-activated protein kinase-activated protein kinase 5 (MAPKAPK5), transcript variant 2, mRNA /cds=(260,1681) /gb=Nm_139078 /gi=21237767 /ug=Hs.30327 /len=2066	NM_003668; NM_139078	Hs.30327	NP_620777
seoc2213	AK026207	cDNA: FLJ22554 fis, clone HSI01092		Hs.93842	NP_631903
fcrb4802	NM_139207	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=Nm_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_004537; NM_139207	Hs.302649	NP_631946

mioc0107	NM_144596	tetratricopeptide repeat domain 8 (TTC8), mRNA /cds=(53,1648) /gb=Nm_144596 /gi=21389382 /ug=Hs.55158 /len=2241	NM_144596	Hs.55158	NP_653197
ncr3976	NM_007200	A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=Nm_007200 /gi=21493028 /ug=Hs.301946 /len=10156	NM_006738; NM_007200; NM_144767	Hs.301946	NP_658913
ncrc3276	NM_144772	apolipoprotein A-I binding protein (APOA1BP), mRNA /cds=(28,894) /gb=Nm_144772 /gi=21426826 /ug=Hs.374850 /len=1120	NM_144772	Hs.374850	NP_658985
mioa4883	NM_144778	muscleblind-like protein MBLL39 (MBLL39), transcript variant 1, mRNA /cds=(782,1885) /gb=Nm_144778 /gi=21464124 /ug=Hs.283609 /len=4665	NM_005757; NM_144778	Hs.283609	NP_659002
seob9435	NM_145040	protein kinase C, delta binding protein (PRKCDBP), mRNA /cds=(35,820) /gb=Nm_145040 /gi=21450786 /ug=Hs.431979 /len=1053	NM_145040	Hs.431979	NP_659477

ncr3197	NM_145080	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=Nm_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
seoa3106	NM_145080	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=Nm_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
ncrc9280	NM_145283	similar to hypothetical protein BC014127 (LOC158046), mRNA	NM_145283	Hs.309216	NP_660326
seoa1427	NM_145690	tyrosine 3- monooxygenase/try ptophan 5- monooxygenase activation protein, zeta polypeptide (YWHAZ), transcript variant 2, mRNA /cds=(127,864) /gb=Nm_145690 /gi=21735624 /ug=Hs.75103 /len=2876	NM_003406; NM_145690	Hs.75103	NP_663723
miob7373	NM_145808	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=Nm_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807

ncr0663	NM_145869	annexin A11 (ANXA11), transcript variant c, mRNA /cds=(484,2001) /gb=Nm_145869 /gi=22165432 /ug=Hs.75510 /len=2731	NM_001157; NM_145868; NM_145869	Hs.75510	NP_665876
seob9820	NM_002624	prefoldin 5 (PFDN5), transcript variant 1, mRNA /cds=(36,500) /gb=Nm_002624 /gi=22202632 /ug=Hs.288856 /len=661	NM_002624; NM_145896; NM_145897	Hs.288856	NP_665904
miob4055	NM_007203	A kinase (PRKA) anchor protein 2 (AKAP2), transcript variant 1, mRNA /cds=(181,3492) /gb=Nm_007203 /gi=22325354 /ug=Hs.42322 /len=7522	NM_007203; NM_147150	Hs.42322	NP_671492
mioc7471	NM_006277	intersectin 2 (ITSN2), transcript variant 1, mRNA /cds=(242,5332) /gb=Nm_006277 /gi=22325384 /ug=Hs.166184 /len=6092	NM_006277; NM_019595; NM_147152	Hs.166184	NP_671494
miob5855	BC042899	Similar to hypothetical protein MGC30540, clone MGC:17342 IMAGE:4342258, mRNA, complete cds /cds=(216,1457) /gb=BC042899 /gi=27552863 /ug=Hs.153716 /len=3028	NM_147156	Hs.153716	NP_671512

seoa7443	NM_021249	sorting nexin 6 (SNX6), transcript variant 1, mRNA /cds=(498,1370) /gb=Nm_021249 /gi=23111048 /ug=Hs.284291 /len=3041	NM_021249; NM_152233	Hs.284291	NP_689419
seob6572	NM_152255	proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), transcript variant 2, mRNA /cds=(116,616) /gb=Nm_152255 /gi=23110947 /ug=Hs.233952 /len=1069	NM_002792; NM_152255	Hs.233952	NP_689468
miod6560	NM_152261	hypothetical protein MGC17943 (MGC17943), mRNA /cds=(214,564) /gb=Nm_152261 /gi=22748614 /ug=Hs.106390 /len=3167	NM_152261	Hs.106390	NP_689474
fcrc6043	NM_152344	hypothetical protein FLJ30656 (FLJ30656), mRNA /cds=(52,639) /gb=Nm_152344 /gi=22748746 /ug=Hs.349887 /len=2212	NM_152344	Hs.349887	NP_689557
seob5632	NM_152391	hypothetical protein MGC33602 (MGC33602), mRNA /cds=(140,748) /gb=Nm_152391 /gi=22748836 /ug=Hs.274415 /len=1790	NM_152391	Hs.274415	NP_689604

miob7550	NM_152392	hypothetical protein DKFZp564C236 (DKFZp564C236), mRNA /cds=(1590,2003) /gb=Nm_152392 /gi=22748838 /ug=Hs.378856 /len=2161	NM_152392	Hs.378856	NP_689605
mioc7570	NM_152392	hypothetical protein DKFZp564C236 (DKFZp564C236), mRNA /cds=(1590,2003) /gb=Nm_152392 /gi=22748838 /ug=Hs.378856 /len=2161	NM_152392	Hs.378856	NP_689605
miod2886	NM_152520	hypothetical protein FLJ25270 (FLJ25270), mRNA /cds=(244,1353) /gb=Nm_152520 /gi=22749086 /ug=Hs.6295 /len=2493	NM_152520	Hs.6295	NP_689733
hfcr2389	NM_152544	hypothetical protein FLJ35725 (FLJ35725), mRNA /cds=(201,1298) /gb=Nm_152544 /gi=22749134 /ug=Hs.380632 /len=1851	NM_152544	Hs.380632	NP_689757
seoc4762	NM_152553	hypothetical protein MGC26996 (MGC26996), mRNA /cds=(344,1171) /gb=Nm_152553 /gi=22749144 /ug=Hs.307526 /len=1804	NM_152553	Hs.307526	NP_689766

ncrc4508	NM_152576	hypothetical protein MGC24103 (MGC24103), mRNA /cds=(445,549) /gb=Nm_152576 /gi=22749194 /ug=Hs.287447 /len=1767	NM_152576	Hs.287447	NP_689789
ncrc5648	NM_152862	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA /cds=(113,1015) /gb=Nm_152862 /gi=23238210 /ug=Hs.83583 /len=1462	NM_005731; NM_152862	Hs.83583	NP_690601
ncrc0849	NM_152306	ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=Nm_152306 /gi=23312361 /ug=Hs.348602 /len=3720	NM_152306; NM_152896	Hs.348602	NP_690856
seob0426	NM_152932	glycosyltransferase AD-017 (AD-017), transcript variant 1, mRNA /cds=(140,1255) /gb=Nm_152932 /gi=23510345 /ug=Hs.283737 /len=1635	NM_018446; NM_152932	Hs.283737	NP_690909
seob4030	NM_153012	tumor necrosis factor (ligand) superfamily, member 12 (TNFSF12), transcript variant 2, mRNA /cds=(97,501) /gb=Nm_153012 /gi=23510440 /ug=Hs.26401 /len=1642	NM_003809; NM_153012	Hs.26401	NP_694557

miod3983	AK057950	cDNA FLJ25221 fis, clone STM00723	NM_153013	Hs.81907	NP_694558
fcrc5713	NM_021090	myotubularin related protein 3 (MTMR3), transcript variant 3, mRNA /cds=(288,3884) /gb=Nm_021090 /gi=23510385 /ug=Hs.63302 /len=5963	NM_021090; NM_153050; NM_153051	Hs.63302	NP_694691
miod1924	NM_153208	hypothetical protein MGC35048 (MGC35048), mRNA /cds=(700,1563) /gb=Nm_153208 /gi=23397455 /ug=Hs.367493 /len=2603	NM_153208	Hs.367493	NP_694940
miod1814	NM_153267	hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=Nm_153267 /gi=23397567 /ug=Hs.131987 /len=1727	NM_153267	Hs.131987	NP_694999
ncr9587	NM_003334	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1), transcript variant 1, mRNA /cds=(130,3306) /gb=Nm_003334 /gi=23510337 /ug=Hs.2055 /len=3504	NM_003334; NM_153280	Hs.2055	NP_695012
fcrb3843	BC028002	clone IMAGE:5212110, mRNA /gb=BC028002 /gi=24081066 /ug=Hs.386507 /len=2415	NM_032921; NM_153373	Hs.386507	NP_699204



seoa4598	NM_153425	TNFRSF1A-associated via death domain (TRADD), transcript variant 2, mRNA /cds=(731,1489) /gb=Nm_153425 /gi=24234725 /ug=Hs.89862 /len=1959	NM_003789; NM_153425	Hs.89862	NP_700474
miob8816	NM_004516	interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 2, mRNA	NM_004516; NM_012218; NM_153464	Hs.256583	NP_703194
miob8578	NM_153638	pantothenate kinase 2 (Hallervorden-Spatz syndrome) (PANK2), transcript variant 1, mRNA /cds=(56,1399) /gb=Nm_153638 /gi=24430170 /ug=Hs.286212 /len=1959	NM_024960; NM_153637; NM_153638; NM_153639; NM_153640; NM_153641	Hs.286212	NP_705905
fcrb7833	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=Nm_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
mioc2021	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=Nm_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
fcrb3739	NM_018951	homeo box A10 (HOXA10), transcript variant 1, mRNA /cds=(50,1231) /gb=Nm_018951 /gi=24497548 /ug=Hs.110637 /len=2618	NM_018951; NM_153715	Hs.110637	NP_714926

ncrc0807	AI498805	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:216 3256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460		Hs.436349	NP_722550
ncr1218	NM_170662	Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA	NM_170662		NP_733762
miob3898	NM_006930	S-phase kinase- associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=Nm_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779
seoa1739	NM_006930	S-phase kinase- associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=Nm_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779
ncrc3358	NM_006930	S-phase kinase- associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=Nm_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779

fcrb2162	NM_170707	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=Nm_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_005572; NM_170707; NM_170708	Hs.377973	NP_733822
ncrb0303	NM_170746	selenoprotein H (SELH), mRNA /cds=(243,611) /gb=Nm_170746 /gi=25014108 /ug=Hs.290874 /len=834	NM_170746	Hs.290874	NP_734467
miob3249	NM_013411	adenylate kinase 2 (AK2), nuclear gene encoding mitochondrial protein, transcript variant AK2B, mRNA /cds=(43,741) /gb=Nm_013411 /gi=26665888 /ug=Hs.294008 /len=2146	NM_001625; NM_013411; NM_172199	Hs.294008	NP_751949
ncrc9736	NM_018672	ATP-binding cassette, sub- family A (ABC1), member 5 (ABCA5), transcript variant 1, mRNA /cds=(1219,6147) /gb=Nm_018672 /gi=27262623 /ug=Hs.180513 /len=7044	NM_018672; NM_172232	Hs.180513	NP_758424
miod7367	NM_006186	nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA /cds=(336,2132) /gb=Nm_006186 /gi=27894347 /ug=Hs.82120 /len=3447	NM_006186; NM_173171; NM_173172; NM_173173	Hs.82120	NP_775265

seoc4316	NM_006333	nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=Nm_006333 /gi=27894371 /ug=Hs.15164 /len=1200	NM_006333; NM_173177	Hs.15164	NP_775269
fcrb4375	NM_173354	SNF1-like kinase (SNF1LK), mRNA /cds=(98,2449) /gb=Nm_173354 /gi=27597093 /ug=Hs.380991 /len=4726	NM_173354	Hs.380991	NP_775490
ncrb8220	NM_173471	hypothetical protein LOC115286 (LOC115286), mRNA /cds=(189,740) /gb=Nm_173471 /gi=27735034 /ug=Hs.379386 /len=1873	NM_173471	Hs.379386	NP_775742
miob2067	NM_173474	hypothetical protein LOC123803 (LOC123803), mRNA /cds=(15,947) /gb=Nm_173474 /gi=27735048 /ug=Hs.351573 /len=1146	NM_173474	Hs.351573	NP_775745
ncrb3373	NM_006785	mucosa associated lymphoid tissue lymphoma translocation gene 1 (MALT1), transcript variant 1, mRNA /cds=(259,2733) /gb=Nm_006785 /gi=27886564 /ug=Hs.180566 /len=5029	NM_006785; NM_173844	Hs.180566	NP_776216

seoc4356	NM_173852	keratinocytes associated protein 2 (KCP2), mRNA /cds=(1,489) /gb=Nm_173852 /gi=27777660 /ug=Hs.374854 /len=489	NM_173852	Hs.374854	NP_776251
mioa4628	NM_002816	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA /cds=(44,1414) /gb=Nm_002816 /gi=4506220 /ug=Hs.4295 /len=3548	NM_002816; NM_174871	Hs.4295	NP_777360
miod0468	BC042754	Similar to low density lipoprotein receptor-related protein 2, clone IMAGE:4828259, mRNA, partial cds /cds=(1,1059) /gb=BC042754 /gi=27769271 /ug=Hs.205865 /len=3814	NM_174902	Hs.205865	NP_777562
miod5984	BC028585	hypothetical gene supported by AK000174; AK055070; AK055612, clone IMAGE:4836971, mRNA		Hs.374538	NP_777569
seob7613	NM_004349	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), transcript variant 1, mRNA /cds=(412,2145) /gb=Nm_004349 /gi=28329413 /ug=Hs.31551 /len=3463	NM_004349; NM_175634; NM_175635; NM_175636	Hs.31551	NP_783554

seoa3885	AK090822	cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339	NM_175893	Hs.356719	NP_787089
seoa1559	AB011108	hypothetical protein (KIAA0536)	NM_003913; NM_176800	Hs.198891	NP_789770
seoc2470	BC033859	chromosome 20 open reading frame 178, clone MGC:45387 IMAGE:5173394, mRNA, complete cds	NM_176812	Hs.352579	NP_789782
seob7547	NM_014599	melanoma antigen, family D, 2 (MAGED2), mRNA /cds=(97,1917) /gb=NM_014599 /gi=21264316 /ug=Hs.4943 /len=2077	NM_014599; NM_177433	Hs.4943	NP_803182
fcrc1974	NM_014782	armadillo repeat protein ALEX2 (ALEX2), mRNA /cds=(458,2356) /gb=NM_014782 /gi=21361239 /ug=Hs.48924 /len=2788	NM_177949	Hs.48924	NP_808818
fcrb3476	NM_021131	protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740 /len=2661	NM_021131; NM_178000; NM_178001; NM_178002; NM_178003	Hs.400740	NP_821070
seob5640	BC013374	clone MGC:16435 IMAGE:3946253, mRNA, complete cds /cds=(137,1471) /gb=BC013374 /gi=15426525 /ug=Hs.179661 /len=2519	NM_178014	Hs.179661	NP_821133

fcrb7780	NM_178148	solute carrier family 35, member B2 (SLC35B2), mRNA	NM_178148		NP_835361
fcrb8973	NM_030789	histocompatibility (minor) 13 (HM13), mRNA /cds=(86,1219) /gb=Nm_030789 /gi=23308606 /ug=Hs.386538 /len=1584	NM_030789	Hs.386538	NP_848697
ncrc4320	NM_015339	activity-dependent neuroprotector (ADNP), mRNA /cds=(346,3654) /gb=Nm_015339 /gi=12229216 /ug=Hs.3657 /len=4713	NM_015339	Hs.3657	NP_852107
hfcr2890	NM_144601	chemokine-like factor super family 3 (CKLFSF3), mRNA /cds=(527,1075) /gb=Nm_144601 /gi=21389400 /ug=Hs.7773 /len=2318	NM_144601	Hs.7773	NP_853533
seob6131	NM_002916	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=Nm_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_853551
ncrc7040	NM_012094	peroxiredoxin 5 (PRDX5), mRNA /cds=(37,681) /gb=Nm_012094 /gi=6912237 /ug=Hs.31731 /len=805	NM_012094	Hs.31731	NP_857635
mioc4994	AK026583	cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600		Hs.90790	NP_858042

seob7409	NM_006534	nuclear receptor coactivator 3 (NCOA3), mRNA /cds=(184,4422) /gb=Nm_006534 /gi=5729725 /ug=Hs.225977 /len=6754	NM_006534	Hs.225977	NP_858045
ncrc5688	NM_003605	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine: polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2040,4802) /gb=Nm_003605 /gi=6006036 /ug=Hs.100293 /len=5733	NM_003605	Hs.100293	NP_858059
fcrc0631	AL834355	mRNA; cDNA DKFZp547F237 (from clone DKFZp547F237); complete cds (=AK024813.1)		Hs.6820	NP_859049
ncrc7016	NM_012381	origin recognition complex, subunit 3-like (yeast) (ORC3L), mRNA /cds=(27,2162) /gb=Nm_012381 /gi=6912561 /ug=Hs.74420 /len=2510	NM_012381	Hs.74420	NP_862820
fcrc5313	NM_002654	pyruvate kinase, muscle (PKM2), mRNA /cds=(110,1705) /gb=Nm_002654 /gi=4505838 /ug=Hs.198281 /len=2287	NM_002654	Hs.198281	NP_872271



mioa1163	BU727332	UI-E-CQ1-act-a-04-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-act-a-04-0-UI 3', mRNA sequence /clone=UI-E-CQ1-act-a-04-0-UI /clone_end=3' /gb=BU727332 /gi=23648099 /ug=Hs.116567 /len=1621		Hs.116567	NP_872297
seoa5090	NM_006754	synaptophysin-like protein (SYPL), mRNA /cds=(34,813) /gb=Nm_006754 /gi=5803184 /ug=Hs.80919 /len=2130	NM_006754	Hs.80919	NP_874384
seob7229	NM_002493	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa (NDUFB6), mRNA /cds=(104,490) /gb=Nm_002493 /gi=20149518 /ug=Hs.109646 /len=733	NM_002493	Hs.109646	NP_877416
seob4039	NM_021960	myeloid cell leukemia sequence 1 (BCL2-related) (MCL1), mRNA /cds=(64,1116) /gb=Nm_021960 /gi=19923213 /ug=Hs.86386 /len=3953	NM_021960	Hs.86386	NP_877495
fcr5176	NM_001675	activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA /cds=(882,1937) /gb=Nm_001675 /gi=4502264 /ug=Hs.181243 /len=2015	NM_001675	Hs.181243	NP_877962

fcrb5840	NM_016240	scavenger receptor class A, member 3 (SCARA3), mRNA /cds=(142,1962) /gb=Nm_016240 /gi=7705335 /ug=Hs.128856 /len=3636	NM_016240	Hs.128856	NP_878185
mioa1055	NM_016106	vesicle transport- related protein (RA410), mRNA /cds=(8,1930) /gb=Nm_016106 /gi=7706370 /ug=Hs.27023 /len=2149	NM_016106; NM_016163	Hs.27023	NP_878255
mioa1708	NM_001969	eukaryotic translation initiation factor 5 (EIF5), mRNA /cds=(469,1764) /gb=Nm_001969 /gi=21361336 /ug=Hs.433702 /len=3899	NM_001969	Hs.433702	NP_892116
fcr0018	NM_016208	vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=Nm_016208 /gi=7705884 /ug=Hs.339697 /len=928	NM_016208	Hs.339697	NP_898880
seob6510	NM_000311	prion protein (p27- 30) (Creutzfeld- Jakob disease, Gerstmann- Strausler-Scheinker syndrome, fatal familial insomnia) (PRNP), mRNA /cds=(50,811) /gb=Nm_000311 /gi=4506112 /ug=Hs.74621 /len=2415	NM_000311	Hs.74621	NP_898902
miod0533	AF253417	microsomal epoxide hydrolase (EPHX1) gene, complete cds	NM_000120		NP_000111

seoa5679	X66503	adenylosuccinate synthetase mRNA	NM_001126		NP_001117
mioa1077	NM_018212	enabled (Drosophila) (ENAH), mRNA /cds=(77,646) /gb=Nm_018212 /gi=8922657 /ug=Hs.14838 /len=2943	NM_018212	Hs.14838	NP_060682
fcrb8910	NM_006083	IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(112,1785) /gb=Nm_006083 /gi=11038650 /ug=Hs.8024 /len=1785	NM_006083	Hs.8024	NP_006074
mioa4677	AJ010770	hyperion gene, exons 1-50	NM_005751; NM_147166; NM_147171; NM_147185		NP_005742; NP_671695; NP_671700; NP_671714
fcr4024	AF058293	D-dopachrome tautomerase (=U49785; Y11151)	NM_001355		NP_001346
seob3386	AB017563	IGSF4 gene, exon 10 and complete cds	NM_014333		NP_055148
ncrc1032	NM_147185	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 3, mRNA	NM_005751; NM_147166; NM_147171; NM_147185		NP_005742; NP_671695; NP_671700; NP_671714
ncr3139	AF038042	BRCA1-associated RING domain protein (BARD1) gene, exons 10, 11 and complete cds	NM_000465		NP_000456
seob6096	NM_002223	inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA	NM_002223		NP_002214
mioc5061	NM_000489	alpha thalassemia/mental retardation syndrome X-linked (RAD54 S. cerevisiae) (ATRX), transcript variant 1,	NM_000489; NM_138270; NM_138271		NP_000480; NP_612114; NP_612115

		mRNA			
seob8489	NM_152724	hypothetical protein FLJ31034 (FLJ31034), mRNA /cds=(598,1023) /gb=Nm_152724 /gi=22749438 /ug=Hs.351342 /len=2267	NM_152724	Hs.351342	NP_689937

**Table 6c:** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for marked OA only

Common name	Genbank	Description	RefSeq	UniGene	Rep_prot
mioc9900	NM_000019	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) (ACAT1), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1360) /gb=Nm_000019 /gi=4557236 /ug=Hs.37 /len=1518	NM_000019	Hs.37	NP_000010
ncrb5699	NM_000064	complement component 3 (C3), mRNA /cds=(61,5052) /gb=Nm_000064 /gi=4557384 /ug=Hs.284394 /len=5067	NM_000064	Hs.284394	NP_000055

fcr0459	NM_000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=Nm_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
fcrc5190	NM_000093	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=Nm_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM_000093	Hs.146428	NP_000084
seob2139	NM_000176	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA /cds=(133,2466) /gb=Nm_000176 /gi=4504132 /ug=Hs.75772 /len=4788	NM_000176	Hs.75772	NP_000167
fcr7019	NM_000178	glutathione synthetase (GSS), mRNA /cds=(41,1465) /gb=Nm_000178 /gi=4504168 /ug=Hs.82327 /len=1856	NM_000178	Hs.82327	NP_000169
seoa2854	NM_000216	Kallmann syndrome 1 sequence (KAL1), mRNA /cds=(151,2193) /gb=Nm_000216 /gi=4557682 /ug=Hs.89591 /len=6314	NM_000216	Hs.89591	NP_000207

fcrb6099	NM_000293	phosphorylase kinase, beta (PHKB), mRNA /cds=(25,3306) /gb=Nm_000293 /gi=4505782 /ug=Hs.78060 /len=4284	NM_000293	Hs.78060	NP_000284
miob1115	NM_000297	polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA /cds=(67,2973) /gb=Nm_000297 /gi=4505834 /ug=Hs.82001 /len=5057	NM_000297	Hs.82001	NP_000288
mioc4557	NM_000351	steroid sulfatase (microsomal), arylsulfatase C, isozyme S (STS), mRNA /cds=(221,1972) /gb=Nm_000351 /gi=13162281 /ug=Hs.79876 /len=6520	NM_000351	Hs.79876	NP_000342
fcrb7178	NM_000582	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA /cds=(88,990) /gb=Nm_000582 /gi=4759165 /ug=Hs.313 /len=1524	NM_000582	Hs.313	NP_000573

ncrb0513	NM_000903	NAD(P)H dehydrogenase, quinone 1 (NQO1), mRNA /cds=(51,875) /gb=NM_000903 /gi=4505414 /ug=Hs.406515 /len=2447	NM_000903	Hs.406515	NP_000894
ncrc9867	NM_000968	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
seob7575	NM_000968	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
fcrb5272	NM_000998	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989
ncr0847	NM_001001	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
seob5579	NM_001012	ribosomal protein S8 (RPS8), mRNA /cds=(24,650) /gb=NM_001012 /gi=4506742 /ug=Hs.399720 /len=705	NM_001012	Hs.399720	NP_001003

seob9734	NM_001090	ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1), mRNA /cds=(95,2518) /gb=Nm_001090 /gi=10947134 /ug=Hs.9573 /len=3141	NM_001090	Hs.9573	NP_001081
fcr1462	NM_001319	casein kinase 1, gamma 2 (CSNK1G2), mRNA /cds=(54,1301) /gb=Nm_001319 /gi=21314777 /ug=Hs.181390 /len=2446	NM_001319	Hs.181390	NP_001310
seob6484	NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCL2), mRNA /cds=(166,2082) /gb=Nm_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
seoc3835	NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCL2), mRNA /cds=(166,2082) /gb=Nm_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
seoa3908	NM_001404	eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA /cds=(38,1351) /gb=Nm_001404 /gi=25453475 /ug=Hs.256184 /len=1429	NM_001404	Hs.256184	NP_001395



hfcr5971	NM_001446	fatty acid binding protein 7, brain (FABP7), mRNA /cds=(187,585) /gb=Nm_001446 /gi=16950660 /ug=Hs.26770 /len=888	NM_001446	Hs.26770	NP_001437
hfcr1671	NM_001457	filamin B, beta (actin binding protein 278) (FLNB), mRNA /cds=(132,7940) /gb=Nm_001457 /gi=4503746 /ug=Hs.81008 /len=9432	NM_001457	Hs.81008	NP_001448
hfcr6434	NM_001539	DnaJ (Hsp40) subfamily A, member 1 (DNAJA1), mRNA /cds=(83,1276) /gb=Nm_001539 /gi=4504510 /ug=Hs.94 /len=1438	NM_001539	Hs.94	NP_001530
fcrb2913	NM_001555	immunoglobulin superfamily, member 1 (IGSF1), mRNA /cds=(81,4091) /gb=Nm_001555 /gi=4504624 /ug=Hs.22111 /len=4381	NM_001555	Hs.22111	NP_001546
hfcr4444	NM_001634	S-adenosylmethionine decarboxylase 1 (AMD1), mRNA /cds=(321,1325) /gb=Nm_001634 /gi=5209326 /ug=Hs.262476 /len=3414	NM_001634	Hs.262476	NP_001625

fcr0416	NM_001685	ATP synthase, H transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial protein, mRNA /cds=(693,1019) /gb=Nm_001685 /gi=19913429 /ug=Hs.73851 /len=1178	NM_001685	Hs.73851	NP_001676
fcrb8509	NM_001698	AU RNA binding protein/enoyl- Coenzyme A hydratase (AUH), nuclear gene encoding mitochondrial protein, mRNA /cds=(5,1024) /gb=Nm_001698 /gi=4502326 /ug=Hs.81886 /len=1548	NM_001698	Hs.81886	NP_001689
ncrc6620	NM_001792	cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA /cds=(206,2926) /gb=Nm_001792 /gi=14589888 /ug=Hs.161 /len=4122	NM_001792	Hs.161	NP_001783
fcr1760	NM_001855	collagen, type XV, alpha 1 (COL15A1), mRNA /cds=(166,4332) /gb=Nm_001855 /gi=18641349 /ug=Hs.83164 /len=5222	NM_001855	Hs.83164	NP_001846

ncrc9401	NM_001861	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=Nm_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
mioa2493	NM_001864	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=Nm_001864 /gi=18105034 /ug=Hs.421621 /len=783	NM_001864	Hs.421621	NP_001855
mioa8648	NM_001873	carboxypeptidase E (CPE), mRNA /cds=(291,1721) /gb=Nm_001873 /gi=4503008 /ug=Hs.75360 /len=2443	NM_001873	Hs.75360	NP_001864
seob6680	NM_001923	damage-specific DNA binding protein 1, 127kDa (DDB1), mRNA /cds=(110,3532) /gb=Nm_001923 /gi=13435358 /ug=Hs.108327 /len=4221	NM_001923	Hs.108327	NP_001914
seob8260	BC033736	dermatopontin, clone MGC:45278 IMAGE:5176855, mRNA, complete cds		Hs.80552	NP_001928

seob9960	NM_001951	E2F transcription factor 5, p130-binding (E2F5), mRNA /cds=(35,1075) /gb=Nm_001951 /gi=12669916 /ug=Hs.2331 /len=1752	NM_001951	Hs.2331	NP_001942
bfcw0492	NM_001964	early growth response 1 (EGR1), mRNA /cds=(271,1902) /gb=Nm_001964 /gi=4503492 /ug=Hs.326035 /len=3132	NM_001964	Hs.326035	NP_001955
seob5260	NM_002006	fibroblast growth factor 2 (basic) (FGF2), mRNA /cds=(302,934) /gb=Nm_002006 /gi=15451897 /ug=Hs.284244 /len=6802	NM_002006	Hs.284244	NP_001997
hfcr1140	NM_002018	flightless I (Drosophila) (FLII), mRNA /cds=(52,3861) /gb=Nm_002018 /gi=22547155 /ug=Hs.83849 /len=4176	NM_002018	Hs.83849	NP_002009
mioc1963	NM_002027	farnesyltransferase, CAAX box, alpha (FNTA), mRNA /cds=(7,1146) /gb=Nm_002027 /gi=4503770 /ug=Hs.356463 /len=1644	NM_002027	Hs.356463	NP_002018

fcrb4599	NM_002032	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
seoa1901	NM_002035	follicular lymphoma variant translocation 1 (FVT1), mRNA /cds=(108,1106) /gb=NM_002035 /gi=4503816 /ug=Hs.74050 /len=2272	NM_002035	Hs.74050	NP_002026
ncrb4472	NM_002065	glutamate-ammonia ligase (glutamine synthase) (GLUL), mRNA /cds=(461,1582) /gb=NM_002065 /gi=21361767 /ug=Hs.170171 /len=3137	NM_002065	Hs.170171	NP_002056
ncrb2247	NM_002245	potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901	NM_002245	Hs.79351	NP_002236
seoc0384	NM_002439	mutS 3 (E. coli) (MSH3), mRNA /cds=(17,3403) /gb=NM_002439 /gi=4505248 /ug=Hs.42674 /len=4374	NM_002439	Hs.42674	NP_002430

hfc5003	NM_002475	myosin light chain 1 slow a (MLC1SA), mRNA /cds=(48,674) /gb=Nm_002475 /gi=17986280 /ug=Hs.90318 /len=778	NM_002475	Hs.90318	NP_002466
seob2966	NM_002480	protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA /cds=(1,3093) /gb=Nm_002480 /gi=4505316 /ug=Hs.16533 /len=4613	NM_002480	Hs.16533	NP_002471
ncr0176	NM_002512	non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA /cds=(73,531) /gb=Nm_002512 /gi=4505408 /ug=Hs.433416 /len=670	NM_002512	Hs.433416	NP_002503
fcr2908	NM_002579	paralemmin (PALM), mRNA /cds=(146,1309) /gb=Nm_002579 /gi=4557041 /ug=Hs.78482 /len=2823	NM_002579	Hs.78482	NP_002570

ncrb0897	NM_002600	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce Drosophila) (PDE4B), mRNA /cds=(766,2460) /gb=Nm_002600 /gi=4505662 /ug=Hs.188 /len=4068	NM_002600	Hs.188	NP_002591
mioa1657	NM_002715	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA /cds=(210,1139) /gb=Nm_002715 /gi=4506016 /ug=Hs.91773 /len=2181	NM_002715	Hs.91773	NP_002706
hfcf0470	NM_002721	protein phosphatase 6, catalytic subunit (PPP6C), mRNA /cds=(69,986) /gb=Nm_002721 /gi=20127429 /ug=Hs.356739 /len=1563	NM_002721	Hs.356739	NP_002712
fcrb3629	NM_002736	protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA /cds=(167,1423) /gb=Nm_002736 /gi=4506064 /ug=Hs.77439 /len=3259	NM_002736	Hs.77439	NP_002727

seoc4856	NM_002765	phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA /cds=(61,1017) /gb=Nm_002765 /gi=4506128 /ug=Hs.2910 /len=2457	NM_002765	Hs.2910	NP_002756
mioa8804	NM_002793	proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA /cds=(48,773) /gb=Nm_002793 /gi=22538462 /ug=Hs.407981 /len=872	NM_002793	Hs.407981	NP_002784
hfcr1324	NM_002811	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 (PSMD7), mRNA /cds=(128,1102) /gb=Nm_002811 /gi=25777614 /ug=Hs.155543 /len=1673	NM_002811	Hs.155543	NP_002802
seob1172	NM_002857	peroxisomal farnesylated protein (PXF), mRNA /cds=(11,910) /gb=Nm_002857 /gi=4506338 /ug=Hs.168670 /len=3662	NM_002857	Hs.168670	NP_002848
fcrc1601	BC050558	RAB5B, member RAS oncogene family, clone IMAGE:6191566, mRNA, partial cds			NP_002859



seoa9409	NM_002937	ribonuclease, RNase A family, 4 (RNASE4), mRNA /cds=(173,616) /gb=Nm_002937 /gi=20070170 /ug=Hs.283749 /len=1414	NM_002937	Hs.283749	NP_002928
ncrb4843	NM_002945	replication protein A1, 70kDa (RPA1), mRNA /cds=(44,1894) /gb=Nm_002945 /gi=20070171 /ug=Hs.84318 /len=2824	NM_002945	Hs.84318	NP_002936
hfcr2554	NM_002998	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), mRNA /cds=(460,1065) /gb=Nm_002998 /gi=27804306 /ug=Hs.1501 /len=2172	NM_002998	Hs.1501	NP_002989
fcrc3497	NM_003001	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa (SDHC), nuclear gene encoding mitochondrial protein, mRNA /cds=(27,536) /gb=Nm_003001 /gi=9257243 /ug=Hs.433982 /len=1315	NM_003001	Hs.433982	NP_002992
seoa8906	AB011538	mRNA for MEGF5, partial cds	NM_003062	Hs.57929	NP_003053
ncrc3172	BC034956	clone IMAGE:4821017, mRNA		Hs.77196	NP_003118

fcr4414	NM_003142	Sjogren syndrome antigen B (autoantigen La) (SSB), mRNA /cds=(73,1299) /gb=Nm_003142 /gi=10835066 /ug=Hs.83715 /len=1619	NM_003142	Hs.83715	NP_003133
fcrb8872	NM_003164	syntaxin 5A (STX5A), mRNA /cds=(27,932) /gb=Nm_003164 /gi=4507292 /ug=Hs.302300 /len=1507	NM_003164	Hs.302300	NP_003155
mioc8840	NM_003193	tubulin-specific chaperone e (TBCE), mRNA /cds=(81,1664) /gb=Nm_003193 /gi=6006029 /ug=Hs.343564 /len=1882	NM_003193	Hs.343564	NP_003184
ncrc6925	NM_003265	toll-like receptor 3 (TLR3), mRNA /cds=(102,2816) /gb=Nm_003265 /gi=19718735 /ug=Hs.29499 /len=3057	NM_003265	Hs.29499	NP_003256
ncrc4323	NM_003295	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=Nm_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
hfcr2808	NM_003310	tumor suppressing subtransferable candidate 1 (TSSC1), mRNA /cds=(152,1315) /gb=Nm_003310 /gi=4507702 /ug=Hs.4992 /len=1705	NM_003310	Hs.4992	NP_003301

mioa1608	NM_003359	UDP-glucose dehydrogenase (UGDH), mRNA /cds=(79,1563) /gb=Nm_003359 /gi=4507812 /ug=Hs.28309 /len=2950	NM_003359	Hs.28309	NP_003350
seoa0256	NM_003380	vimentin (VIM), mRNA /cds=(123,1523) /gb=Nm_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_003371
hfc1848	X59739	ZFX mRNA for put. transcription activator, isoform 2	NM_003410	Hs.2074	NP_003401
ncrc7043	NM_003418	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=Nm_003418 /gi=4827070 /ug=Hs.2110 /len=1500	NM_003418	Hs.2110	NP_003409
fcr3528	AF062089	leucine zipper protein Fip3p (=AF074382 Ikb kinase gamma subunit)	NM_003639	Hs.43505	NP_003630
ncr8843	NM_003640	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA /cds=(304,4302) /gb=Nm_003640 /gi=4504628 /ug=Hs.31323 /len=4803	NM_003640	Hs.31323	NP_003631

seoa7086	NM_003750	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa (EIF3S10), mRNA /cds=(114,4262) /gb=Nm_003750 /gi=4503508 /ug=Hs.154796 /len=5256	NM_003750	Hs.154796	NP_003741
ncrb1337	NM_003753	eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67kDa (EIF3S7), mRNA /cds=(372,2018) /gb=Nm_003753 /gi=23238220 /ug=Hs.55682 /len=2169	NM_003753	Hs.55682	NP_003744
fcr2541	NM_003836	delta-like 1 (Drosophila) (DLK1), mRNA /cds=(163,1314) /gb=Nm_003836 /gi=21361079 /ug=Hs.169228 /len=1556	NM_003836	Hs.169228	NP_003827
fcr4878	NM_003918	glycogenin 2 (GYG2), mRNA /cds=(284,1789) /gb=Nm_003918 /gi=5453673 /ug=Hs.380757 /len=3267	NM_003918	Hs.380757	NP_003909
hfc1428	NM_003981	protein regulator of cytokinesis 1 (PRC1), mRNA /cds=(79,1941) /gb=Nm_003981 /gi=4506038 /ug=Hs.344037 /len=3044	NM_003981	Hs.344037	NP_003972

fcrb2356	NM_004127	G protein pathway suppressor 1 (GPS1), mRNA /cds=(21,1523) /gb=Nm_004127 /gi=13435380 /ug=Hs.268530 /len=1866	NM_004127	Hs.268530	NP_004118
fcr1337	NM_004145	myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=Nm_004145 /gi=4758749 /ug=Hs.159629 /len=6069	NM_004145	Hs.159629	NP_004136
seob2336	NM_004147	developmentally regulated GTP binding protein 1 (DRG1), mRNA /cds=(66,1169) /gb=Nm_004147 /gi=4758795 /ug=Hs.115242 /len=1383	NM_004147	Hs.115242	NP_004138
seoa6724	AL831917	mRNA; cDNA DKFZp761F0118 (from clone DKFZp761F0118) /cds=(1,6490) /gb=AL831917 /gi=21732430 /ug=Hs.6685 /len=7334		Hs.6685	NP_004232
mioa7299	NM_004247	U5 snRNP-specific protein, 116 kD (U5-116KD), mRNA /cds=(61,2979) /gb=Nm_004247 /gi=4759279 /ug=Hs.151787 /len=3784	NM_004247	Hs.151787	NP_004238

mioa1303	NM_004279	peptidase (mitochondrial processing) beta (PMPCB), mRNA /cds=(14,1483) /gb=Nm_004279 /gi=4758733 /ug=Hs.184211 /len=1771	NM_004279	Hs.184211	NP_004270
mioc5692	NM_004330	BCL2/adenovirus E1B 19kDa interacting protein 2 (BNIP2), mRNA /cds=(212,1156) /gb=Nm_004330 /gi=4757855 /ug=Hs.155596 /len=2382	NM_004330	Hs.155596	NP_004321
ncr7839	NM_004415	desmoplakin (DPI, DPII) (DSP), mRNA /cds=(280,8895) /gb=Nm_004415 /gi=4758199 /ug=Hs.349499 /len=9588	NM_004415	Hs.349499	NP_004406
ncr1699	NM_004446	glutamyl-prolyl-tRNA synthetase (EPRS), mRNA /cds=(59,4381) /gb=Nm_004446 /gi=4758293 /ug=Hs.55921 /len=4586	NM_004446	Hs.55921	NP_004437
mioa2965	NM_004450	enhancer of rudimentary (Drosophila) (ERH), mRNA /cds=(72,386) /gb=Nm_004450 /gi=4758301 /ug=Hs.433413 /len=815	NM_004450	Hs.433413	NP_004441

seoa2467	NM_004505	ubiquitin specific protease 6 (Tre-2 oncogene) (USP6), mRNA /cds=(1697,4057) /gb=NM_004505 /gi=4758563 /ug=Hs.111065 /len=7878	NM_004505	Hs.111065	NP_004496
mioa6913	NM_004551	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
hfcr5956	NM_004554	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 (NFATC4), mRNA /cds=(294,3002) /gb=NM_004554 /gi=27886562 /ug=Hs.77810 /len=3399	NM_004554	Hs.77810	NP_004545
mioa1370	NM_004630	splicing factor 1 (SF1), mRNA /cds=(383,2254) /gb=NM_004630 /gi=4759339 /ug=Hs.180677 /len=3131	NM_004630	Hs.180677	NP_004621
seoc2955	AK057605	cDNA FLJ33043 fis, clone THYMU2000440		Hs.193145	NP_004645

miod1389	NM_004663	RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=Nm_004663 /gi=20149549 /ug=Hs.75618 /len=2474	NM_004663	Hs.75618	NP_004654
ncr5046	NM_004719	splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA /cds=(1211,4657) /gb=Nm_004719 /gi=4759171 /ug=Hs.51957 /len=5307	NM_004719	Hs.51957	NP_004710
mioc4923	NM_004827	ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), mRNA /cds=(205,2172) /gb=Nm_004827 /gi=4757849 /ug=Hs.194720 /len=2719	NM_004827	Hs.194720	NP_004818
seoa9916	NM_005008	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=Nm_005008 /gi=4826859 /ug=Hs.182255 /len=1475	NM_005008	Hs.182255	NP_004999



ncrc3256	NM_005121	thyroid hormone receptor-associated protein, 240 kDa subunit (TRAP240), mRNA /cds=(78,6602) /gb=Nm_005121 /gi=4827043 /ug=Hs.11861 /len=7389	NM_005121	Hs.11861	NP_005112
mioa8899	NM_005345	heat shock 70kDa protein 1A (HSPA1A), mRNA /cds=(198,2123) /gb=Nm_005345 /gi=26787973 /ug=Hs.75452 /len=2383	NM_005345	Hs.75452	NP_005336
seob8301	NM_005415	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=Nm_005415 /gi=7382462 /ug=Hs.78452 /len=3220	NM_005415	Hs.78452	NP_005406
fcrc4551	NM_005452	chromosome 6 open reading frame 11 (C6orf11), mRNA /cds=(54,1886) /gb=Nm_005452 /gi=14550417 /ug=Hs.17930 /len=2074	NM_005452	Hs.17930	NP_005443
fcrb2637	NM_005482	phosphatidylinositol glycan, class K (PIGK), mRNA /cds=(25,1212) /gb=Nm_005482 /gi=23199982 /ug=Hs.62187 /len=1897	NM_005482	Hs.62187	NP_005473

seob5523	NM_005496	SMC4 structural maintenance of chromosomes 4-like 1 (yeast) (SMC4L1), mRNA /cds=(233,4099) /gb=Nm_005496 /gi=21361251 /ug=Hs.50758 /len=5261	NM_005496	Hs.50758	NP_005487
seoc2904	NM_005499	SUMO-1 activating enzyme subunit 2 (UBA2), mRNA /cds=(26,1948) /gb=Nm_005499 /gi=4885648 /ug=Hs.4311 /len=2617	NM_005499	Hs.4311	NP_005490
ncrc7188	AA705851	ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412		Hs.443872	NP_005495
fcrb4784	NM_005514	major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=Nm_005514 /gi=21327676 /ug=Hs.77961 /len=1310	NM_005514	Hs.77961	NP_005505

ncrb6846	NM_005536	inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA /cds=(99,932) /gb=Nm_005536 /gi=8393607 /ug=Hs.171776 /len=2349	NM_005536	Hs.171776	NP_005527
miob3595	NM_005587	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA /cds=(415,1938) /gb=Nm_005587 /gi=5031906 /ug=Hs.182280 /len=2975	NM_005587	Hs.182280	NP_005578
ncrc2607	NM_005594	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=Nm_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
hfcr6573	NM_005626	splicing factor, arginine/serine-rich 4 (SFRS4), mRNA /cds=(107,1591) /gb=Nm_005626 /gi=21361281 /ug=Hs.76122 /len=2167	NM_005626	Hs.76122	NP_005617

fcr61607	NM_005628	solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(591,2216) /gb=Nm_005628 /gi=5032092 /ug=Hs.183556 /len=2856	NM_005628	Hs.183556	NP_005619
fcr2530	NM_005770	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=Nm_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761
fcrb7751	NM_005839	serine/arginine repetitive matrix 1 (SRRM1), mRNA /cds=(6,2468) /gb=Nm_005839 /gi=5032118 /ug=Hs.18192 /len=3698	NM_005839	Hs.18192	NP_005830
fcr6248	NM_006191	proliferation-associated 2G4, 38kDa (PA2G4), mRNA /cds=(98,1282) /gb=Nm_006191 /gi=5453841 /ug=Hs.374491 /len=1697	NM_006191	Hs.374491	NP_006182
fcrb1720	NM_006294	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=Nm_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285

seoa1611	NM_006346	progesterone-induced blocking factor 1 (PIBF1), mRNA /cds=(1,2277) /gb=Nm_006346 /gi=5453889 /ug=Hs.43913 /len=2277	NM_006346	Hs.43913	NP_006337
fcrb3119	NM_006482	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA /cds=(161,1966) /gb=Nm_006482 /gi=5922003 /ug=Hs.173135 /len=3615	NM_003583; NM_006482	Hs.173135	NP_006473
seob3455	NM_006519	t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=Nm_006519 /gi=5730084 /ug=Hs.266940 /len=713	NM_006519	Hs.266940	NP_006510
miod0526	NM_006620	HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=Nm_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
hfcr4423	NM_006640	MLL septin-like fusion (MSF), mRNA /cds=(258,1964) /gb=Nm_006640 /gi=19923366 /ug=Hs.181002 /len=3929	NM_006640	Hs.181002	NP_006631

mioa1392	NM_006699	mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA /cds=(521,2446) /gb=Nm_006699 /gi=5729912 /ug=Hs.367638 /len=2792	NM_006699	Hs.367638	NP_006690
fcrb5996	NM_006757	troponin T3, skeletal, fast (TNNT3), mRNA /cds=(13,789) /gb=Nm_006757 /gi=5803202 /ug=Hs.73454 /len=1000	NM_006757	Hs.73454	NP_006748
miob9470	NM_006773	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA /cds=(72,2084) /gb=Nm_006773 /gi=13787205 /ug=Hs.100555 /len=2753	NM_006773	Hs.100555	NP_006764
ncrb8569	NM_006820	chromosome 1 open reading frame 29 (C1orf29), mRNA /cds=(242,1483) /gb=Nm_006820 /gi=5803026 /ug=Hs.75470 /len=2058	NM_006820	Hs.75470	NP_006811
seob5012	NM_006965	zinc finger protein 24 (KOX 17) (ZNF24), mRNA /cds=(165,1271) /gb=Nm_006965 /gi=5902161 /ug=Hs.183593 /len=2513	NM_006965	Hs.183593	NP_008896

ncr7672	NM_006988	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=Nm_006988 /gi=11038653 /ug=Hs.8230 /len=4459	NM_006988	Hs.8230	NP_008919
fcrb2452	NM_006997	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=Nm_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
ncr3419	NM_007106	ubiquitin-like 3 (UBL3), mRNA /cds=(110,463) /gb=Nm_007106 /gi=6005927 /ug=Hs.173091 /len=3323	NM_007106	Hs.173091	NP_009037
mioa5836	NM_007115	tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(77,910) /gb=Nm_007115 /gi=26051242 /ug=Hs.29352 /len=1440	NM_007115	Hs.29352	NP_009046
ncr1055	NM_007268	Ig superfamily protein (Z39IG), mRNA /cds=(46,1245) /gb=Nm_007268 /gi=6005957 /ug=Hs.8904 /len=1787	NM_007268	Hs.8904	NP_009199

ncrb2027	NM_007344	transcription termination factor, RNA polymerase I (TTF1), mRNA /cds=(45,2705) /gb=Nm_007344 /gi=6678454 /ug=Hs.54780 /len=2847	NM_007344	Hs.54780	NP_031370
seoa1496	NM_007361	nidogen 2 (osteonidogen) (NID2), mRNA /cds=(1,4131) /gb=Nm_007361 /gi=6679055 /ug=Hs.82733 /len=4829	NM_007361	Hs.82733	NP_031387
mioc3590	NM_007373	soc-2 suppressor of clear (C. elegans) (SHOC2), mRNA /cds=(278,2026) /gb=Nm_007373 /gi=6677944 /ug=Hs.104315 /len=3872	NM_007373	Hs.104315	NP_031399
seoc7694	BC008272	Mus musculus neuron specific gene family member 1, mRNA (cDNA clone MGC:11446 IMAGE:3603440), complete cds	NM_010942	Mm.7414	NP_035072
ncrc5363	NM_012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=Nm_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333



fcrb5122	NM_012215	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(396,3146) /gb=Nm_012215 /gi=11024697 /ug=Hs.5734 /len=5147	NM_012215	Hs.5734	NP_036347
mioa1058	NM_012257	HMG-box containing protein 1 (HBP1), mRNA /cds=(187,1731) /gb=Nm_012257 /gi=21361410 /ug=Hs.10882 /len=2857	NM_012257	Hs.10882	NP_036389
fcrb9390	NM_012322	U6 snRNA-associated Sm-like protein (LSM5), mRNA /cds=(1,276) /gb=Nm_012322 /gi=6912487 /ug=Hs.227280 /len=749	NM_012322	Hs.227280	NP_036454
mioc6385	NM_012332	likely ortholog of mouse acyl-Coenzyme A thioesterase 2, mitochondrial (ACATE2), mRNA /cds=(148,1368) /gb=Nm_012332 /gi=6912517 /ug=Hs.18625 /len=1954	NM_012332	Hs.18625	NP_036464
fcr0148	NM_012333	c-myc binding protein (MYCBP), mRNA /cds=(39,350) /gb=Nm_012333 /gi=8850230 /ug=Hs.78221 /len=2070	NM_012333	Hs.78221	NP_036465

fcrc3288	NM_012339	transmembrane 4 superfamily member tetraspan NET-7 (NET-7), mRNA /cds=(122,1006) /gb=Nm_012339 /gi=21264576 /ug=Hs.95583 /len=1727	NM_012339	Hs.95583	NP_036471
ncrc2273	NM_013234	muscle specific gene (M9), mRNA /cds=(172,828) /gb=Nm_013234 /gi=10801344 /ug=Hs.283781 /len=911	NM_013234	Hs.283781	NP_037366
mioc6374	NM_014033	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=Nm_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752
fcrb8467	NM_014041	signal peptidase 12kDa (SPC12), mRNA /cds=(169,444) /gb=Nm_014041 /gi=7661745 /ug=Hs.11125 /len=798	NM_014041	Hs.11125	NP_054760
fcrb3618	NM_014138	PRO0659 protein (PRO0659), mRNA /cds=(60,584) /gb=Nm_014138 /gi=7662583 /ug=Hs.6451 /len=1416	NM_014138	Hs.6451	NP_054857
fcrc5593	AK025603	cDNA: FLJ21950 fis, clone HEP04949	NM_014181	Hs.372208	NP_054900

ncr4539	NM_014285	of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease (RRP4), mRNA	NM_014285	Hs.211973	NP_055100
ncr3511	NM_014347	zinc finger protein (ZF5128), mRNA /cds=(95,1756) /gb=Nm_014347 /gi=7657692 /ug=Hs.296365 /len=3000	NM_014347	Hs.296365	NP_055162
hfc1163	NM_014399	transmembrane 4 superfamily member tetraspan NET-6 (NET-6), mRNA /cds=(207,821) /gb=Nm_014399 /gi=21264573 /ug=Hs.284243 /len=1875	NM_014399	Hs.284243	NP_055214
miob9024	NM_014411	brain and nasopharyngeal carcinoma susceptibility protein (NSG-X), mRNA /cds=(186,518) /gb=Nm_014411 /gi=14149650 /ug=Hs.26937 /len=1897	NM_014411	Hs.26937	NP_055226
seoa7608	NM_014453	putative breast adenocarcinoma marker (32kD) (BC-2), mRNA /cds=(130,798) /gb=Nm_014453 /gi=7656921 /ug=Hs.12107 /len=903	NM_014453	Hs.12107	NP_055268

seob9292	NM_014489	FGF receptor activating protein 1 (FRAG1), mRNA /cds=(129,1076) /gb=Nm_014489 /gi=7657101 /ug=Hs.133968 /len=2040	NM_014489	Hs.133968	NP_055304
seoc6779	NM_014500	HIV TAT specific factor 1 (HTATSF1), mRNA /cds=(183,2450) /gb=Nm_014500 /gi=21361436 /ug=Hs.171595 /len=2785	NM_014500	Hs.171595	NP_055315
seob1770	NM_014608	cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA /cds=(53,3814) /gb=Nm_014608 /gi=24307968 /ug=Hs.77257 /len=4394	NM_014608	Hs.77257	NP_055423
miob3420	NM_014669	KIAA0095 gene product (KIAA0095), mRNA /cds=(67,2526) /gb=Nm_014669 /gi=7661901 /ug=Hs.155314 /len=2681	NM_014669	Hs.155314	NP_055484
ncr5651	NM_014739	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=Nm_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554

ncrc5813	NM_014764	DAZ associated protein 2 (DAZAP2), mRNA /cds=(70,576) /gb=Nm_014764 /gi=7661885 /ug=Hs.75416 /len=1897	NM_014764	Hs.75416	NP_055579
ncr7136	NM_014774	KIAA0494 gene product (KIAA0494), mRNA /cds=(978,2465) /gb=Nm_014774 /gi=7662159 /ug=Hs.62515 /len=5766	NM_014774	Hs.62515	NP_055589
seoa4070	NM_014781	RB1-inducible coiled-coil 1 (RB1CC1), mRNA /cds=(516,5291) /gb=Nm_014781 /gi=7661991 /ug=Hs.50421 /len=6614	NM_014781	Hs.50421	NP_055596
seoa8443	NM_014880	C-type lectin BIMLEC precursor (BIMLEC), mRNA /cds=(12,710) /gb=Nm_014880 /gi=26892292 /ug=Hs.2441 /len=1033	NM_014880	Hs.2441	NP_055695
ncrc3700	D87466	mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185		Hs.240112	NP_055930
fcrb4706	D31888	KIAA0071 mRNA, partial cds	NM_015156	Hs.78398	NP_055971

miob6597	NM_015161	ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA /cds=(70,681) /gb=Nm_015161 /gi=24308006 /ug=Hs.75249 /len=2280	NM_015161	Hs.75249	NP_055976
hfc1760	AL096857	Novel mRNA from chromosome 1, which has similarities to BAT2 genes /cds=(58,8163) /gb=AL096857 /gi=5541862 /ug=Hs.69559 /len=10174	NM_015172	Hs.69559	NP_055987
ncrc3927	NM_015469	DKFZp564D177 protein (DKFZp564D177), mRNA /cds=(106,849) /gb=Nm_015469 /gi=22267435 /ug=Hs.24608 /len=1664	NM_015469	Hs.24608	NP_056284
ncrb2449	BC001336	Similar to nectin 3; DKFZP566B0846 protein, clone IMAGE:3461033, mRNA, partial cds	NM_015480	Hs.21201	NP_056295
fcr5026	NM_015570	autism susceptibility candidate 2 (AUTS2), mRNA /cds=(322,4101) /gb=Nm_015570 /gi=17864089 /ug=Hs.32168 /len=5972	NM_015570	Hs.32168	NP_056385

seoa7647	NM_015571	SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=Nm_015571 /gi=7662311 /ug=Hs.27197 /len=4210	NM_015571	Hs.27197	NP_056386
miod1265	NM_015577	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=Nm_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
fcrb3330	NM_015640	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=Nm_015640 /gi=7661625 /ug=Hs.165998 /len=2201	NM_015640	Hs.165998	NP_056455
miod5195	BC032345	DKFZP586D0824 protein, clone MGC:40527 IMAGE:5208411, mRNA, complete cds /cds=(65,1078) /gb=BC032345 /gi=21595443 /ug=Hs.128797 /len=1499	NM_015660	Hs.128797	NP_056475
ncrc2404	NM_015683	hypothetical protein CLONE24945 (CLONE24945), mRNA /cds=(144,1367) /gb=Nm_015683 /gi=18373304 /ug=Hs.30882 /len=2518	NM_015683	Hs.30882	NP_056498

fcr5259	NM_015866	PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA	NM_012231; NM_015866	Hs.26719	NP_056950
ncr5168	NM_015902	progesterone induced protein (DD5), mRNA /cds=(34,8433) /gb=Nm_015902 /gi=15147336 /ug=Hs.278428 /len=8838	NM_015902	Hs.278428	NP_056986
mioc2188	NM_015952	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=Nm_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036
fcr6655	BC010867	Similar to lymphocyte activation-associated protein, clone IMAGE:3892557, mRNA (=AK001698.1)		Hs.272239	NP_057074
miod5612	NM_016009	SH3-domain GRB2-like endophilin B1 (SH3GLB1), mRNA /cds=(82,1179) /gb=Nm_016009 /gi=21359904 /ug=Hs.136309 /len=1561	NM_016009	Hs.136309	NP_057093
seob4079	NM_016037	CGI-94 protein (CGI-94), mRNA /cds=(70,831) /gb=Nm_016037 /gi=7705808 /ug=Hs.111449 /len=1025	NM_016037	Hs.111449	NP_057121



miob7750	NM_016052	CGI-115 protein (CGI-115), mRNA /cds=(35,814) /gb=Nm_016052 /gi=7705619 /ug=Hs.56043 /len=1308	NM_016052	Hs.56043	NP_057136
miob2714	NM_016065	mitochondrial ribosomal protein S16 (MRPS16), nuclear gene encoding mitochondrial protein, mRNA /cds=(170,583) /gb=Nm_016065 /gi=16554612 /ug=Hs.180312 /len=704	NM_016065	Hs.180312	NP_057149
miob1746	NM_016146	PTD009 protein (PTD009), mRNA	NM_016146	Hs.279901	NP_057230
fcrb6431	NM_016250	NDRG family member 2 (NDRG2), mRNA /cds=(97,1170) /gb=Nm_016250 /gi=10280619 /ug=Hs.243960 /len=2024	NM_016250	Hs.243960	NP_057334
seoa2181	NM_016312	WW domain binding protein 11 (WBP11), mRNA /cds=(162,2087) /gb=Nm_016312 /gi=18375679 /ug=Hs.334811 /len=2690	NM_016312	Hs.334811	NP_057396
ncr8112	NM_016360	clone HQ0477 PRO0477p (LOC51204), mRNA /cds=(201,1094) /gb=Nm_016360 /gi=27545314 /ug=Hs.174134 /len=1491	NM_016360	Hs.174134	NP_057444

ncrc0194	NM_016494	hypothetical protein LOC51255 (LOC51255), mRNA /cds=(31,492) /gb=NM_016494 /gi=24475978 /ug=Hs.11156 /len=601	NM_016494	Hs.11156	NP_057578
ncrc0095	NM_016525	ubiquitin associated protein 1 (UBAP1), mRNA /cds=(236,1744) /gb=NM_016525 /gi=22212941 /ug=Hs.75425 /len=2757	NM_016525	Hs.75425	NP_057609
seob6486	NM_016578	hepatitis B virus x associated protein (HBXAP), mRNA /cds=(1062,4631) /gb=NM_016578 /gi=10835261 /ug=Hs.20509 /len=5323	NM_016578	Hs.20509	NP_057662
ncrc5232	NM_016929	chloride intracellular channel 5 (CLIC5), mRNA /cds=(298,1053) /gb=NM_016929 /gi=8393146 /ug=Hs.283021 /len=2380	NM_016929	Hs.283021	NP_058625
mioc8531	NM_017571	hypothetical protein LOC55580 (LOC55580), mRNA /cds=(759,2987) /gb=NM_017571 /gi=8923837 /ug=Hs.254122 /len=3109	NM_017571	Hs.254122	NP_060041

mioc5182	NM_017599	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=Nm_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
fcrb8622	NM_017611	likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=Nm_017611 /gi=18252046 /ug=Hs.274453 /len=2630	NM_014096; NM_017611	Hs.274453	NP_060081
mioc8117	AJ420591	mRNA full length insert cDNA clone EUROIMAGE 701679		Hs.10784	NP_060103
miod4437	NM_017661	hypothetical protein FLJ20086 (FLJ20086), mRNA /cds=(48,1313) /gb=Nm_017661 /gi=8923096 /ug=Hs.46821 /len=3572	NM_017661	Hs.46821	NP_060131
miod0228	NM_017798	chromosome 20 open reading frame 21 (C20orf21), mRNA /cds=(10,603) /gb=Nm_017798 /gi=8923363 /ug=Hs.11747 /len=2429	NM_017798	Hs.11747	NP_060268
seoc0068	NM_017807	O-sialoglycoprotein endopeptidase (OSGEP), mRNA /cds=(130,1137) /gb=Nm_017807 /gi=8923379 /ug=Hs.108894 /len=1394	NM_017807	Hs.108894	NP_060277

seoa3758	NM_017822	hypothetical protein FLJ20436 (FLJ20436), mRNA /cds=(505,963) /gb=Nm_017822 /gi=8923410 /ug=Hs.268189 /len=1901	NM_017822	Hs.268189	NP_060292
seob6883	NM_017837	hypothetical protein FLJ20477 (FLJ20477), mRNA /cds=(332,1813) /gb=Nm_017837 /gi=21361770 /ug=Hs.26994 /len=2380	NM_017837	Hs.26994	NP_060307
hfcr5228	NM_017991	hypothetical protein FLJ10081 (FLJ10081), mRNA /cds=(437,2812) /gb=Nm_017991 /gi=21361733 /ug=Hs.7871 /len=5249	NM_017991	Hs.7871	NP_060461
ncrc3908	NM_018107	RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=Nm_018107 /gi=21361701 /ug=Hs.4997 /len=2442	NM_018107	Hs.4997	NP_060577
ncr1646	NM_018155	hypothetical protein FLJ10618 (FLJ10618), mRNA /cds=(210,1142) /gb=Nm_018155 /gi=8922550 /ug=Hs.42484 /len=2001	NM_018155	Hs.42484	NP_060625

fcrb4760	NM_018204	cytoskeleton associated protein 2 (CKAP2), mRNA /cds=(97,2145) /gb=NM_018204 /gi=19923520 /ug=Hs.24641 /len=3626	NM_018204	Hs.24641	NP_060674
fcrb8625	NM_018385	hypothetical protein FLJ11301 (FLJ11301), mRNA /cds=(21,1997) /gb=NM_018385 /gi=14149719 /ug=Hs.301724 /len=3290	NM_018385	Hs.301724	NP_060855
miob8012	NM_018405	hypothetical protein, clone 2746033 (HSA272196), mRNA /cds=(39,593) /gb=NM_018405 /gi=24475639 /ug=Hs.8179 /len=861	NM_018405	Hs.8179	NP_060875
ncrb0163	NM_018475	TPA regulated locus (TPARL), mRNA /cds=(195,1169) /gb=NM_018475 /gi=8923860 /ug=Hs.236510 /len=1913	NM_018475	Hs.236510	NP_060945
seob6675	NM_018489	hypothetical protein ASH1 (ASH1), mRNA /cds=(310,9219) /gb=NM_018489 /gi=8922080 /ug=Hs.102652 /len=9926	NM_018489	Hs.102652	NP_060959
fcrb1922	NM_018579	mitochondrial solute carrier protein (MSCP), mRNA	NM_016612; NM_018579	Hs.283716	NP_061049

miob7134	NM_018589	chromosome 14 open reading frame 116 (C14orf116), mRNA /cds=(270,458) /gb=Nm_018589 /gi=20127573 /ug=Hs.60548 /len=1654	NM_018589	Hs.60548	NP_061059
fcrb9565	NM_018649	H2A histone family, member Y2 (H2AFY2), mRNA /cds=(214,1332) /gb=Nm_018649 /gi=8923919 /ug=Hs.92023 /len=1932	NM_018649	Hs.92023	NP_061119
miob4822	NM_018981	ER-resident protein ERdj5 (ERdj5), mRNA /cds=(416,2797) /gb=Nm_018981 /gi=24308126 /ug=Hs.1098 /len=4193	NM_018981	Hs.1098	NP_061854
seob8261	NM_019000	hypothetical protein FLJ20152 (FLJ20152), mRNA /cds=(217,1287) /gb=Nm_019000 /gi=21361616 /ug=Hs.82273 /len=2989	NM_019000	Hs.82273	NP_061873
ncrb3417	NM_019058	HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=Nm_019058 /gi=9506686 /ug=Hs.111244 /len=1760	NM_019058	Hs.111244	NP_061931
ncr8171	BC009777	clone MGC:13446 IMAGE:4275731, mRNA, complete cds	NM_019071	Hs.143198	NP_061944

mioc8220	NM_020062	SLC2A4 regulator (SLC2A4RG), mRNA /cds=(1,1164) /gb=Nm_020062 /gi=13236503 /ug=Hs.170088 /len=1727	NM_020062	Hs.170088	NP_064446
fcrb9292	NM_020187	DC12 protein (DC12), mRNA	NM_020187	Hs.166096	NP_064572
mioc7440	NM_020188	DC13 protein (DC13), mRNA /cds=(176,415) /gb=Nm_020188 /gi=9910183 /ug=Hs.6879 /len=716	NM_020188	Hs.6879	NP_064573
ncr3686	NM_020307	cyclin L ania-6a (LOC57018), mRNA /cds=(55,1635) /gb=Nm_020307 /gi=9945319 /ug=Hs.4859 /len=2076	NM_020307	Hs.4859	NP_064703
seoc5267	NM_020432	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=Nm_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
fcrb4226	NM_020470	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=Nm_020470 /gi=9994168 /ug=Hs.406422 /len=1078	NM_020470	Hs.406422	NP_065203

mioc3413	NM_020648	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=Nm_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
miob8396	AK022459	cDNA FLJ12397 fis, clone MAMMA1002769, weakly similar to cell cycle progression restoration 8 protein (CPR8) mRNA	NM_004748	Hs.82506	NP_065790
hfcr3404	NM_020873	KIAA1497 protein (KIAA1497), mRNA /cds=(10,1305) /gb=Nm_020873 /gi=23308734 /ug=Hs.126085 /len=2728	NM_020873	Hs.126085	NP_065924
mioa1383	BC043352	Similar to RIKEN cDNA 2310026P19 gene, clone MGC:49935 IMAGE:6175382, mRNA, complete cds /cds=(288,3329) /gb=BC043352 /gi=27694113 /ug=Hs.35096 /len=5900		Hs.35096	NP_065950
miob9734	NM_020978	amylase, alpha 2B; pancreatic (AMY2B), mRNA /cds=(365,1900) /gb=Nm_020978 /gi=20070311 /ug=Hs.335493 /len=1963	NM_020978	Hs.335493	NP_066188



fcrb7533	NM_015270	adenylate cyclase 6 (ADCY6), transcript variant 1, mRNA /cds=(695,4201) /gb=Nm_015270 /gi=10947059 /ug=Hs.12373 /len=6594	NM_015270; NM_020983	Hs.12373	NP_066193
seoc6689	NM_021190	polypyrimidine tract binding protein 2 (PTBP2), mRNA /cds=(53,1648) /gb=Nm_021190 /gi=10863996 /ug=Hs.34956 /len=3054	NM_021190	Hs.34956	NP_067013
mioa8747	NM_021633	kelch-like protein C3IP1 (C3IP1), mRNA /cds=(201,1907) /gb=Nm_021633 /gi=21361889 /ug=Hs.3826 /len=3338	NM_021633	Hs.3826	NP_067646
fcrb1503	NM_021738	supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=Nm_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_003174; NM_021738	Hs.154567	NP_068506
ncrb6640	NM_021820	MDS024 protein (MDS024), mRNA /cds=(65,838) /gb=Nm_021820 /gi=11141892 /ug=Hs.425659 /len=2103	NM_021820	Hs.425659	NP_068592

hfc2229	NM_021826	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=Nm_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598
mioc2662	NM_022063	hypothetical protein FLJ13188 (FLJ13188), mRNA /cds=(247,948) /gb=Nm_022063 /gi=11545770 /ug=Hs.11859 /len=2746	NM_022063	Hs.11859	NP_071346
mioa8273	AK026797	cDNA: FLJ23144 fis, clone LNG09262	NM_022068	Hs.293907	NP_071351
fcr6461	NM_022366	transcription factor B2, mitochondrial (TFB2M), mRNA /cds=(125,1315) /gb=Nm_022366 /gi=11641288 /ug=Hs.7395 /len=1803	NM_022366	Hs.7395	NP_071761
mioc8481	NM_022763	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=Nm_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600
seob1730	NM_022772	EPS8-related protein 2 (EPS8R2), mRNA /cds=(273,2420) /gb=Nm_022772 /gi=21264615 /ug=Hs.55016 /len=3181	NM_022772	Hs.55016	NP_073609

fcrc6002	NM_022780	hypothetical protein FLJ13910 (FLJ13910), mRNA /cds=(99,1274) /gb=NM_022780 /gi=19923839 /ug=Hs.75277 /len=3239	NM_022780	Hs.75277	NP_073617
ncr2930	NM_022802	C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 /len=3780	NM_001329; NM_022802	Hs.171391	NP_073713
fcrc3895	NM_023018	NAD kinase (FLJ13052), mRNA /cds=(206,1978) /gb=NM_023018 /gi=20070325 /ug=Hs.220324 /len=3676	NM_023018	Hs.220324	NP_075394
ncrc7086	AK025702	cDNA: FLJ22049 fis, clone HEP09444. /gb=AK025702 /gi=10438304 /ug=Hs.423737 /len=2435		Hs.423737	NP_075447
seoa8870	NM_023039	ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154 /len=2048	NM_023039	Hs.239154	NP_075526

ncrb4248	NM_024051	hypothetical protein MGC3077 (MGC3077), mRNA /cds=(137,703) /gb=Nm_024051 /gi=13129017 /ug=Hs.433404 /len=1195	NM_024051	Hs.433404	NP_076956
mioc1019	M80902	AHNAK nucleoprotein mRNA, 5' end		Hs.165215	NP_076965
ncr8827	NM_024065	likely ortholog of mouse phosducin-like 2 (PDCL2), mRNA /cds=(101,820) /gb=Nm_024065 /gi=13129043 /ug=Hs.94576 /len=1044	NM_024065	Hs.94576	NP_076970
miod6210	BE966653	601661342R1 NIH_MGC_72 cDNA clone IMAGE:3915994 3', mRNA sequence /clone=IMAGE:3915994 /clone_end=3' /gb=BE966653 /gi=11772295 /ug=Hs.330958 /len=703		Hs.330958	NP_076974
fcrb6635	NM_024102	MEP50 protein (MEP50), mRNA /cds=(40,1068) /gb=Nm_024102 /gi=20127622 /ug=Hs.11039 /len=2428	NM_024102	Hs.11039	NP_077007

ncr1168	NM_024120	chromosome 20 open reading frame 7 (C20orf7), mRNA /cds=(31,507) /gb=Nm_024120 /gi=13129143 /ug=Hs.44296 /len=1715	NM_024120	Hs.44296	NP_077025
mioc7764	NM_024571	hypothetical protein FLJ22940 (FLJ22940), mRNA /cds=(984,1382) /gb=Nm_024571 /gi=13443017 /ug=Hs.15277 /len=1704	NM_024571	Hs.15277	NP_078847
seob8853	NM_024941	hypothetical protein FLJ13611 (FLJ13611), mRNA /cds=(207,1271) /gb=Nm_024941 /gi=13376418 /ug=Hs.282958 /len=2726	NM_024941	Hs.282958	NP_079217
mioc5536	NM_025057	hypothetical protein FLJ23189 (FLJ23189), mRNA /cds=(60,746) /gb=Nm_025057 /gi=13376590 /ug=Hs.287733 /len=2157	NM_025057	Hs.287733	NP_079333
fcrc1803	NM_030571	Nedd4 family interacting protein 1 (NDFIP1), mRNA /cds=(105,770) /gb=Nm_030571 /gi=13386479 /ug=Hs.9788 /len=1837	NM_030571	Hs.9788	NP_085048

miod0110	BQ228526	AGENCOURT_7591767 NIH_MGC_92 cDNA clone IMAGE:6067123 5', mRNA sequence /clone=IMAGE:6067123 /clone_end=5' /gb=BQ228526 /gi=20409926 /ug=Hs.282204 /len=1263		Hs.282204	NP_110390
seob4775	NM_030786	intermediate filament protein syncoilin (SYNCOILIN), mRNA /cds=(169,624) /gb=Nm_030786 /gi=13540560 /ug=Hs.348415 /len=2114	NM_030786	Hs.348415	NP_110413
seoc7016	NM_030918	sorting nexin 27 (SNX27), mRNA	NM_030918	Hs.67619	NP_112180
fcrb8333	NM_031219	hypothetical protein MGC12904 (MGC12904), mRNA /cds=(196,951) /gb=Nm_031219 /gi=13654293 /ug=Hs.7739 /len=1143	NM_031219	Hs.7739	NP_112496
seoc2336	NM_031447	hypothetical protein MGC13033 (MGC13033), mRNA /cds=(201,305) /gb=Nm_031447 /gi=13899280 /ug=Hs.423808 /len=1339	NM_031447	Hs.423808	NP_113635

miod5338	NM_031866	frizzled 8 (Drosophila) (FZD8), mRNA /cds=(6,2090) /gb=Nm_031866 /gi=13994189 /ug=Hs.302634 /len=3195	NM_031866	Hs.302634	NP_114072
fcrb9169	NM_031934	RAB34, member RAS oncogene family (RAB34), mRNA /cds=(206,985) /gb=Nm_031934 /gi=21361998 /ug=Hs.301853 /len=1340	NM_031934	Hs.301853	NP_114140
seoc4416	NM_005016	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=Nm_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016; NM_031989	Hs.63525	NP_114366
seob0817	NM_032025	CDA02 protein (CDA02), mRNA /cds=(3,1832) /gb=Nm_032025 /gi=14042940 /ug=Hs.332404 /len=2179	NM_032025	Hs.332404	NP_114414
seoc6099	NM_032141	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=Nm_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517

fcrb8430	NM_032377	hypothetical protein MGC4549 (MGC4549), mRNA /cds=(29,280) /gb=NM_032377 /gi=14150202 /ug=Hs.326422 /len=991	NM_032377	Hs.326422	NP_115753
fcrc6234	NM_032378	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA /cds=(198,2141) /gb=NM_032378 /gi=25453473 /ug=Hs.334798 /len=2216	NM_001960; NM_032378	Hs.334798	NP_115754
fcrc7358	NM_023005	bromodomain adjacent to zinc finger domain, 1B (BAZ1B), transcript variant 1, mRNA /cds=(353,4804) /gb=NM_023005 /gi=14670389 /ug=Hs.194688 /len=6079	NM_023005; NM_032408	Hs.194688	NP_115784
fcrc5734	AB058707	mRNA for KIAA1804 protein, partial cds	NM_032435	Hs.50883	NP_115811
seoc6288	NM_032476	mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding mitochondrial protein, mRNA /cds=(124,501) /gb=NM_032476 /gi=16554615 /ug=Hs.424751 /len=959	NM_032476	Hs.424751	NP_115865



seob9750	NM_032557	HP43.8KD protein (HP43.8KD), mRNA /cds=(507,3635) /gb=NM_032557 /gi=27545312 /ug=Hs.332841 /len=4684	NM_032557	Hs.332841	NP_115946
mioc3549	NM_032739	hypothetical protein MGC5370 (MGC5370), mRNA /cds=(189,269) /gb=NM_032739 /gi=14249363 /ug=Hs.332938 /len=974	NM_032739	Hs.332938	NP_116128
ncrb0550	NM_032810	hypothetical protein FLJ14600 (FLJ14600), mRNA /cds=(309,764) /gb=NM_032810 /gi=14249497 /ug=Hs.100861 /len=2334	NM_032810	Hs.100861	NP_116199
miob9054	NM_032832	hypothetical protein FLJ14735 (FLJ14735), mRNA /cds=(7,1509) /gb=NM_032832 /gi=14249539 /ug=Hs.334762 /len=3260	NM_032832	Hs.334762	NP_116221
seoa8750	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259

fcrb9354	NM_032997	ZW10 interactor (ZWINT), transcript variant 2, mRNA /cds=(25,858) /gb=Nm_032997 /gi=14602426 /ug=Hs.42650 /len=1851	NM_007057; NM_032997	Hs.42650	NP_127490
ncr7090	BC009336	clone MGC:16714 IMAGE:4128220, mRNA, complete cds	NM_033116	Hs.7200	NP_149107
miob3594	NM_033535	F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 2, mRNA /cds=(586,2283) /gb=Nm_033535 /gi=21536439 /ug=Hs.5548 /len=3475	NM_012161; NM_033535	Hs.5548	NP_277077
ncr0097	NM_015414	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=Nm_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414; NM_033643	Hs.433411	NP_378669
miob9875	NM_052957	acidic repeat containing (ACRC), mRNA /cds=(3,2078) /gb=Nm_052957 /gi=16445032 /ug=Hs.135167 /len=2692	NM_052957	Hs.135167	NP_443189
fcrb4340	NM_053045	hypothetical protein MGC14327 (MGC14327), mRNA /cds=(225,635) /gb=Nm_053045 /gi=16596685 /ug=Hs.231029 /len=1576	NM_053045	Hs.231029	NP_444273

seoc1791	NM_057159	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA /cds=(394,1488) /gb=Nm_057159 /gi=16950637 /ug=Hs.75794 /len=2732	NM_001401; NM_057159	Hs.75794	NP_476500
ncr8413	NM_003479	protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=Nm_003479 /gi=18104974 /ug=Hs.82911 /len=3925	NM_003479; NM_080391; NM_080392	Hs.82911	NP_536317
mioc1784	NM_080737	synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA /cds=(333,2348) /gb=Nm_080737 /gi=18152766 /ug=Hs.247525 /len=3914	NM_080737	Hs.247525	NP_542775
seoa5382	NM_080597	oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, mRNA /cds=(175,3027) /gb=Nm_080597 /gi=19718740 /ug=Hs.252716 /len=4165	NM_018030; NM_080597; NM_133268	Hs.252716	NP_579802

fcrb3518	NM_133367	chromosome 6 open reading frame 33 (C6orf33), mRNA /cds=(165,1229) /gb=Nm_133367 /gi=19115959 /ug=Hs.239388 /len=4650	NM_133367	Hs.239388	NP_588608
fcr4477	NM_134264	SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=Nm_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_015626; NM_134264; NM_134265	Hs.187991	NP_599027
seoa9537	NM_138792	hypothetical protein BC018147 (LOC123169), mRNA /cds=(29,2029) /gb=Nm_138792 /gi=20270336 /ug=Hs.296420 /len=2174	NM_138792	Hs.296420	NP_620147
fcrb8994	NM_004357	CD151 antigen (CD151), transcript variant 1, mRNA /cds=(130,891) /gb=Nm_004357 /gi=21237747 /ug=Hs.75564 /len=1552	NM_004357; NM_139030	Hs.75564	NP_620599
fcrb5629	AK026207	cDNA: FLJ22554 fis, clone HSI01092		Hs.93842	NP_631903
seoa3268	AK095110	cDNA FLJ37791 fis, clone BRHIP3000131. /gb=AK095110 /gi=21754304 /ug=Hs.350534 /len=3820	NM_144628	Hs.350534	NP_653229

miob9726	NM_144721	hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=Nm_144721 /gi=21389506 /ug=Hs.143692 /len=2260	NM_144721	Hs.143692	NP_653322
ncrc2763	NM_003188	mitogen-activated protein kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=Nm_003188 /gi=21735560 /ug=Hs.7510 /len=2912	NM_003188; NM_145331; NM_145332; NM_145333	Hs.7510	NP_663306
seob5906	AJ295983	mRNA for hypothetical protein (ORF1), clone Telethon(Italy_B41)_Strait15106_FL304		Hs.292653	NP_689526
mioa8032	NM_152388	hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=Nm_152388 /gi=22748830 /ug=Hs.346509 /len=2078	NM_152388	Hs.346509	NP_689601
ncrc2529	NM_152408	hypothetical protein FLJ35779 (FLJ35779), mRNA /cds=(42,1694) /gb=Nm_152408 /gi=22748864 /ug=Hs.432726 /len=1698	NM_152408	Hs.432726	NP_689621

seob1646	NM_152520	hypothetical protein FLJ25270 (FLJ25270), mRNA /cds=(244,1353) /gb=NM_152520 /gi=22749086 /ug=Hs.6295 /len=2493	NM_152520	Hs.6295	NP_689733
fcrb2722	NM_012425	Ras suppressor protein 1 (RSU1), mRNA /cds=(70,903) /gb=NM_012425 /gi=10800408 /ug=Hs.75551 /len=1436	NM_012425	Hs.75551	NP_689937
fcrb9649	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
seoc6266	NM_138962	musashi 2 (Drosophila) (MSI2), transcript variant 1, mRNA	NM_138962; NM_170721	Hs.103512	NP_733839
miod7470	NM_172070	similar to F10G7.10.p (KIAA2024), mRNA /cds=(343,1374) /gb=NM_172070 /gi=25453393 /ug=Hs.46826 /len=3703	NM_172070	Hs.46826	NP_742067
fcrb9184	NM_172239	exonuclease GOR (GOR), mRNA /cds=(628,1584) /gb=NM_172239 /gi=26665874 /ug=Hs.373854 /len=6609	NM_172239	Hs.373854	NP_758439

mioc3936	NM_003971	sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=Nm_003971 /gi=27436919 /ug=Hs.129872 /len=4663	NM_003971; NM_172345	Hs.129872	NP_758853
miod0441	NM_176824	Bardet-Biedl syndrome 7 (BBS7), transcript variant 1, mRNA	NM_018190; NM_176824		NP_789794
fcr0485	BC013374	clone MGC:16435 IMAGE:3946253, mRNA, complete cds /cds=(137,1471) /gb=BC013374 /gi=15426525 /ug=Hs.179661 /len=2519	NM_178014	Hs.179661	NP_821133
seob7765	AK023762	cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN	NM_003128; NM_178313	Hs.107164	NP_842565
fcrb4334	NM_004953	eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA /cds=(369,4559) /gb=Nm_004953 /gi=4826709 /ug=Hs.433750 /len=5018	NM_004953	Hs.433750	NP_886553

ncrc5310	NM_018682	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326 /ug=Hs.333300 /len=6543	NM_018682	Hs.333300	NP_891847
miod3546	AL833458	mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297		Hs.428760	NP_037387
ncrb4962	U55184	G protein Golf alpha gene, exon 12 and complete cds	NM_002071		NP_002062
fcrb5966	U18270	thymopoietin (TMPO) gene, exons 4 and 5, and complete cds for thymopoietin alpha	NM_003276		NP_003267
seob6525	NM_131105	Danio rerio alpha-tropomyosin (tpma), mRNA	NM_131105	Dr.20815	NP_571180
mioa3679	NM_138713	nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), transcript variant 2, mRNA	NM_006599; NM_138713; NM_138714; NM_173214; NM_173215		NP_006590; NP_619727; NP_619728; NP_775321; NP_775322
seoa0491	J00123	preproenkephalin precursor (PEN) gene, exon 3 and complete cds	NM_006211		NP_006202
seob4068	AB030001	gene for SGRF, complete cds	NM_016584		NP_057668



seoc0951	NM_033071	spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant longest, mRNA	NM_015293; NM_033071; NM_133650		NP_056108; NP_149062; NP_598411
seob9302	NM_025199	hypothetical protein FLJ20886 (FLJ20886), mRNA	NM_025199	Hs.241558	NP_079475
seoc6222	AL832582	mRNA; cDNA DKFZp451G0416 (from clone DKFZp451G0416)	NM_015878; NM_148174		NP_056962; NP_680479
seoc7548	AY207372	cyclin I (CCNI) gene, complete cds			AA013492
seob1128	AF539738	Danio rerio troponin mRNA, complete cds			AAN31755

**Table 6d:** depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for severe OA only

Clone name	Genbank	Description	RefSeq	UniGene	Rep_prot
ncrb8285	NM_000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
ncrc2319	NM_000146	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137

mioc4119	NM_000161	GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA /cds=(149,901) /gb=Nm_000161 /gi=4503948 /ug=Hs.86724 /len=2921	NM_000161	Hs.86724	NP_000152
fcrc1965	NM_000175	glucose phosphate isomerase (GPI), mRNA /cds=(104,1780) /gb=Nm_000175 /gi=18201904 /ug=Hs.406458 /len=2075	NM_000175	Hs.406458	NP_000166
mioa9147	NM_000237	lipoprotein lipase (LPL), mRNA /cds=(175,1602) /gb=Nm_000237 /gi=4557726 /ug=Hs.180878 /len=3549	NM_000237	Hs.180878	NP_000228
seob2750	NM_000291	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=Nm_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
mioa0218	NM_000361	thrombomodulin (THBD), mRNA /cds=(542,2269) /gb=Nm_000361 /gi=4507482 /ug=Hs.2030 /len=4050	NM_000361	Hs.2030	NP_000352

ncrb7675	NM_000380	xeroderma pigmentosum, complementation group A (XPA), mRNA /cds=(27,848) /gb=NM_000380 /gi=4507936 /ug=Hs.192803 /len=1377	NM_000380	Hs.192803	NP_000371
fcr7059	NM_000386	bleomycin hydrolase (BLMH), mRNA /cds=(79,1446) /gb=NM_000386 /gi=4557366 /ug=Hs.78943 /len=1932	NM_000386	Hs.78943	NP_000377
seoc0394	NM_000406	gonadotropin-releasing hormone receptor (GNRHR), mRNA /cds=(1749,2735) /gb=NM_000406 /gi=4504058 /ug=Hs.73064 /len=2735	NM_000406	Hs.73064	NP_000397
fcrb2704	NM_000517	hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575	NM_000517	Hs.347939	NP_000508
fcr2546	NM_000598	insulin-like growth factor binding protein 3 (IGFBP3), mRNA /cds=(88,963) /gb=NM_000598 /gi=19923110 /ug=Hs.77326 /len=2506	NM_000598	Hs.77326	NP_000589

fcrb3205	NM_000633	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA /cds=(32,751) /gb=Nm_000633 /gi=4557354 /ug=Hs.79241 /len=6030	NM_000633; NM_000657	Hs.79241	NP_000648
fcrb9371	NM_000701	ATPase, Na /K transporting, alpha 1 polypeptide (ATP1A1), mRNA /cds=(262,3333) /gb=Nm_000701 /gi=21361180 /ug=Hs.76549 /len=3680	NM_000701	Hs.76549	NP_000692
fcrb3704	NM_000786	cytochrome P450, family 51 (CYP51), mRNA /cds=(332,1861) /gb=Nm_000786 /gi=13929427 /ug=Hs.226213 /len=3381	NM_000786	Hs.226213	NP_000777
ncr5719	NM_000898	monoamine oxidase B (MAOB), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,1640) /gb=Nm_000898 /gi=4505092 /ug=Hs.82163 /len=2491	NM_000898	Hs.82163	NP_000889
ncrc3544	NM_000970	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=Nm_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961

seob7309	NM_000970	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=Nm_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
mioa0607	NM_000971	ribosomal protein L7 (RPL7), mRNA /cds=(22,768) /gb=Nm_000971 /gi=15431300 /ug=Hs.153 /len=838	NM_000971	Hs.153	NP_000962
ncrc5230	NM_000976	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=Nm_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
seoa7605	NM_000981	ribosomal protein L19 (RPL19), mRNA /cds=(29,619) /gb=Nm_000981 /gi=17158042 /ug=Hs.426977 /len=698	NM_000981	Hs.426977	NP_000972
miod2225	NM_000985	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=Nm_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
fcrb6000	NM_000998	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=Nm_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989

mioa0909	NM_001000	ribosomal protein L39 (RPL39), mRNA /cds=(68,223) /gb=Nm_001000 /gi=16306563 /ug=Hs.300141 /len=401	NM_001000	Hs.300141	NP_000991
fcrb5503	NM_001007	ribosomal protein S4, X-linked (RPS4X), mRNA /cds=(36,827) /gb=Nm_001007 /gi=17981705 /ug=Hs.389933 /len=916	NM_001007	Hs.389933	NP_000998
mioa8984	NM_001012	ribosomal protein S8 (RPS8), mRNA /cds=(24,650) /gb=Nm_001012 /gi=4506742 /ug=Hs.399720 /len=705	NM_001012	Hs.399720	NP_001003
mioa3987	NM_001021	ribosomal protein S17 (RPS17), mRNA /cds=(26,433) /gb=Nm_001021 /gi=14591913 /ug=Hs.5174 /len=515	NM_001021	Hs.5174	NP_001012
fcrb5756	NM_001102	actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=Nm_001102 /gi=12025669 /ug=Hs.119000 /len=3398	NM_001102	Hs.119000	NP_001093
fcrb1809	NM_001207	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=Nm_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198

seoa3555	NM_001207	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=Nm_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
seob5942	NM_001239	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=Nm_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP_001230
fcr7060	NM_001428	enolase 1, (alpha) (ENO1), mRNA /cds=(152,1456) /gb=Nm_001428 /gi=16507965 /ug=Hs.254105 /len=1812	NM_001428	Hs.254105	NP_001419
hfcr2664	NM_001428	enolase 1, (alpha) (ENO1), mRNA /cds=(152,1456) /gb=Nm_001428 /gi=16507965 /ug=Hs.254105 /len=1812	NM_001428	Hs.254105	NP_001419
ncrc1531	AF001862	FYN binding protein mRNA, complete cds	NM_001465	Hs.58435	NP_001456
seob6156	NM_001494	GDP dissociation inhibitor 2 (GDI2), mRNA /cds=(153,1490) /gb=Nm_001494 /gi=6598322 /ug=Hs.56845 /len=2274	NM_001494	Hs.56845	NP_001485
miob2257	BC039726	Similar to general transcription factor IIH, polypeptide 3, 34kDa, clone IMAGE:5582960, mRNA		Hs.30724	NP_001507

fcrb6574	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=Nm_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
fcrb2745	NM_001613	actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA /cds=(48,1181) /gb=Nm_001613 /gi=4501882 /ug=Hs.195851 /len=1330	NM_001613	Hs.195851	NP_001604
mioa8034	NM_001690	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=Nm_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
ncr1428	NM_001693	ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 (ATP6V1B2), mRNA /cds=(208,1743) /gb=Nm_001693 /gi=19913427 /ug=Hs.1697 /len=3054	NM_001693	Hs.1697	NP_001684



seob1860	NM_001754	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), mRNA /cds=(445,1887) /gb=Nm_001754 /gi=19923197 /ug=Hs.129914 /len=6212	NM_001754	Hs.129914	NP_001745
ncr3642	NM_001759	cyclin D2 (CCND2), mRNA /cds=(270,1139) /gb=Nm_001759 /gi=16950656 /ug=Hs.75586 /len=6480	NM_001759	Hs.75586	NP_001750
fcrb3966	NM_001766	CD1D antigen, d polypeptide (CD1D), mRNA /cds=(165,1172) /gb=Nm_001766 /gi=4502648 /ug=Hs.1799 /len=1903	NM_001766	Hs.1799	NP_001757
seoa0913	NM_001769	CD9 antigen (p24) (CD9), mRNA /cds=(112,798) /gb=Nm_001769 /gi=21237762 /ug=Hs.1244 /len=1246	NM_001769	Hs.1244	NP_001760
seob0752	NM_001827	CDC28 protein kinase regulatory subunit 2 (CKS2), mRNA /cds=(96,335) /gb=Nm_001827 /gi=4502858 /ug=Hs.83758 /len=627	NM_001827	Hs.83758	NP_001818
seoa0526	BC025372	calponin 3, acidic, clone MGC:1775 IMAGE:3505668, mRNA, complete cds	NM_001839	Hs.194662	NP_001830

fcrb2993	NM_001861	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=Nm_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
fcr4308	NM_001878	cellular retinoic acid binding protein 2 (CRABP2), mRNA /cds=(138,554) /gb=Nm_001878 /gi=6382069 /ug=Hs.183650 /len=969	NM_001878	Hs.183650	NP_001869
fcr7656	NM_001896	casein kinase 2, alpha prime polypeptide (CSNK2A2), mRNA /cds=(164,1216) /gb=Nm_001896 /gi=4503096 /ug=Hs.82201 /len=1677	NM_001896	Hs.82201	NP_001887
ncrc2495	NM_001967	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=Nm_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912	NP_001958
fcr6452	NM_002047	glycyl-tRNA synthetase (GARS), mRNA /cds=(519,2576) /gb=Nm_002047 /gi=6996009 /ug=Hs.293885 /len=2742	NM_002047	Hs.293885	NP_002038

ncr5066	NM_002117	major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(16,1116) /gb=Nm_002117 /gi=19557676 /ug=Hs.277477 /len=1549	NM_002117	Hs.277477	NP_002108
seoc5963	AL110194	mRNA; cDNA DKFZp566M063 (from clone DKFZp566M063)		Hs.6727	NP_002119
seob5976	NM_002210	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV), mRNA /cds=(42,3188) /gb=Nm_002210 /gi=4504762 /ug=Hs.295726 /len=5717	NM_002210	Hs.295726	NP_002201
ncrc9228	NM_002295	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=Nm_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
seob0810	NM_002305	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=Nm_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296

ncr8780	NM_002395	malic enzyme 1, NADP( )-dependent, cytosolic (ME1), mRNA /cds=(108,1826) /gb=NM_002395 /gi=13435400 /ug=Hs.14732 /len=2212	NM_002395	Hs.14732	NP_002386
hfc2696	NM_002417	antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA /cds=(197,9967) /gb=NM_002417 /gi=19923216 /ug=Hs.80976 /len=12515	NM_002417	Hs.80976	NP_002408
fcr2218	NM_002477	myosin, light polypeptide 5, regulatory (MYL5), mRNA /cds=(106,627) /gb=NM_002477 /gi=4505304 /ug=Hs.170482 /len=661	NM_002477	Hs.170482	NP_002468
seoa4400	BC045606	Similar to nidogen (enactin), clone MGC:33141 IMAGE:5271590, mRNA, complete cds		Hs.356624	NP_002499
seoa2726	NM_002526	5'-nucleotidase, ecto (CD73) (NT5E), mRNA	NM_002526	Hs.153952	NP_002517

hfcr1724	NM_002615	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 (SERPINF1), mRNA /cds=(39,1082) /gb=Nm_002615 /gi=4505708 /ug=Hs.173594 /len=1199	NM_002615	Hs.173594	NP_002606
ncrb8191	NM_002616	period 1 (Drosophila) (PER1), mRNA /cds=(188,4060) /gb=Nm_002616 /gi=4505712 /ug=Hs.68398 /len=4656	NM_002616	Hs.68398	NP_002607
hfcr1689	NM_002676	phosphomannomutase 1 (PMM1), mRNA /cds=(5,793) /gb=Nm_002676 /gi=4505904 /ug=Hs.75835 /len=1210	NM_002676	Hs.75835	NP_002667
ncrb4402	NM_002696	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=Nm_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687

miob0175	NM_002734	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036	NM_002734	Hs.183037	NP_002725
fcrb9420	NM_002778	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
seob0928	NM_002790	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002790	Hs.76913	NP_002781
fcrb8937	J03580	parathyroid-like protein (associated with humoral hypercalcemia of malignancy) mRNA, complete cds	NM_002820	Hs.89626	NP_002811

ncrc1247	NM_002835	protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(30,2372) /gb=Nm_002835 /gi=18375651 /ug=Hs.62 /len=3161	NM_002835	Hs.62	NP_002826
seob6395	NM_002841	protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA /cds=(718,5055) /gb=Nm_002841 /gi=18860897 /ug=Hs.89627 /len=5787	NM_002841	Hs.89627	NP_002832
ncrb3989	BC050558	RAB5B, member RAS oncogene family, clone IMAGE:6191566, mRNA, partial cds			NP_002859
fcr4984	NM_002951	ribophorin II (RPN2), mRNA /cds=(289,2184) /gb=Nm_002951 /gi=4506676 /ug=Hs.406532 /len=2509	NM_002951	Hs.406532	NP_002942
fcr2427	NM_002997	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=Nm_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988
seob6153	NM_003113	nuclear antigen Sp100 (SP100), mRNA /cds=(32,2671) /gb=Nm_003113 /gi=19923235 /ug=Hs.77617 /len=3579	NM_003113	Hs.77617	NP_003104

seob0376	NM_003392	wingless-type MMTV integration site family, member 5A (WNT5A), mRNA /cds=(758,1855) /gb=Nm_003392 /gi=17402917 /ug=Hs.152213 /len=4428	NM_003392	Hs.152213	NP_003383
fcr3001	NM_003405	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (YWHAH), mRNA /cds=(198,938) /gb=Nm_003405 /gi=21464102 /ug=Hs.349530 /len=1775	NM_003405	Hs.349530	NP_003396
mioa0400	AF025771	C2H2 zinc finger protein splicing variant b2 (ZNF189) mRNA, complete cds	NM_003452	Hs.50123	NP_003443
mioa3528	NM_003455	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=Nm_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
hfr6164	NM_003505	frizzled 1 (Drosophila) (FZD1), mRNA /cds=(414,2357) /gb=Nm_003505 /gi=4503824 /ug=Hs.94234 /len=4350	NM_003505	Hs.94234	NP_003496



miob3252	NM_003613	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA /cds=(130,3684) /gb=Nm_003613 /gi=4502844 /ug=Hs.151407 /len=4175	NM_003613	Hs.151407	NP_003604
miob5675	NM_003630	peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=Nm_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621
ncr0179	NM_003729	RTC domain containing 1 (RTCD1), mRNA /cds=(171,1271) /gb=Nm_003729 /gi=4506588 /ug=Hs.27076 /len=1539	NM_003729	Hs.27076	NP_003720
fcrb7588	NM_003746	dynein, cytoplasmic, light polypeptide 1 (DNCL1), mRNA /cds=(94,363) /gb=Nm_003746 /gi=4505812 /ug=Hs.5120 /len=643	NM_003746	Hs.5120	NP_003737
ncr3948	NM_003851	cellular repressor of E1A-stimulated genes (CREG), mRNA /cds=(34,696) /gb=Nm_003851 /gi=4503036 /ug=Hs.5710 /len=1989	NM_003851	Hs.5710	NP_003842

seob1078	NM_003881	WNT1 inducible signaling pathway protein 2 (WISP2), mRNA /cds=(148,900) /gb=Nm_003881 /gi=18491001 /ug=Hs.194679 /len=1433	NM_003881	Hs.194679	NP_003872
ncrc6678	NM_003906	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (MCM3AP), mRNA /cds=(38,5980) /gb=Nm_003906 /gi=19923190 /ug=Hs.168481 /len=6114	NM_003906	Hs.168481	NP_003897
seob3869	NM_003919	sarcoglycan, epsilon (SGCE), mRNA /cds=(69,1382) /gb=Nm_003919 /gi=10835046 /ug=Hs.110708 /len=1658	NM_003919	Hs.110708	NP_003910
hfcr3444	NM_003992	CDC-like kinase 3 (CLK3), transcript variant phclk3, mRNA /cds=(57,1529) /gb=Nm_003992 /gi=4502884 /ug=Hs.73987 /len=1762	NM_001292; NM_003992	Hs.73987	NP_003983
fcrb6181	NM_004152	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=Nm_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143

fcr1182	NM_004181	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA /cds=(75,746) /gb=NM_004181 /gi=21361090 /ug=Hs.76118 /len=1119	NM_004181	Hs.76118	NP_004172
fcr6915	NM_004192	acetylserotonin O-methyltransferase-like (ASMTL), mRNA /cds=(1,1890) /gb=NM_004192 /gi=4757793 /ug=Hs.70327 /len=1890	NM_004192	Hs.70327	NP_004183
hfc1639	NM_004265	fatty acid desaturase 2 (FADS2), mRNA /cds=(151,1485) /gb=NM_004265 /gi=14141180 /ug=Hs.184641 /len=3149	NM_004265	Hs.184641	NP_004256
fcrb5455	NM_004269	cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa (CRSP8), mRNA /cds=(1,822) /gb=NM_004269 /gi=4758065 /ug=Hs.374262 /len=822	NM_004269	Hs.374262	NP_004260
ncrb5254	NM_004339	pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA /cds=(211,753) /gb=NM_004339 /gi=11038670 /ug=Hs.111126 /len=2737	NM_004339	Hs.111126	NP_004330

ncr3825	NM_004344	centrin, EF-hand protein, 2 (CETN2), mRNA /cds=(48,566) /gb=Nm_004344 /gi=4757901 /ug=Hs.82794 /len=1087	NM_004344	Hs.82794	NP_004335
ncrc5464	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) (NDUFS5), mRNA /cds=(72,392) /gb=Nm_004552 /gi=4758789 /ug=Hs.409829 /len=540	NM_004552	Hs.409829	NP_004543
seob7928	NM_004642	CDK2-associated protein 1 (CDK2AP1), mRNA /cds=(523,870) /gb=Nm_004642 /gi=17978492 /ug=Hs.433201 /len=1627	NM_004642	Hs.433201	NP_004633
miob0496	NM_004719	splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA /cds=(1211,4657) /gb=Nm_004719 /gi=4759171 /ug=Hs.51957 /len=5307	NM_004719	Hs.51957	NP_004710
seoa4102	NM_004780	transcription elongation factor A (SII)-like 1 (TCEAL1), mRNA /cds=(165,638) /gb=Nm_004780 /gi=4759215 /ug=Hs.95243 /len=1174	NM_004780	Hs.95243	NP_004771

seoa6930	NM_004798	kinesin family member 3B (KIF3B), mRNA	NM_004798	Hs.301206	NP_004789
ncrc0174	NM_004837	geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA /cds=(233,1135) /gb=Nm_004837 /gi=21359876 /ug=Hs.55498 /len=1489	NM_004837	Hs.55498	NP_004828
seob2161	NM_004905	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2) (AOP2), mRNA /cds=(44,718) /gb=Nm_004905 /gi=4758637 /ug=Hs.120 /len=1653	NM_004905	Hs.120	NP_004896
seoa0066	NM_005006	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (NDUFS1), mRNA /cds=(85,2268) /gb=Nm_005006 /gi=28269700 /ug=Hs.8248 /len=2382	NM_005006	Hs.8248	NP_004997
ncr7915	NM_005083	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 1 (U2AF1RS1), mRNA /cds=(112,1551) /gb=Nm_005083 /gi=13186299 /ug=Hs.103962 /len=1566	NM_005083	Hs.103962	NP_005074

ncr3380	NM_005178	B-cell CLL/lymphoma 3 (BCL3), mRNA /cds=(42,1382) /gb=Nm_005178 /gi=20336471 /ug=Hs.31210 /len=1813	NM_005178	Hs.31210	NP_005169
fcrb3288	NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST), mRNA /cds=(60,1430) /gb=Nm_005216 /gi=20070196 /ug=Hs.34789 /len=2045	NM_005216	Hs.34789	NP_005207
seoa4548	NM_005336	high density lipoprotein binding protein (vigilin) (HDLBP), mRNA	NM_005336	Hs.177516	NP_005327
seoc3552	BC041849	Similar to Rho-associated, coiled-coil containing protein kinase 1, clone IMAGE:5269982, mRNA		Hs.17820	NP_005397
seoa5473	NM_005408	chemokine (C-C motif) ligand 13 (CCL13), mRNA /cds=(76,372) /gb=Nm_005408 /gi=22538799 /ug=Hs.11383 /len=861	NM_005408	Hs.11383	NP_005399
seoc4060	AF006516	eps8 binding protein e3B1 mRNA, complete cds	NM_005470	Hs.24752	NP_005461

miob7231	AA705851	ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412		Hs.443872	NP_005495
fcrb0623	NM_005517	high-mobility group nucleosomal binding domain 2 (HMGN2), mRNA /cds=(108,380) /gb=Nm_005517 /gi=5031748 /ug=Hs.181163 /len=1198	NM_005517	Hs.181163	NP_005508
seoc0514	NM_005531	interferon, gamma-inducible protein 16 (IFI16), mRNA /cds=(265,2454) /gb=Nm_005531 /gi=5031778 /ug=Hs.155530 /len=2709	NM_005531	Hs.155530	NP_005522
seoa6393	NM_005537	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=Nm_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528

fcr0535	NM_005539	inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA /cds=(102,1193) /gb=Nm_005539 /gi=5031796 /ug=Hs.124029 /len=2640	NM_005539	Hs.124029	NP_005530
seoa2639	NM_005545	immunoglobulin superfamily containing leucine-rich repeat (ISLR), mRNA /cds=(99,1385) /gb=Nm_005545 /gi=5031808 /ug=Hs.102171 /len=2110	NM_005545	Hs.102171	NP_005536
mioc1440	NM_005578	LIM domain containing preferred translocation partner in lipoma (LPP), mRNA /cds=(247,2085) /gb=Nm_005578 /gi=5031886 /ug=Hs.180398 /len=5656	NM_005578	Hs.180398	NP_005569
seoa0737	NM_005591	MRE11 meiotic recombination 11 A (S. cerevisiae) (MRE11A), transcript variant 1, mRNA /cds=(160,2286) /gb=Nm_005591 /gi=24234691 /ug=Hs.20555 /len=4852	NM_005590; NM_005591	Hs.20555	NP_005582
seoa8669	NM_005638	synaptobrevin-like 1 (SYBL1), mRNA /cds=(115,777) /gb=Nm_005638 /gi=27545446 /ug=Hs.24167 /len=2588	NM_005638	Hs.24167	NP_005629



seob1744	NM_005652	telomeric repeat binding factor 2 (TERF2), mRNA /cds=(126,1628) /gb=Nm_005652 /gi=21536372 /ug=Hs.100030 /len=2909	NM_005652	Hs.100030	NP_005643
seoa7910	AK055659	cDNA FLJ31097 fis, clone IMR321000210	NM_005723	Hs.8037	NP_005714
miod5622	NM_005725	tetraspan 2 (TSPAN-2), mRNA /cds=(33,698) /gb=Nm_005725 /gi=21264579 /ug=Hs.234863 /len=3179	NM_005725	Hs.234863	NP_005716
mioc5226	NM_005786	serologically defined colon cancer antigen 33 (SDCCAG33), mRNA /cds=(295,2358) /gb=Nm_005786 /gi=15451922 /ug=Hs.284217 /len=2858	NM_005786	Hs.284217	NP_005777
mioc8793	NM_005795	calcitonin receptor-like (CALCRL), mRNA /cds=(555,1940) /gb=Nm_005795 /gi=5031620 /ug=Hs.152175 /len=3018	NM_005795	Hs.152175	NP_005786
mioa6807	NM_005800	highly charged protein (D13S106E), mRNA /cds=(178,3456) /gb=Nm_005800 /gi=5031648 /ug=Hs.151236 /len=3650	NM_005800	Hs.151236	NP_005791

miob5010	NM_005849	immunoglobulin superfamily, member 6 (IGSF6), mRNA /cds=(45,770) /gb=Nm_005849 /gi=5031672 /ug=Hs.135194 /len=1019	NM_005849	Hs.135194	NP_005840
mioa9510	NM_005857	zinc metalloproteinase (STE24 yeast) (ZMPSTE24), mRNA /cds=(166,1593) /gb=Nm_005857 /gi=18379365 /ug=Hs.25846 /len=3103	NM_005857	Hs.25846	NP_005848
mioa3080	NM_005903	MAD, mothers against decapentaplegic 5 (Drosophila) (MADH5), mRNA /cds=(193,1590) /gb=Nm_005903 /gi=20070216 /ug=Hs.37501 /len=2049	NM_005903	Hs.37501	NP_005894
ncrc2289	NM_005907	mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA /cds=(443,2404) /gb=Nm_005907 /gi=24497518 /ug=Hs.25253 /len=4139	NM_005907	Hs.25253	NP_005898

seob1161	NM_006003	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(91,915) /gb=NM_006003 /gi=5174742 /ug=Hs.3712 /len=1203	NM_006003	Hs.3712	NP_005994
fcrb9454	NM_006067	neighbor of COX4 (NOC4), mRNA /cds=(209,841) /gb=NM_006067 /gi=19923775 /ug=Hs.173162 /len=1950	NM_006067	Hs.173162	NP_006058
hfcr4114	NM_006086	tubulin, beta, 4 (TUBB4), mRNA /cds=(1,1353) /gb=NM_006086 /gi=5174736 /ug=Hs.159154 /len=1648	NM_006086	Hs.159154	NP_006077
fcrb5181	NM_006184	nucleobindin 1 (NUCB1), mRNA /cds=(27,1412) /gb=NM_006184 /gi=20070227 /ug=Hs.172609 /len=2311	NM_006184	Hs.172609	NP_006175

seob3148	NM_006216	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPINE2), mRNA /cds=(210,1406) /gb=Nm_006216 /gi=24307906 /ug=Hs.21858 /len=2129	NM_006216	Hs.21858	NP_006207
fcr2611	NM_006230	polymerase (DNA directed), delta 2, regulatory subunit 50kDa (POLD2), mRNA /cds=(79,1488) /gb=Nm_006230 /gi=5453923 /ug=Hs.74598 /len=1584	NM_006230	Hs.74598	NP_006221
hfc6600	NM_006233	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa (POLR2I), mRNA /cds=(36,413) /gb=Nm_006233 /gi=14589954 /ug=Hs.47062 /len=458	NM_006233	Hs.47062	NP_006224
seoa1582	NM_006306	SMC1 structural maintenance of chromosomes 1-like 1 (yeast) (SMC1L1), mRNA	NM_006306	Hs.211602	NP_006297

fcrb8162	NM_006322	tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA /cds=(85,2808) /gb=Nm_006322 /gi=5453659 /ug=Hs.9884 /len=3795	NM_006322	Hs.9884	NP_006313
fcr3367	NM_006325	RAN, member RAS oncogene family (RAN), mRNA /cds=(115,765) /gb=Nm_006325 /gi=6042206 /ug=Hs.10842 /len=1656	NM_006325	Hs.10842	NP_006316
ncr5509	NM_006329	fibulin 5 (FBLN5), mRNA /cds=(463,1809) /gb=Nm_006329 /gi=19743802 /ug=Hs.11494 /len=2646	NM_006329	Hs.11494	NP_006320
hfcr4446	NM_006353	high mobility group nucleosomal binding domain 4 (HMGN4), mRNA /cds=(239,511) /gb=Nm_006353 /gi=23238232 /ug=Hs.236774 /len=1980	NM_006353	Hs.236774	NP_006344
hfcr2524	NM_006372	NS1-associated protein 1 (NSAP1), mRNA /cds=(526,2397) /gb=Nm_006372 /gi=23397426 /ug=Hs.373499 /len=2932	NM_006372	Hs.373499	NP_006363

mioa0072	NM_006409	actin related protein 2/3 complex, subunit 1A, 41kDa (ARPC1A), mRNA /cds=(148,1260) /gb=Nm_006409 /gi=22907051 /ug=Hs.90370 /len=1619	NM_006409	Hs.90370	NP_006400
seob5792	NM_006431	chaperonin containing TCP1, subunit 2 (beta) (CCT2), mRNA /cds=(58,1665) /gb=Nm_006431 /gi=5453602 /ug=Hs.432970 /len=1935	NM_006431	Hs.432970	NP_006422
seoc1058	NM_006474	lung type-I cell membrane-associated glycoprotein (T1A-2), mRNA /cds=(234,722) /gb=Nm_006474 /gi=18767663 /ug=Hs.135150 /len=1081	NM_006474	Hs.135150	NP_006465
ncrb7586	NM_006530	glioma-amplified sequence-41 (GAS41), mRNA /cds=(222,905) /gb=Nm_006530 /gi=5729837 /ug=Hs.4029 /len=1404	NM_006530	Hs.4029	NP_006521
hfcr3007	NM_006561	CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA /cds=(35,1564) /gb=Nm_006561 /gi=5729815 /ug=Hs.211610 /len=5516	NM_006561	Hs.211610	NP_006552

ncr9502	NM_006682	fibrinogen-like 2 (FGL2), mRNA /cds=(34,1353) /gb=Nm_006682 /gi=5730074 /ug=Hs.351808 /len=1496	NM_006682	Hs.351808	NP_006673
fcrc1738	NM_006701	similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=Nm_006701 /gi=20070233 /ug=Hs.433683 /len=1415	NM_006701	Hs.433683	NP_006692
fcrc5160	NM_002313	actin binding LIM protein 1 (ABLIM1), transcript variant ABLIM-1, mRNA /cds=(100,2436) /gb=Nm_002313 /gi=21284382 /ug=Hs.158203 /len=7581	NM_002313; NM_006719; NM_006720	Hs.158203	NP_006711
ncrb3541	NM_006766	runt-related transcription factor binding protein 2 (RUNXBP2), mRNA /cds=(394,6408) /gb=Nm_006766 /gi=5803097 /ug=Hs.82210 /len=7869	NM_006766	Hs.82210	NP_006757
ncrc3690	BG166990	602344930F1 NIH_MGC_89 cDNA clone IMAGE:4454934 5', mRNA sequence /clone=IMAGE:4454934 /clone_end=5' /gb=BG166990 /gi=12673693 /ug=Hs.440568 /len=1137		Hs.440568	NP_006764

mioc5751	NM_006795	EH-domain containing 1 (EHD1), mRNA /cds=(247,1851) /gb=Nm_006795 /gi=5803008 /ug=Hs.155119 /len=3508	NM_006795	Hs.155119	NP_006786
hfc1918	NM_006868	RAB31, member RAS oncogene family (RAB31), mRNA /cds=(61,645) /gb=Nm_006868 /gi=5803130 /ug=Hs.223025 /len=921	NM_006868	Hs.223025	NP_006859
fcr6409	AF022654	homeodomain protein (OG12) mRNA, complete cds	NM_003030; NM_006884	Hs.55967	NP_006875
fcr0955	NM_006886	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=Nm_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
miob5752	NM_006925	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=Nm_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856



ncrb0462	NM_006996	solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), mRNA /cds=(238,1731) /gb=Nm_006996 /gi=27734718 /ug=Hs.30246 /len=3668	NM_006996	Hs.30246	NP_008927
mioc3107	NM_006997	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=Nm_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
fcrb1406	NM_007007	cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=Nm_007007 /gi=5901927 /ug=Hs.64542 /len=3426	NM_007007	Hs.64542	NP_008938
fcrb6874	NM_007100	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) /gb=Nm_007100 /gi=6005716 /ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
fcrb2334	NM_007104	ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=Nm_007104 /gi=15431287 /ug=Hs.425293 /len=700	NM_007104	Hs.425293	NP_009035

miob7223	NM_007149	zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA /cds=(268,2523) /gb=Nm_007149 /gi=24307934 /ug=Hs.158174 /len=3095	NM_007149	Hs.158174	NP_009080
seoc1561	NM_007218	patched related protein translocated in renal cancer (TRC8), mRNA /cds=(215,2209) /gb=Nm_007218 /gi=21314653 /ug=Hs.28285 /len=2481	NM_007218	Hs.28285	NP_009149
fcrb0993	NM_007242	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (DBP5 yeast) (DDX19), mRNA /cds=(105,1544) /gb=Nm_007242 /gi=13787207 /ug=Hs.289097 /len=1806	NM_007242	Hs.289097	NP_009173
fcrb4860	NM_007255	xylosylprotein beta 1,4- galactosyltransferase, polypeptide 7 (galactosyltransferase I) (B4GALT7), mRNA /cds=(41,1024) /gb=Nm_007255 /gi=6005951 /ug=Hs.54702 /len=1669	NM_007255	Hs.54702	NP_009186
hfcr6394	NM_007263	coatamer protein complex, subunit epsilon (COPE), mRNA /cds=(43,969) /gb=Nm_007263 /gi=6005734 /ug=Hs.10326 /len=1130	NM_007263	Hs.10326	NP_009194

fcrb7051	NM_007358	putative DNA binding protein (M96), mRNA /cds=(244,2025) /gb=Nm_007358 /gi=6678763 /ug=Hs.31016 /len=2648	NM_007358	Hs.31016	NP_031384
fcrb7852	NM_012073	chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717) /gb=Nm_012073 /gi=24307938 /ug=Hs.1600 /len=1961	NM_012073	Hs.1600	NP_036205
miod5114	NM_012086	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=Nm_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
hfc2201	NM_012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=Nm_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333
fcr6866	NM_012321	U6 snRNA-associated Sm-like protein (LSM4), mRNA /cds=(49,468) /gb=Nm_012321 /gi=6912485 /ug=Hs.76719 /len=1033	NM_012321	Hs.76719	NP_036453

fcrb9448	AK022921	cDNA FLJ12859 fis, clone NT2RP2003522, highly similar to zinc finger DNA binding protein 99 (ZNF281) mRNA		Hs.59757	NP_036614
seoc3229	NM_013250	zinc finger protein 215 (ZNF215), mRNA /cds=(589,2142) /gb=Nm_013250 /gi=7019582 /ug=Hs.161427 /len=3480	NM_013250	Hs.161427	NP_037382
seoc6295	NM_013252	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(198,764) /gb=Nm_013252 /gi=10281668 /ug=Hs.126355 /len=3510	NM_013252	Hs.126355	NP_037384
hfcr6376	NM_013277	Rac GTPase activating protein 1 (RACGAP1), mRNA /cds=(225,2123) /gb=Nm_013277 /gi=21361396 /ug=Hs.23900 /len=3237	NM_013277	Hs.23900	NP_037409
ncr0531	NM_013332	hypoxia-inducible protein 2 (HIG2), mRNA /cds=(206,397) /gb=Nm_013332 /gi=7019408 /ug=Hs.61762 /len=1372	NM_013332	Hs.61762	NP_037464

mioc5113	NM_013943	chloride intracellular channel 4 (CLIC4), mRNA /cds=(198,959) /gb=Nm_013943 /gi=7330334 /ug=Hs.25035 /len=4318	NM_013943	Hs.25035	NP_039234
miob7970	NM_014033	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=Nm_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752
ncrc5335	NM_014046	mitochondrial ribosomal protein S18B (MRPS18B), nuclear gene encoding mitochondrial protein, mRNA /cds=(38,814) /gb=Nm_014046 /gi=16554601 /ug=Hs.274417 /len=1439	NM_014046	Hs.274417	NP_054765
fcrb1890	NM_014077	DKFZP586O0120 protein (DKFZP586O0120), mRNA /cds=(21,359) /gb=Nm_014077 /gi=7661695 /ug=Hs.4766 /len=1465	NM_014077	Hs.4766	NP_054796
seob5629	AK096676	cDNA FLJ39357 fis, clone PEBLM2003914. /gb=AK096676 /gi=21756220 /ug=Hs.22635 /len=2315		Hs.22635	NP_054874

seoa6395	NM_014160	HSPC070 protein (HSPC070), mRNA /cds=(332,1582) /gb=Nm_014160 /gi=8850222 /ug=Hs.279474 /len=3050	NM_014160	Hs.279474	NP_054879
mioa3411	NM_014210	ecotropic viral integration site 2A (EVI2A), mRNA /cds=(220,918) /gb=Nm_014210 /gi=7657074 /ug=Hs.70499 /len=1563	NM_014210	Hs.70499	NP_055025
mioa1944	NM_014280	DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=Nm_014280 /gi=7657610 /ug=Hs.433540 /len=1525	NM_014280	Hs.433540	NP_055095
seob4197	NM_014287	pM5 protein (PM5), mRNA /cds=(1,3669) /gb=Nm_014287 /gi=10947030 /ug=Hs.439182 /len=4182	NM_014287	Hs.439182	NP_055102
fcrb7760	NM_014292	chromobox 6 (CBX6), mRNA /cds=(30,1268) /gb=Nm_014292 /gi=10140848 /ug=Hs.107374 /len=6014	NM_014292	Hs.107374	NP_055107
ncrc2227	NM_014319	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=Nm_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014319	Hs.7256	NP_055134

miod2255	NM_014333	immunoglobulin superfamily, member 4 (IGSF4), mRNA /cds=(4,1332) /gb=Nm_014333 /gi=22095346 /ug=Hs.70337 /len=3512	NM_014333	Hs.70337	NP_055148
seoa0388	NM_014341	mitochondrial carrier 1 (MTCH1), nuclear gene encoding mitochondrial protein, mRNA /cds=(1,1119) /gb=Nm_014341 /gi=7657344 /ug=Hs.279939 /len=1890	NM_014341	Hs.279939	NP_055156
seob9574	NM_014394	growth hormone inducible transmembrane protein (GHITM), mRNA /cds=(130,1089) /gb=Nm_014394 /gi=7657479 /ug=Hs.433957 /len=2374	NM_014394	Hs.433957	NP_055209
mioa4770	NM_014409	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa (TAF5L), mRNA /cds=(98,1867) /gb=Nm_014409 /gi=21269865 /ug=Hs.26782 /len=3065	NM_014409	Hs.26782	NP_055224

miob0487	NM_014575	schwannomin interacting protein 1 (SCHIP1), mRNA /cds=(70,1533) /gb=Nm_014575 /gi=7657539 /ug=Hs.61490 /len=2112	NM_014575	Hs.61490	NP_055390
fcr6801	NM_014628	gene predicted from cDNA with a complete coding sequence (CMT2), mRNA /cds=(4,828) /gb=Nm_014628 /gi=7661917 /ug=Hs.124 /len=1233	NM_014628	Hs.124	NP_055443
seoa7542	NM_014656	KIAA0040 gene product (KIAA0040), mRNA /cds=(921,1382) /gb=Nm_014656 /gi=7657258 /ug=Hs.158282 /len=4564	NM_014656	Hs.158282	NP_055471
seob3105	NM_014730	KIAA0152 gene product (KIAA0152), mRNA /cds=(129,1007) /gb=Nm_014730 /gi=7661947 /ug=Hs.181418 /len=6322	NM_014730	Hs.181418	NP_055545
fcr4376	D14657	hypothetical protein (KIAA0101)	NM_014736	Hs.81892	NP_055551
miod4140	NM_014781	RB1-inducible coiled-coil 1 (RB1CC1), mRNA /cds=(516,5291) /gb=Nm_014781 /gi=7661991 /ug=Hs.50421 /len=6614	NM_014781	Hs.50421	NP_055596



fcr5029	NM_014828	chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=Nm_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643
miob0986	NM_014828	chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=Nm_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643
ncrb3942	NM_014892	KIAA1116 protein (KIAA1116), mRNA /cds=(186,4001) /gb=Nm_014892 /gi=7662491 /ug=Hs.227602 /len=4664	NM_014892	Hs.227602	NP_055707
miob3314	NM_014950	zinc finger and BTB domain containing 1 (ZBTB1), mRNA /cds=(263,2197) /gb=Nm_014950 /gi=7662437 /ug=Hs.372699 /len=3990	NM_014950	Hs.372699	NP_055765
miod1316	NM_014953	mitotic control protein dis3 (DIS3), mRNA /cds=(37,2913) /gb=Nm_014953 /gi=19923415 /ug=Hs.323346 /len=7320	NM_014953	Hs.323346	NP_055768

mioa9062	NM_014999	RAB21, member RAS oncogene family (RAB21), mRNA /cds=(256,933) /gb=Nm_014999 /gi=7661921 /ug=Hs.184627 /len=2630	NM_014999	Hs.184627	NP_055814
mioc1697	BC014378	clone IMAGE:4044107, mRNA		Hs.64691	NP_055991
mioc2082	NM_015247	cylindromatosis (turban tumor syndrome) (CYLD), mRNA /cds=(392,3262) /gb=Nm_015247 /gi=14165257 /ug=Hs.18827 /len=5371	NM_015247	Hs.18827	NP_056062
mioa6404	NM_015252	KIAA0903 protein (KIAA0903), mRNA /cds=(349,4044) /gb=Nm_015252 /gi=24308022 /ug=Hs.16218 /len=5048	NM_015252	Hs.16218	NP_056067
seoa4422	NM_015338	additional sex combs like 1 (Drosophila) (ASXL1), mRNA /cds=(259,4884) /gb=Nm_015338 /gi=27734730 /ug=Hs.3686 /len=6864	NM_015338	Hs.3686	NP_056153
fcrc5789	NM_015416	cervical cancer 1 protooncogene (DKFZP586A011), mRNA /cds=(9,1091) /gb=Nm_015416 /gi=21166356 /ug=Hs.75884 /len=2118	NM_015416	Hs.75884	NP_056231

mioa4196	NM_015435	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=Nm_015435 /gi=19923421 /ug=Hs.48320 /len=4357	NM_015435	Hs.48320	NP_056250
mioa8607	NM_015440	DKFZP586G1517 protein (DKFZP586G1517), mRNA /cds=(127,2328) /gb=Nm_015440 /gi=24308062 /ug=Hs.44155 /len=2749	NM_015440	Hs.44155	NP_056255
mioc7209	AL833852	mRNA; cDNA DKFZp761G0111 (from clone DKFZp761G0111)	NM_015472	Hs.24341	NP_056287
seoa7373	NM_015558	synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), mRNA /cds=(61,1251) /gb=Nm_015558 /gi=27754185 /ug=Hs.154429 /len=3723	NM_015558	Hs.154429	NP_056373
ncrc2507	AB014542	mRNA for KIAA0642 protein, partial cds. /cds=(200,4189) /gb=AB014542 /gi=20521116 /ug=Hs.323317 /len=5937		Hs.323317	NP_056390
fcrb6587	NM_015702	hypothetical protein CL25022 (CL25022), mRNA /cds=(158,1048) /gb=Nm_015702 /gi=7661547 /ug=Hs.5324 /len=1416	NM_015702	Hs.5324	NP_056517

seoa5665	NM_015899	putative glycolipid transfer protein (LOC51054), mRNA /cds=(538,1713) /gb=Nm_015899 /gi=7705683 /ug=Hs.334649 /len=1839	NM_015899	Hs.334649	NP_056983
seob2155	AL833555	mRNA; cDNA DKFZp686A1444 (from clone DKFZp686A1444)		Hs.278428	NP_056986
fcrb2353	NM_015965	cell death-regulatory protein GRIM19 (GRIM19), mRNA /cds=(212,895) /gb=Nm_015965 /gi=21361821 /ug=Hs.279574 /len=1023	NM_015965	Hs.279574	NP_057049
mioc2891	NM_016059	peptidylprolyl isomerase (cyclophilin)-like 1 (PPIL1), mRNA /cds=(222,722) /gb=Nm_016059 /gi=22035675 /ug=Hs.27693 /len=1723	NM_016059	Hs.27693	NP_057143
fcr6011	AK055223	cDNA FLJ30661 fis, clone DFNES2000526		Hs.432729	NP_057178
mioa5729	NM_016103	GTP-binding protein Sara (LOC51128), mRNA /cds=(151,747) /gb=Nm_016103 /gi=7705826 /ug=Hs.279582 /len=1280	NM_016103	Hs.279582	NP_057187

ncrc6888	NM_016107	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=Nm_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191
seob7369	NM_016129	COP9 constitutive photomorphogenic subunit 4 (Arabidopsis) (COPS4), mRNA /cds=(7,1224) /gb=Nm_016129 /gi=7705844 /ug=Hs.6671 /len=1613	NM_016129	Hs.6671	NP_057213
seoa4464	NM_000965	retinoic acid receptor, beta (RARβ), transcript variant 1, mRNA /cds=(469,1815) /gb=Nm_000965 /gi=14916493 /ug=Hs.171495 /len=3119	NM_000965; NM_016152	Hs.171495	NP_057236
fcrb5166	NM_016221	dynactin 4 (p62) (DCTN4), mRNA /cds=(22,1404) /gb=Nm_016221 /gi=19923450 /ug=Hs.328865 /len=3837	NM_016221	Hs.328865	NP_057305
miob4793	NM_016258	high-glucose-regulated protein 8 (HGRG8), mRNA /cds=(151,1863) /gb=Nm_016258 /gi=7705410 /ug=Hs.20993 /len=2730	NM_016258	Hs.20993	NP_057342

seoa3578	NM_016302	protein x 0001 (LOC51185), mRNA /cds=(34,1044) /gb=Nm_016302 /gi=10047097 /ug=Hs.18925 /len=1668	NM_016302	Hs.18925	NP_057386
miob6721	NM_016315	CED-6 protein (CED-6), mRNA /cds=(429,1343) /gb=Nm_016315 /gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056	NP_057399
mioa5902	NM_016331	zinc finger protein ANC_2H01 (LOC51193), mRNA /cds=(446,1903) /gb=Nm_016331 /gi=7705934 /ug=Hs.22879 /len=3013	NM_016331	Hs.22879	NP_057415
fcrb4280	NM_016404	hypothetical protein HSPC152 (HSPC152), mRNA /cds=(36,413) /gb=Nm_016404 /gi=7705476 /ug=Hs.79259 /len=612	NM_016404	Hs.79259	NP_057488
seoa7583	NM_016570	CDA14 (LOC51290), mRNA /cds=(89,1225) /gb=Nm_016570 /gi=7706104 /ug=Hs.26813 /len=1378	NM_016570	Hs.26813	NP_057654
ncrc6015	NM_016617	hypothetical protein BM-002 (BM-002), mRNA /cds=(40,297) /gb=Nm_016617 /gi=7705299 /ug=Hs.367646 /len=2529	NM_016617	Hs.367646	NP_057701

seob7614	NM_016648	HDCMA18P protein (HDCMA18P), mRNA /cds=(532,1176) /gb=NM_016648 /gi=7705400 /ug=Hs.278635 /len=1438	NM_016648	Hs.278635	NP_057732
seob5556	NM_016947	chromosome 6 open reading frame 48 (C6orf48), mRNA /cds=(42,422) /gb=NM_016947 /gi=8393383 /ug=Hs.109798 /len=711	NM_016947	Hs.109798	NP_058643
miod5060	NM_017426	nucleoporin 54kDa (NUP54), mRNA /cds=(129,1652) /gb=NM_017426 /gi=26051236 /ug=Hs.9082 /len=2358	NM_017426	Hs.9082	NP_059122
fcrb3615	NM_017510	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510	Hs.279929	NP_059980
fcr5836	NM_017510	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510	Hs.279929	NP_059980

fcrb5536	NM_017607	protein phosphatase 1, regulatory (inhibitor) subunit 12C (PPP1R12C), mRNA /cds=(19,2367) /gb=Nm_017607 /gi=14149715 /ug=Hs.235975 /len=2944	NM_017607	Hs.235975	NP_060077
mioc0222	NM_017654	hypothetical protein FLJ20073 (FLJ20073), mRNA /cds=(17,1909) /gb=Nm_017654 /gi=8923080 /ug=Hs.65641 /len=3401	NM_017654	Hs.65641	NP_060124
miod3739	NM_017851	hypothetical protein FLJ20509 (FLJ20509), mRNA /cds=(418,1041) /gb=Nm_017851 /gi=8923470 /ug=Hs.30634 /len=2369	NM_017851	Hs.30634	NP_060321
ncr2842	NM_017876	hypothetical protein FLJ20552 (FLJ20552), mRNA /cds=(130,1065) /gb=Nm_017876 /gi=21361772 /ug=Hs.69554 /len=1681	NM_017876	Hs.69554	NP_060346
ncr1941	NM_017987	RUN and FYVE domain containing 2 (RUFY2), mRNA /cds=(12,1832) /gb=Nm_017987 /gi=24850106 /ug=Hs.154091 /len=2080	NM_017987	Hs.154091	NP_060457



fcrc0039	NM_018011	hypothetical protein FLJ10154 (FLJ10154), mRNA /cds=(246,1067) /gb=Nm_018011 /gi=8922258 /ug=Hs.179972 /len=1734	NM_018011	Hs.179972	NP_060481
ncr8156	NM_018013	hypothetical protein FLJ10159 (FLJ10159), mRNA /cds=(1,807) /gb=Nm_018013 /gi=8922262 /ug=Hs.22505 /len=2070	NM_018013	Hs.22505	NP_060483
seoc5911	NM_018019	hypothetical protein FLJ10193 (FLJ10193), mRNA /cds=(57,497) /gb=Nm_018019 /gi=22907057 /ug=Hs.235195 /len=2222	NM_018019	Hs.235195	NP_060489
fcrc5850	NM_018067	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=Nm_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537
mioa3939	NM_018158	solute carrier family 4 (anion exchanger), member 1, adaptor protein (SLC4A1AP), mRNA /cds=(283,2673) /gb=Nm_018158 /gi=8922556 /ug=Hs.306000 /len=2954	NM_018158	Hs.306000	NP_060628

miod6646	NM_018178	hypothetical protein FLJ10687 (FLJ10687), mRNA /cds=(46,903) /gb=Nm_018178 /gi=21361715 /ug=Hs.29379 /len=2992	NM_018178	Hs.29379	NP_060648
fcrb6202	NM_018182	hypothetical protein FLJ10700 (FLJ10700), mRNA /cds=(184,1872) /gb=Nm_018182 /gi=8922595 /ug=Hs.295909 /len=3434	NM_018182	Hs.295909	NP_060652
seoc1163	AF225871	polybromo-1 (PB1) mRNA, complete cds, alternatively spliced	NM_018165; NM_018313	Hs.44143	NP_060783
seob6139	NM_018352	hypothetical protein FLJ11184 (FLJ11184), mRNA /cds=(113,724) /gb=Nm_018352 /gi=8922922 /ug=Hs.267446 /len=1748	NM_018352	Hs.267446	NP_060822
seob6084	NM_018421	TBC1 domain family, member 2 (TBC1D2), mRNA /cds=(1622,3028) /gb=Nm_018421 /gi=8922166 /ug=Hs.135917 /len=3431	NM_018421	Hs.135917	NP_060891
mioc6970	NM_018465	uncharacterized hematopoietic stem/progenitor cells protein MDS030 (MDS030), mRNA /cds=(206,649) /gb=Nm_018465 /gi=8923931 /ug=Hs.181385 /len=927	NM_018465	Hs.181385	NP_060935

ncrc0151	NM_018507	hypothetical protein PRO1843 (PRO1843), mRNA /cds=(965,1255) /gb=Nm_018507 /gi=8924082 /ug=Hs.283330 /len=1268	NM_018507	Hs.283330	NP_060977
ncrb0757	BC029427	clone MGC:32681 IMAGE:4809776, mRNA, complete cds		Hs.410294	NP_061008
mioc6360	NM_018675	zinc finger protein 302 (ZNF302), mRNA /cds=(337,1773) /gb=Nm_018675 /gi=11034834 /ug=Hs.125287 /len=2978	NM_018443; NM_018675	Hs.125287	NP_061145
ncr0004	NM_018847	KIAA1354 protein (KIAA1354), mRNA /cds=(514,2367) /gb=Nm_018847 /gi=24308180 /ug=Hs.106283 /len=4373	NM_018847	Hs.106283	NP_061335
seoa5586	AL133623	mRNA; cDNA DKFZp434P0721 (from clone DKFZp434P0721); partial cds /cds=(1,3481) /gb=AL133623 /gi=6599261 /ug=Hs.82501 /len=8281		Hs.82501	NP_061874
fcrb6613	NM_019095	chromosome 20 open reading frame 155 (C20orf155), mRNA	NM_019095	Hs.3569	NP_061968

seoc2614	NM_019095	hypothetical protein (LOC54675), mRNA /cds=(1,906) /gb=Nm_019095 /gi=10092646 /ug=Hs.3569 /len=906	NM_019095	Hs.3569	NP_061968
mioc5039	NM_020038	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA /cds=(71,1603) /gb=Nm_020038 /gi=9955973 /ug=Hs.90786 /len=5380	NM_003786; NM_020037; NM_020038	Hs.90786	NP_064422
fcrb2317	NM_020150	SAR1 protein (SAR1), mRNA /cds=(125,721) /gb=Nm_020150 /gi=21361614 /ug=Hs.110796 /len=3003	NM_020150	Hs.110796	NP_064535
mioa5059	NM_020166	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=Nm_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
seoc3854	NM_020368	disrupter of silencing 10 (SAS10), mRNA /cds=(162,1601) /gb=Nm_020368 /gi=9966798 /ug=Hs.322901 /len=2035	NM_020368	Hs.322901	NP_065101

miob2601	NM_020443	neuron navigator 1 (NAV1), mRNA /cds=(348,5972) /gb=Nm_020443 /gi=27262621 /ug=Hs.6298 /len=11365	NM_020443	Hs.6298	NP_065176
miod0935	AL080079	mRNA; cDNA DKFZp564D0462 (from clone DKFZp564D0462)	NM_020455	Hs.44197	NP_065188
fcr4056	AF004876	54TMp (54tm) (=S83365 RAB5- interaction protein)	NM_020470	Hs.406422	NP_065203
ncrc9528	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B- cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=Nm_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
mioa7955	NM_020905	retinol dehydrogenase 14 (all- trans and 9-cis) (RDH14), mRNA /cds=(64,1074) /gb=Nm_020905 /gi=10190745 /ug=Hs.288880 /len=1538	NM_020905	Hs.288880	NP_065956
fcrb8134	NM_021070	latent transforming growth factor beta binding protein 3 (LTBP3), mRNA /cds=(1,3771) /gb=Nm_021070 /gi=18497287 /ug=Hs.289019 /len=4064	NM_021070	Hs.289019	NP_066548

seoa0302	NM_021088	zinc finger protein 2 (A1-5) (ZNF2), mRNA /cds=(855,1733) /gb=Nm_021088 /gi=20304090 /ug=Hs.192285 /len=2630	NM_021088	Hs.192285	NP_066574
seoa0040	NM_021109	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=Nm_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
miob0931	NM_021111	reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA /cds=(93,3008) /gb=Nm_021111 /gi=11863155 /ug=Hs.29640 /len=4414	NM_021111	Hs.29640	NP_066934
seoc7910	NM_021183	hypothetical protein similar to small G proteins, especially RAP- 2A (LOC57826), mRNA /cds=(17,568) /gb=Nm_021183 /gi=10880976 /ug=Hs.225979 /len=3165	NM_021183	Hs.225979	NP_067006
fcrb5961	NM_021227	DC2 protein (DC2), mRNA /cds=(60,509) /gb=Nm_021227 /gi=24308270 /ug=Hs.103180 /len=1090	NM_021227	Hs.103180	NP_067050

fcrb6279	NM_004069	adaptor-related protein complex 2, sigma 1 subunit (AP2S1), transcript variant AP17, mRNA /cds=(71,499) /gb=Nm_004069 /gi=11038644 /ug=Hs.119591 /len=781	NM_004069; NM_021575	Hs.119591	NP_067586
seob3404	NM_021632	zinc-finger protein ZBRK1 (ZBRK1), mRNA /cds=(184,1782) /gb=Nm_021632 /gi=11056003 /ug=Hs.130965 /len=2260	NM_021632	Hs.130965	NP_067645
fcrb5051	NM_021825	hypothetical protein MDS025 (MDS025), mRNA /cds=(363,1127) /gb=Nm_021825 /gi=21361605 /ug=Hs.154938 /len=1585	NM_021825	Hs.154938	NP_068597
seoc1216	AL049447	mRNA; cDNA DKFZp586A0722 (from clone DKFZp586A0722)		Hs.433334	NP_068603
fcrb1547	NM_022003	FXD domain containing ion transport regulator 6 (FXD6), mRNA /cds=(67,354) /gb=Nm_022003 /gi=11612654 /ug=Hs.3807 /len=1677	NM_022003	Hs.3807	NP_071286
seoa9665	NM_022145	leucine zipper protein FKSG14 (FKSG14), mRNA /cds=(265,1074) /gb=Nm_022145 /gi=16905072 /ug=Hs.192843 /len=1794	NM_022145	Hs.192843	NP_071428

miod7052	NM_022483	hypothetical protein FLJ21657 (FLJ21657), mRNA /cds=(342,989) /gb=Nm_022483 /gi=19923589 /ug=Hs.26498 /len=2995	NM_022483	Hs.26498	NP_071928
mioa2851	NM_022731	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=Nm_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
mioc0121	NM_022731	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=Nm_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
ncrc9642	NM_022756	hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=Nm_022756 /gi=20149668 /ug=Hs.17118 /len=1558	NM_022756	Hs.17118	NP_073593
mioa8074	NM_022763	FAD104 (FAD104), mRNA	NM_022763	Hs.299883	NP_073600
seob3747	NM_022763	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=Nm_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600
miod6988	NM_022845	core-binding factor, beta subunit (CBFB), transcript variant 1, mRNA	NM_001755; NM_022845	Hs.179881	NP_074036



seoc0422	AL161991	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324	NM_022913	Hs.71252	NP_075064
seob4011	AL161991	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324	NM_022913	Hs.71252	NP_075064
ncrc3116	NM_023926	hypothetical protein FLJ12895 (FLJ12895), mRNA /cds=(410,1942) /gb=Nm_023926 /gi=21314715 /ug=Hs.235390 /len=2804	NM_023926	Hs.235390	NP_076415
fcrc1849	NM_024297	hypothetical protein MGC2941 (MGC2941), mRNA /cds=(172,969) /gb=Nm_024297 /gi=13236519 /ug=Hs.288217 /len=2005	NM_024297	Hs.288217	NP_077273
miob2944	NM_024520	hypothetical protein FLJ22555 (FLJ22555), mRNA /cds=(323,1198) /gb=Nm_024520 /gi=13375659 /ug=Hs.3592 /len=1530	NM_024520	Hs.3592	NP_078796

ncrc7038	NM_024551	hypothetical protein FLJ21432 (FLJ21432), mRNA /cds=(110,886) /gb=Nm_024551 /gi=13375714 /ug=Hs.334854 /len=3500	NM_024551	Hs.334854	NP_078827
seob8986	NM_024568	chromodomain helicase DNA binding protein 1-like (CHD1L), mRNA /cds=(332,1897) /gb=Nm_024568 /gi=24308292 /ug=Hs.14570 /len=2936	NM_024568	Hs.14570	NP_078844
seoa6389	BC013945	Similar to hypothetical protein FLJ21212, clone MGC:24384 IMAGE:4064736, mRNA, complete cds	NM_024642	Hs.47099	NP_078918
ncr2899	NM_024657	hypothetical protein FLJ11565 (FLJ11565), mRNA /cds=(19,2301) /gb=Nm_024657 /gi=21362027 /ug=Hs.61763 /len=3037	NM_024657	Hs.61763	NP_078933
miod4023	NM_024659	hypothetical protein FLJ11753 (FLJ11753), mRNA /cds=(14,832) /gb=Nm_024659 /gi=13375910 /ug=Hs.62348 /len=1868	NM_024659	Hs.62348	NP_078935
mioc4929	NM_024699	hypothetical protein FLJ14007 (FLJ14007), mRNA /cds=(15,821) /gb=Nm_024699 /gi=13375984 /ug=Hs.99519 /len=1793	NM_024699	Hs.99519	NP_078975

mioa7617	NM_024755	hypothetical protein FLJ13213 (FLJ13213), mRNA /cds=(234,1670) /gb=Nm_024755 /gi=13376087 /ug=Hs.331328 /len=2617	NM_024755	Hs.331328	NP_079031
ncr7532	NM_024945	hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=Nm_024945 /gi=13376426 /ug=Hs.284137 /len=3413	NM_024945	Hs.284137	NP_079221
seoc3801	AL832993	mRNA; cDNA DKFZp666L233 (from clone DKFZp666L233)	NM_030571	Hs.9788	NP_085048
mioa4183	NM_002380	matrilin 2 (MATN2), transcript variant 1, mRNA /cds=(126,2996) /gb=Nm_002380 /gi=13518036 /ug=Hs.19368 /len=3496	NM_002380; NM_030583	Hs.19368	NP_085072
mioa2970	NM_030751	transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA /cds=(25,3399) /gb=Nm_030751 /gi=28077090 /ug=Hs.232068 /len=3952	NM_030751	Hs.232068	NP_110378
miob9233	BC050366	thioredoxin domain containing, clone IMAGE:5764221, mRNA			NP_110382

seoa3274	NM_031214	hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=Nm_031214 /gi=13654285 /ug=Hs.300624 /len=1138	NM_031214	Hs.300624	NP_112491
seob7637	NM_031216	sec13-like protein (SEC13L), mRNA /cds=(107,1189) /gb=Nm_031216 /gi=14591917 /ug=Hs.301048 /len=3492	NM_031216	Hs.301048	NP_112493
fcrb2933	NM_031286	SH3 domain binding glutamic acid-rich protein like 3 (SH3BGRL3), mRNA /cds=(72,353) /gb=Nm_031286 /gi=13775197 /ug=Hs.109051 /len=764	NM_031286	Hs.109051	NP_112576
seoa4324	NM_031287	SF3b10 (SF3b10), mRNA	NM_031287	Hs.110695	NP_112577
mioc1808	NM_031452	hypothetical protein MGC2560 (MGC2560), mRNA /cds=(195,551) /gb=Nm_031452 /gi=13899288 /ug=Hs.80624 /len=1229	NM_031452	Hs.80624	NP_113640
fcrb7247	NM_031453	hypothetical protein MGC11034 (MGC11034), mRNA /cds=(246,641) /gb=Nm_031453 /gi=13899290 /ug=Hs.103378 /len=3301	NM_031453	Hs.103378	NP_113641

ncrc2705	NM_031461	CocoaCrisp (LOC83690), mRNA /cds=(376,1878) /gb=Nm_031461 /gi=21314740 /ug=Hs.182364 /len=2962	NM_031461	Hs.182364	NP_113649
miod6896	NM_031469	SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA /cds=(180,503) /gb=Nm_031469 /gi=13899316 /ug=Hs.9167 /len=4676	NM_031469	Hs.9167	NP_113657
mioc3370	NM_031483	itchy E3 ubiquitin protein ligase (mouse) (ITCH), mRNA /cds=(171,2759) /gb=Nm_031483 /gi=27477108 /ug=Hs.98074 /len=6357	NM_031483	Hs.98074	NP_113671
mioa2173	NM_005016	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=Nm_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016; NM_031989	Hs.63525	NP_114366
seoc0861	NM_032041	neurocalcin delta (NCALD), mRNA /cds=(121,702) /gb=Nm_032041 /gi=14042973 /ug=Hs.90063 /len=3300	NM_032041	Hs.90063	NP_114430

mioa9007	NM_032121	hypothetical protein DKFZp564K142 similar to implantation-associated protein (DKFZp564K142), mRNA /cds=(30,1037) /gb=Nm_032121 /gi=14149774 /ug=Hs.323562 /len=2241	NM_032121	Hs.323562	NP_115497
mioc8079	NM_032148	hypothetical protein DKFZp434K0427 (DKFZP434K0427), mRNA /cds=(342,1814) /gb=Nm_032148 /gi=14149818 /ug=Hs.238996 /len=2375	NM_032148	Hs.238996	NP_115524
fcrc0134	NM_032211	lysyl oxidase-like 4 (LOXL4), mRNA /cds=(152,2422) /gb=Nm_032211 /gi=19923658 /ug=Hs.306814 /len=3665	NM_032211	Hs.306814	NP_115587
seob2953	NM_032273	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=Nm_032273 /gi=14150016 /ug=Hs.108338 /len=782	NM_032273	Hs.108338	NP_115649
ncrc9055	NM_032313	hypothetical protein MGC3232 (MGC3232), mRNA /cds=(85,2181) /gb=Nm_032313 /gi=14150077 /ug=Hs.8715 /len=2316	NM_032313	Hs.8715	NP_115689

fcrb8110	NM_032347	zinc finger protein 397 (ZNF397), mRNA /cds=(136,963) /gb=Nm_032347 /gi=14150142 /ug=Hs.269914 /len=1439	NM_032347	Hs.269914	NP_115723
mioa9258	NM_032661	hypothetical protein MGC5139 (MGC5139), mRNA /cds=(14,115) /gb=Nm_032661 /gi=14249217 /ug=Hs.127610 /len=457	NM_032661	Hs.127610	NP_116050
ncr2304	NM_032682	forkhead box P1 (FOXP1), mRNA /cds=(432,2465) /gb=Nm_032682 /gi=19923670 /ug=Hs.274344 /len=4954	NM_032682	Hs.274344	NP_116071
seoc3443	NM_032822	hypothetical protein FLJ14668 (FLJ14668), mRNA /cds=(59,475) /gb=Nm_032822 /gi=14249519 /ug=Hs.334644 /len=1786	NM_032822	Hs.334644	NP_116211
miod2082	NM_032859	hypothetical protein FLJ14906 (FLJ14906), mRNA /cds=(131,736) /gb=Nm_032859 /gi=14249591 /ug=Hs.183528 /len=2492	NM_032859	Hs.183528	NP_116248
ncrc3773	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=Nm_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259

fcrb7573	NM_032907	hypothetical protein MGC14421 (MGC14421), mRNA /cds=(474,1616) /gb=Nm_032907 /gi=14249681 /ug=Hs.334713 /len=1772	NM_032907	Hs.334713	NP_116296
fcr3287	NM_002607	platelet-derived growth factor alpha polypeptide (PDGFA), transcript variant 1, mRNA /cds=(839,1474) /gb=Nm_002607 /gi=15208657 /ug=Hs.37040 /len=2797	NM_002607; NM_033023	Hs.37040	NP_148983
ncr7768	NM_033055	likely ortholog of mouse hippocampus abundant gene transcript 1 (HIAT1), mRNA /cds=(6,1124) /gb=Nm_033055 /gi=24308343 /ug=Hs.21015 /len=2230	NM_033055	Hs.21015	NP_149044
fcr1150	NM_033209	Thy-1 co-transcribed (LOC94105), mRNA /cds=(1289,1717) /gb=Nm_033209 /gi=24475732 /ug=Hs.345643 /len=1818	NM_033209	Hs.345643	NP_149986



fcr6395	NM_003672	CDC14 cell division cycle 14 A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA /cds=(466,2250) /gb=Nm_003672 /gi=15451928 /ug=Hs.65993 /len=4262	NM_003672; NM_033312; NM_033313	Hs.65993	NP_201570
miod2665	NM_033318	hypothetical gene supported by AL449243 (LOC91689), mRNA /cds=(80,403) /gb=Nm_033318 /gi=21314768 /ug=Hs.306083 /len=1586	NM_033318	Hs.306083	NP_201575
mioc2720	NM_033495	KIAA1309 protein (KIAA1309), mRNA /cds=(211,2025) /gb=Nm_033495 /gi=15741229 /ug=Hs.348262 /len=3119	NM_033495	Hs.348262	NP_277030
fcrb1296	NM_015414	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=Nm_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414; NM_033643	Hs.433411	NP_378669
mioa4542	NM_033655	cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA /cds=(408,3872) /gb=Nm_033655 /gi=16306508 /ug=Hs.212839 /len=5017	NM_024879; NM_033655	Hs.212839	NP_387504

ncrc9916	BQ109159	imageqc_6_2001/snk86bdr81.y1 NIH_MGC_12 cDNA clone IMAGE:5110111 5', mRNA sequence /clone=IMAGE:5110111 /clone_end=5' /gb=BQ109159 /gi=20158813 /ug=Hs.433575 /len=604		Hs.433575	NP_387506
fcrb6870	NM_007103	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (NDUFV1), mRNA /cds=(70,1464) /gb=Nm_007103 /gi=20149567 /ug=Hs.7744 /len=1566	NM_007103	Hs.7744	NP_438172
ncrc9758	NM_052966	chromosome 1 open reading frame 24 (C1orf24), mRNA /cds=(195,2981) /gb=Nm_052966 /gi=16757969 /ug=Hs.48778 /len=6919	NM_022083; NM_052966	Hs.48778	NP_443198
ncr1912	NM_053025	myosin, light polypeptide kinase (MYLK), transcript variant 1, mRNA /cds=(120,5864) /gb=Nm_053025 /gi=16950610 /ug=Hs.211582 /len=5925	NM_005965; NM_053025; NM_053026; NM_053027; NM_053028; NM_053029; NM_053030; NM_053031; NM_053032	Hs.211582	NP_444260

ncr5909	BC036034	endothelial differentiation, lysophosphatidic acid G-protein- coupled receptor, 2, clone MGC:33157 IMAGE:5272431, mRNA, complete cds	NM_001401; NM_057159	Hs.75794	NP_476500
seoa2795	NM_080821	chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=Nm_080821 /gi=18201877 /ug=Hs.352413 /len=3026	NM_080821	Hs.352413	NP_543011
miod7066	NM_030781	collectin sub-family member 12 (COLEC12), transcript variant II, mRNA /cds=(172,2040) /gb=Nm_030781 /gi=18641357 /ug=Hs.29423 /len=4685	NM_030781; NM_130386	Hs.29423	NP_569057
mioc8640	NM_133259	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=Nm_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
seoa1661	NM_133493	CD109 (CD109), mRNA /cds=(113,4450) /gb=Nm_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964	NP_598000

mioc2340	NM_133502	zinc finger protein 274 (ZNF274), transcript variant ZNF274c, mRNA /cds=(460,2421) /gb=Nm_133502 /gi=19743800 /ug=Hs.83761 /len=2839	NM_016324; NM_016325; NM_133502	Hs.83761	NP_598009
seob3112	NM_001920	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=Nm_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920; NM_133503; NM_133504; NM_133505; NM_133506; NM_133507	Hs.433989	NP_598014
seob6379	NM_015293	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=Nm_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293; NM_033071; NM_133650	Hs.192102	NP_598411
fcr4784	NM_134269	smoothelin (SMTN), transcript variant 2, mRNA /cds=(219,2966) /gb=Nm_134269 /gi=19913395 /ug=Hs.149098 /len=3294	NM_006932; NM_134269; NM_134270	Hs.149098	NP_599032
seob0047	U09820	helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115	NM_000489; NM_138270; NM_138271	Hs.96264	NP_612115

seoc1948	NM_138436	hypothetical protein BC013035 (LOC114926), mRNA /cds=(128,430) /gb=Nm_138436 /gi=19923964 /ug=Hs.10018 /len=836	NM_138436	Hs.10018	NP_612445
ncr5529	BC014000	clone MGC:20208 IMAGE:3936339, mRNA, complete cds /cds=(330,1832) /gb=BC014000 /gi=15559281 /ug=Hs.58461 /len=2733		Hs.58461	NP_612456
fcrb5507	NM_138455	collagen triple helix repeat containing 1 (CTHRC1), mRNA /cds=(109,840) /gb=Nm_138455 /gi=19923988 /ug=Hs.283713 /len=1245	NM_138455	Hs.283713	NP_612464
fcrb5705	NM_138555	kinesin family member 23 (KIF23), transcript variant 1, mRNA /cds=(118,3000) /gb=Nm_138555 /gi=20143966 /ug=Hs.270845 /len=3636	NM_004856; NM_138555	Hs.270845	NP_612565
fcrb5164	NM_138785	hypothetical protein BC014320 (LOC116254), mRNA /cds=(28,1020) /gb=Nm_138785 /gi=20302037 /ug=Hs.240767 /len=1143	NM_138785	Hs.240767	NP_620140

mioa4326	NM_000919	peptidylglycine alpha-amidating monooxygenase (PAM), transcript variant 1, mRNA /cds=(374,3298) /gb=Nm_000919 /gi=21070983 /ug=Hs.83920 /len=3960	NM_000919; NM_138766; NM_138821; NM_138822	Hs.83920	NP_620177
seoa5894	NM_058183	SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=Nm_058183 /gi=21040317 /ug=Hs.92909 /len=8482	NM_003103; NM_032195; NM_058183; NM_138925; NM_138926; NM_138927	Hs.92909	NP_620305
fcr4896	NM_139168	splicing factor, arginine/serine- rich 12 (SFRS12), mRNA /cds=(342,1868) /gb=Nm_139168 /gi=21040254 /ug=Hs.381165 /len=3811	NM_139168	Hs.381165	NP_631907
seoa1480	NM_139207	nucleosome assembly protein 1- like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=Nm_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_004537; NM_139207	Hs.302649	NP_631946

miod0642	AW071632	wt94d09.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2515121 3', mRNA sequence /clone=IMAGE:2515121 /clone_end=3' /gb=AW071632 /gi=6026630 /ug=Hs.414880 /len=122		Hs.414880	NP_653087
fcrb5439	NM_007040	E1B-55kDa-associated protein 5 (E1B-AP5), transcript variant 1, mRNA /cds=(174,2744) /gb=Nm_007040 /gi=21536325 /ug=Hs.155218 /len=3872	NM_007040; NM_144732; NM_144733; NM_144734	Hs.155218	NP_653335
seoc1504	NM_144976	hypothetical protein MGC26914 (MGC26914), mRNA /cds=(148,1809) /gb=Nm_144976 /gi=21699059 /ug=Hs.202974 /len=2900	NM_144976	Hs.202974	NP_659413
seoc0149	NM_004619	TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA /cds=(194,1867) /gb=Nm_004619 /gi=22027625 /ug=Hs.29736 /len=4132	NM_004619; NM_145759	Hs.29736	NP_665702

seob0850	NM_017613	downstream neighbor of SON (DONSON), transcript variant 1, mRNA /cds=(68,1768) /gb=Nm_017613 /gi=22035582 /ug=Hs.17834 /len=2189	NM_017613; NM_145794; NM_145795	Hs.17834	NP_665738
fcrb5296	NM_015129	sepin 6 (SEPT6), transcript variant II, mRNA /cds=(257,1561) /gb=Nm_015129 /gi=22035575 /ug=Hs.90998 /len=2686	NM_015129; NM_145799; NM_145800; NM_145802	Hs.90998	NP_665801
miob8373	NM_007217	programmed cell death 10 (PDCD10), transcript variant 1, mRNA /cds=(399,1037) /gb=Nm_007217 /gi=22538790 /ug=Hs.28866 /len=1454	NM_007217; NM_145859; NM_145860	Hs.28866	NP_665859
ncrc9784	NM_002624	prefoldin 5 (PFDN5), transcript variant 1, mRNA /cds=(36,500) /gb=Nm_002624 /gi=22202632 /ug=Hs.288856 /len=661	NM_002624; NM_145896; NM_145897	Hs.288856	NP_665904



miob4886	NM_148954	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9), transcript variant 2, mRNA /cds=(52,681) /gb=Nm_148954 /gi=23110931 /ug=Hs.381081 /len=748	NM_002800; NM_148954	Hs.381081	NP_683756
fcrb3519	NM_148980	Williams Beuren syndrome chromosome region 20C (WBSCR20C), transcript variant 3, mRNA /cds=(794,1399) /gb=Nm_148980 /gi=23200003 /ug=Hs.334837 /len=1857	NM_032158; NM_148936; NM_148980; NM_149379	Hs.334837	NP_684281
seoa0511	NM_015976	sorting nexin 7 (SNX7), transcript variant 1, mRNA /cds=(268,1431) /gb=Nm_015976 /gi=23111053 /ug=Hs.127241 /len=1798	NM_015976; NM_152238	Hs.127241	NP_689424
miod1450	NM_152334	hypothetical protein FLJ25005 (FLJ25005), mRNA /cds=(166,1467) /gb=Nm_152334 /gi=22748728 /ug=Hs.181426 /len=2109	NM_152334	Hs.181426	NP_689547

seob7747	NM_152367	hypothetical protein FLJ38716 (FLJ38716), mRNA /cds=(266,1354) /gb=Nm_152367 /gi=22748790 /ug=Hs.376194 /len=3229	NM_152367	Hs.376194	NP_689580
fcrb1687	NM_152573	hypothetical protein FLJ31614 (FLJ31614), mRNA /cds=(312,881) /gb=Nm_152573 /gi=22749180 /ug=Hs.351442 /len=1766	NM_152573	Hs.351442	NP_689786
ncrc9549	NM_152683	hypothetical protein FLJ33167 (FLJ33167), mRNA /cds=(217,1899) /gb=Nm_152683 /gi=22749372 /ug=Hs.351470 /len=2078	NM_152683	Hs.351470	NP_689896
fcr1883	NM_152713	integral membrane protein 1 (ITM1), mRNA /cds=(130,2247) /gb=Nm_152713 /gi=22749414 /ug=Hs.287850 /len=2553	NM_152713	Hs.287850	NP_689926
seoa3109	NM_006597	heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=Nm_006597 /gi=24234684 /ug=Hs.180414 /len=2276	NM_006597; NM_153201	Hs.180414	NP_694881
mioa8831	NM_153225	hypothetical protein FLJ40021 (FLJ40021), mRNA /cds=(364,792) /gb=Nm_153225 /gi=23397486 /ug=Hs.41185 /len=1972	NM_153225	Hs.41185	NP_694957

mioc4009	NM_153348	F-box only protein 29 (FBXO29), mRNA /cds=(88,1884) /gb=Nm_153348 /gi=24158491 /ug=Hs.350985 /len=4874	NM_153348	Hs.350985	NP_699179
mioc0350	NM_153373	hypothetical protein MGC15875 (MGC15875), mRNA /cds=(235,1587) /gb=Nm_153373 /gi=24119276 /ug=Hs.315054 /len=2010	NM_032921; NM_153373	Hs.315054	NP_699204
fcrb8196	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=Nm_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
seoc1167	NM_153812	hypothetical protein MGC43399 (MGC43399), mRNA /cds=(383,1285) /gb=Nm_153812 /gi=24432092 /ug=Hs.7299 /len=3684	NM_153812	Hs.7299	NP_722519
ncr7570	NM_153831	PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA /cds=(231,3389) /gb=Nm_153831 /gi=27886591 /ug=Hs.740 /len=4453	NM_005607; NM_153831	Hs.740	NP_722560

seob5007	NM_170705	isoprenylcysteine carboxyl methyltransferase (ICMT), transcript variant 2, mRNA /cds=(457,1023) /gb=Nm_170705 /gi=24797155 /ug=Hs.183212 /len=3654	NM_012405; NM_170705	Hs.183212	NP_733806
fcrb5146	NM_170707	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=Nm_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_005572; NM_170707; NM_170708	Hs.377973	NP_733822
miob9506	NM_172240	TUWD12 (TUWD12), mRNA /cds=(106,1542) /gb=Nm_172240 /gi=26665868 /ug=Hs.25130 /len=2984	NM_172240	Hs.25130	NP_758440
ncrc4907	NM_004555	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), transcript variant 2, mRNA /cds=(211,3417) /gb=Nm_004555 /gi=27886542 /ug=Hs.172674 /len=4005	NM_004555; NM_173163; NM_173164; NM_173165	Hs.172674	NP_775188
ncrb8134	NM_173473	hypothetical protein LOC119504 (LOC119504), mRNA /cds=(119,451) /gb=Nm_173473 /gi=27735038 /ug=Hs.426296 /len=1177	NM_173473	Hs.426296	NP_775744

mioc7700	NM_173473	hypothetical protein LOC119504 (LOC119504), mRNA /cds=(119,451) /gb=NM_173473 /gi=27735038 /ug=Hs.426296 /len=1177	NM_173473	Hs.426296	NP_775744
ncr2861	AK074985	cDNA FLJ90504 fis, clone NT2RP3004090, weakly similar to GOLIATH PROTEIN. /cds=(103,1305) /gb=AK074985 /gi=22760786 /ug=Hs.171802 /len=2452	NM_173647	Hs.171802	NP_775918
seob9694	NM_173852	keratinocytes associated protein 2 (KCP2), mRNA /cds=(1,489) /gb=NM_173852 /gi=27777660 /ug=Hs.374854 /len=489	NM_173852	Hs.374854	NP_776251
hfcr1694	NM_004135	isocitrate dehydrogenase 3 (NAD ) gamma (IDH3G), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	NM_004135; NM_174869	Hs.75253	NP_777358
mioc1117	NM_174890	hypothetical protein LOC93550 (LOC93550), mRNA /cds=(217,2400) /gb=NM_174890 /gi=28376663 /ug=Hs.377945 /len=3256	NM_174890	Hs.377945	NP_777550

mioc0621	NM_174909	hypothetical protein LOC153339 (LOC153339), mRNA /cds=(21,239) /gb=Nm_174909 /gi=28372532 /ug=Hs.374538 /len=726	NM_174909	Hs.374538	NP_777569
fcrb3285	NM_014599	melanoma antigen, family D, 2 (MAGED2), mRNA /cds=(97,1917) /gb=Nm_014599 /gi=21264316 /ug=Hs.4943 /len=2077	NM_014599; NM_177433	Hs.4943	NP_803182
miod6500	BQ181216	UI-H-EU0-azl-k-15-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5850374 3', mRNA sequence /clone=IMAGE: 5850374 /clone_end=3' /gb=BQ181216 /gi=20356708 /ug=Hs.442170 /len=1044		Hs.442170	NP_835228
miod0500	NM_032023	AD037 protein (AD037), mRNA /cds=(107,1072) /gb=Nm_032023 /gi=23510359 /ug=Hs.296162 /len=2481	NM_032023	Hs.296162	NP_835281
miod4216	BC041375	clone IMAGE:5274527, mRNA /gb=BC041375 /gi=27370608 /ug=Hs.11700 /len=3905	NM_178314	Hs.11700	NP_847884

fcrb6483	NM_020830	WD40 and FYVE domain containing 1 (WDFY1), mRNA /cds=(30,1262) /gb=Nm_020830 /gi=18482372 /ug=Hs.44743 /len=4585	NM_020830	Hs.44743	NP_848127
miob9458	AI377292	te65d01.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2091553 3', mRNA sequence /clone=IMAGE:2091553 /clone_end=3' /gb=AI377292 /gi=4187145 /ug=Hs.410753 /len=238		Hs.410753	NP_848642
mioc2216	NM_006814	proteasome (prosome, macropain) inhibitor subunit 1 (PI31) (PSMF1), mRNA /cds=(127,942) /gb=Nm_006814 /gi=5803122 /ug=Hs.405813 /len=3188	NM_006814	Hs.405813	NP_848694
ncrc3073	NM_006348	component of oligomeric golgi complex 5 (COG5), mRNA /cds=(52,2571) /gb=Nm_006348 /gi=5453669 /ug=Hs.239631 /len=3105	NM_006348	Hs.239631	NP_859422

fcrb7072	AK075459	cDNA PSEC0152 fis, clone PLACE1007885. /cds=(20,1144) /gb=AK075459 /gi=22761560 /ug=Hs.350475 /len=2130		Hs.350475	NP_877437
ncr1692	NM_133171	engulfment and cell motility 2 (ced-12 C. elegans) (ELMO2), transcript variant 1, mRNA /cds=(141,2303) /gb=Nm_133171 /gi=19718768 /ug=Hs.96560 /len=3630	NM_022086; NM_133171	Hs.96560	NP_877496
hfc1433	NM_016240	scavenger receptor class A, member 3 (SCARA3), mRNA /cds=(142,1962) /gb=Nm_016240 /gi=7705335 /ug=Hs.128856 /len=3636	NM_016240	Hs.128856	NP_878185
seoa3752	NM_000935	procollagen-lysine, 2- oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2), mRNA /cds=(1,2214) /gb=Nm_000935 /gi=4505888 /ug=Hs.41270 /len=3503	NM_000935	Hs.41270	NP_891988
seob5748	NM_031268	PRO0461 protein (PRO0461), mRNA /gb=Nm_031268 /gi=20588827 /ug=Hs.25063 /len=1100	NM_031268	Hs.25063	NP_112558



seob7984	AF094481	trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	NM_003663		NP_003654
seoc4654	X07718	fibronectin gene ED-A region	NM_002026; NM_054034		NP_002017; NP_473375
ncrb2544	NM_018996	hypothetical protein FLJ20015 (FLJ20015), mRNA /cds=(32,523) /gb=NM_018996 /gi=9506648 /ug=Hs.375614 /len=1457	NM_018996	Hs.375614	NP_061869
ncrc1316	XM_294901	hypothetical gene supported by U79248; AK056929; BC041875 (LOC339290), mRNA			XP_294901
ncr1954	AB042297	PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds	NM_031938		NP_114144

**Table 7a: depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for (a) mild OA only in OA cartilage as compared to cartilage isolated from normal individuals using the Affymetrix™ U133A Array analysis as disclosed herein.**

Gene name	Common name	Genbank	Description	RefSeq
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203400_s_at		NM_001063	gb:NM_001063.1 /DEF=Homo sapiens transferrin (TF), mRNA. /FEA=mRNA /GEN=TF /PROD=transferrin precursor /DB_XREF=gi:4557870 /UG=Hs.284176 transferrin /FL=gb:M12530.1 gb:NM_001063.1	
214674_at	USP19	AW451502	ubiquitin specific protease 19	
210794_s_at		AF119863	Consensus includes gb:AF119863.1 /DEF=Homo sapiens PRO2160 mRNA, complete cds. /FEA=mRNA /PROD=PRO2160 /DB_XREF=gi:7770162 /UG=Hs.112844 maternally expressed 3 /FL=gb:AF119863.1	

202994_s_at	Z95331	Consensus includes gb:Z95331 /DEF=Human DNA sequence from clone CTA-941F9 on chromosome 22q13 Contains the 3 end of the FBLN1 gene for Fibulin 1 isoforms B, C and D, the first exon of the gene for a novel protein (the ortholog of mouse brain protein E46), ESTs, STSs, GSSs and two... /FEA=mRNA_1 /DB_XREF=gi:6572282 /UG=Hs.79732 fibulin 1 /FL=gb:U01244.1 gb:NM_006486.1
218630_at	NM_017777	gb:NM_017777.1 /DEF=Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA. /FEA=mRNA /GEN=FLJ20345 /PROD=hypothetical protein FLJ20345 /DB_XREF=gi:8923323 /UG=Hs.20558 hypothetical protein FLJ20345 /FL=gb:NM_017777.1

222186_at	AL109684	Consensus includes gb:AL109684.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 27080. /FEA=mRNA /DB_XREF=gi:5689805 /UG=Hs.306329 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 27080
201791_s_at	NM_001360	gb:NM_001360.1 /DEF=Homo sapiens 7-dehydrocholesterol reductase (DHCR7), mRNA. /FEA=mRNA /GEN=DHCR7 /PROD=7-dehydrocholesterol reductase /DB_XREF=gi:4503320 /UG=Hs.11806 7-dehydrocholesterol reductase /FL=gb:BC000054.1 gb:AF034544.1 gb:AF067127.1 gb:AF096305.1 gb:NM_001360.1

213147_at		NM_018951	Consensus includes gb:AI375919 /FEA=EST /DB_XREF=gi:4175909 /DB_XREF=est:tc14d04.x1 /CLONE=IMAGE:2063815 /UG=Hs.110637 homeo box A10 /FL=gb:NM_018951.1	
204153_s_at		NM_002405	gb:NM_002405.1 /DEF=Homo sapiens manic fringe (Drosophila) homolog (MFNG), mRNA. /FEA=mRNA /GEN=MFNG /PROD=manic fringe (Drosophila) homolog /DB_XREF=gi:4505158 /UG=Hs.31939 manic fringe (Drosophila) homolog /FL=gb:U94352.1 gb:NM_002405.1	

205702_at		NM_006608	gb:NM_006608.1 /DEF=Homo sapiens putative homeodomain transcription factor (PHTF1), mRNA. /FEA=mRNA /GEN=PHTF1 /PROD=putative homeodomain transcription factor /DB_XREF=gi:5729975 /UG=Hs.123637 putative homeodomain transcription factor /FL=gb:NM_006608.1	
210355_at		J03580	gb:J03580.1 /DEF=Human, parathyroid-like protein (associated with humoral hypercalcemia of malignancy) mRNA, complete cds. /FEA=mRNA /GEN=PTH1H /DB_XREF=gi:190705 /UG=Hs.89626 parathyroid hormone-like hormone /FL=gb:J03580.1	

211252_x_at		U36759	gb:U36759.1 /DEF=Human pre-T cell receptor alpha-type chain precursor, mRNA, complete cds. /FEA=mRNA /PROD=pre-T cell receptor alpha-type chain precursor /DB_XREF=gi:1127580 /UG=Hs.169002 Human pre TCR alpha mRNA, partial cds /FL=gb:U36759.1	
217566_s_at		BF222018	ESTs, Moderately similar to S71105 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) 4, prostate specific - human [H.sapiens]	
33814_at	PAK4	AF005046	p21(CDKN1A)-activated kinase 4	NM_005884
216521_s_at	c6.1A-TCRC	S72931	This sequence comes from Fig. 1; author's translation differs from conceptual translation; Homo sapiens T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene, partial cds.	

219961_s_at		NM_018474	gb:NM_018474.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HT013 (HT013), mRNA. /FEA=mRNA /GEN=HT013 /PROD=uncharacterized hypothalamus protein HT013 /DB_XREF=gi:8923814 /UG=Hs.173515 uncharacterized hypothalamus protein HT013 /FL=gb:AF220187.1 gb:NM_018474.1	
208463_at		NM_000809	gb:NM_000809.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA. /FEA=CDS /GEN=GABRA4 /PROD=gamma-aminobutyric acid A receptor, alpha 4precursor /DB_XREF=gi:4557604 /UG=Hs.248112 gamma-aminobutyric acid (GABA) A receptor, alpha 4 /FL=gb:NM_000809.1 gb:U30461.1	



218743_at		NM_024591	gb:NM_024591.1 /DEF=Homo sapiens hypothetical protein FLJ11749 (FLJ11749), mRNA. /FEA=mRNA /GEN=FLJ11749 /PROD=hypothetical protein FLJ11749 /DB_XREF=gi:13375782 /UG=Hs.22897 hypothetical protein FLJ11749 /FL=gb:NM_024591.1	
219184_x_at		NM_013337	gb:NM_013337.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 22 (yeast) homolog (TIM22), mRNA. /FEA=mRNA /GEN=TIM22 /PROD=translocase of inner mitochondrial membrane 22(yeast) homolog /DB_XREF=gi:7019552 /UG=Hs.87595 translocase of inner mitochondrial membrane 22 (yeast) homolog /FL=gb:BC002324.1 gb:AF155330.1 gb:NM_013337.1	

219645_at		NM_001231	gb:NM_001231.1 /DEF=Homo sapiens calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=CASQ1 /PROD=skeletal muscle calsequestrin 1 /DB_XREF=gi:4557406 /UG=Hs.60708 calsequestrin 1 (fast-twitch, skeletal muscle) /FL=gb:NM_001231.1 gb:S73775.1	
204479_at		NM_012383	gb:NM_012383.1 /DEF=Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /FEA=mRNA /GEN=OSTF1 /PROD=osteoclast stimulating factor 1 /DB_XREF=gi:6912563 /UG=Hs.95821 osteoclast stimulating factor 1 /FL=gb:U63717.1 gb:NM_012383.1	

201878_at		NM_005744	Consensus includes gb:N25546 /FEA=EST /DB_XREF=gi:1139894 /DB_XREF=est:yx76e05.s1 /CLONE=IMAGE:267680 /UG=Hs.181461 ariadne (Drosophila) homolog, ubiquitin- conjugating enzyme E2-binding protein, 1 /FL=gb:AF072832.1 gb:NM_005744.2	
212729_at		AB033058	Consensus includes gb:AI916274 /FEA=EST /DB_XREF=gi:5636129 /DB_XREF=est:wg99e04.x1 /CLONE=IMAGE:2379390 /UG=Hs.11101 KIAA1232 protein	
212726_at		AB014562	Consensus includes gb:AB014562.1 /DEF=Homo sapiens mRNA for KIAA0662 protein, partial cds. /FEA=mRNA /GEN=KIAA0662 /PROD=KIAA0662 protein /DB_XREF=gi:3327137 /UG=Hs.93868 KIAA0662 gene product	

203338_at		NM_006246	gb:NM_006246.1 /DEF=Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /FEA=mRNA /GEN=PPP2R5E /PROD=protein phosphatase 2, regulatory subunit B(B56), epsilon isoform /DB_XREF=gi:5453955 /UG=Hs.173328 protein phosphatase 2, regulatory subunit B (B56), epsilon isoform /FL=gb:L76703.1 gb:NM_006246.1	
215985_at		X92110	Consensus includes gb:X92110.1 /DEF=H.sapiens mRNA for hcgVIII protein. /FEA=mRNA /DB_XREF=gi:1216163 /UG=Hs.153618 HCGVIII-1 protein	

201511_at		NM_001087	gb:NM_001087.1 /DEF=Homo sapiens angio-associated, migratory cell protein (AAMP), mRNA. /FEA=mRNA /GEN=AAMP /PROD=angio-associated, migratory cell protein /DB_XREF=gi:4557228 /UG=Hs.83347 angio-associated, migratory cell protein /FL=gb:NM_001087.1 gb:M95627.1	
205231_s_at		NM_005670	gb:NM_005670.1 /DEF=Homo sapiens epilepsy, progressive myoclonus type 2, Lafora disease (laforin) (EPM2A), mRNA. /FEA=mRNA /GEN=EPM2A /PROD=epilepsy, progressive myoclonus type 2, Laforadisease (laforin) /DB_XREF=gi:11321612 /UG=Hs.22464 epilepsy, progressive myoclonus type 2, Lafora disease (laforin) /FL=gb:AF284580.1 gb:NM_005670.1 gb:AF084535.2	
212337_at		AI687738	ESTs	

219920_s_at		NM_021971	gb:NM_021971.1 /DEF=Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 2, mRNA. /FEA=mRNA /GEN=GMPPB /PROD=GDP-mannose pyrophosphorylase B, isoform 2 /DB_XREF=gi:11761620 /UG=Hs.28077 GDP-mannose pyrophosphorylase B /FL=gb:NM_021971.1 gb:BC001141.1 gb:AF135421.1	
211139_s_at		AF045452	gb:AF045452.1 /DEF=Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds. /FEA=mRNA /PROD=transcriptional regulatory protein p54 /DB_XREF=gi:3282824 /UG=Hs.107474 NGFI-A binding protein 1 (ERG1 binding protein 1) /FL=gb:AF045452.1	

209984_at		AB037901	gb:AB037901.1 /DEF=Homo sapiens GASC-1 mRNA, complete cds. /FEA=mRNA /GEN=GASC-1 /DB_XREF=gi:10567163 /UG=Hs.149918 gene amplified in squamous cell carcinoma 1; KIAA0780 protein /FL=gb:AB037901.1	
218761_at		NM_017610	gb:NM_017610.1 /DEF=Homo sapiens hypothetical protein DKFZp761D081 (DKFZp761D081), mRNA. /FEA=mRNA /GEN=DKFZp761D081 /PROD=hypothetical protein DKFZp761D081 /DB_XREF=gi:8922164 /UG=Hs.12504 hypothetical protein DKFZp761D081 /FL=gb:NM_017610.1	
201983_s_at	EGFR	AW157070	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	
215499_at	MAP2K3	AA780381	mitogen-activated protein kinase kinase 3	

219626_at		NM_024597	gb:NM_024597.1 /DEF=Homo sapiens hypothetical protein FLJ12649 (FLJ12649), mRNA. /FEA=mRNA /GEN=FLJ12649 /PROD=hypothetical protein FLJ12649 /DB_XREF=gi:13375794 /UG=Hs.24078 hypothetical protein FLJ12649 /FL=gb:NM_024597.1	
222209_s_at		AK000684	Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fis, clone KAIA4183. /FEA=mRNA /DB_XREF=gi:7020930 /UG=Hs.183887 hypothetical protein FLJ22104	



203300_x_at		NM_003916	gb:NM_003916.1 /DEF=Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA. /FEA=mRNA /GEN=AP1S2 /PROD=adaptor-related protein complex 1, sigma 2subunit /DB_XREF=gi:4506956 /UG=Hs.40368 adaptor-related protein complex 1, sigma 2 subunit /FL=gb:AF251295.1 gb:BC001117.1 gb:AB015320.1 gb:NM_003916.1	
203269_at		NM_003580	gb:NM_003580.1 /DEF=Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /FEA=mRNA /GEN=NSMAF /PROD=neutral sphingomyelinase (N-SMase) activationassociated factor /DB_XREF=gi:4505464 /UG=Hs.78687 neutral sphingomyelinase (N-SMase) activation associated factor /FL=gb:NM_003580.1	

214151_s_at	PIGB	AU144243	phosphatidylinositol glycan, class B	
212989_at	TUBGCP2	AI377497	tubulin, gamma complex associated protein 2	
201661_s_at		NM_004457	gb:NM_004457.2 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3), mRNA. /FEA=mRNA /GEN=FACL3 /PROD=long-chain fatty-acid-Coenzyme A ligase 3 /DB_XREF=gi:12669907 /UG=Hs.268012 fatty-acid-Coenzyme A ligase, long-chain 3 /FL=gb:NM_004457.2 gb:D89053.1 gb:AF116690.1	

201664_at	AL136877	<p>gb:AL136877.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434F205 (from clone DKFZp434F205); complete cds. /FEA=mRNA /GEN=DKFZp434F205 /PROD=hypothetical protein /DB_XREF=gi:6807670 /UG=Hs.50758 SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 /FL=gb:AB019987.1 gb:NM_005496.1 gb:AL136877.1</p>
201681_s_at	AB011155	<p>Consensus includes gb:AB011155.1 /DEF=Homo sapiens mRNA for KIAA0583 protein, partial cds. /FEA=mRNA /GEN=KIAA0583 /PROD=KIAA0583 protein /DB_XREF=gi:3043689 /UG=Hs.170290 discs, large (Drosophila) homolog 5 /FL=gb:U61843.1 gb:NM_004747.1</p>

210653_s_at		M55575	gb:M55575.1 /DEF=Human branched chain alpha-keto acid dehydrogenase (BCKDHB) E1-beta subunit mRNA, complete cds. /FEA=mRNA /GEN=BCKDHB /PROD=branched chain alpha-keto acid dehydrogenaseE1-beta subunit /DB_XREF=gi:179361 /UG=Hs.1265 branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) /FL=gb:M55575.1	
210691_s_at		AF275803	gb:AF275803.1 /DEF=Homo sapiens PNAS-107 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-107 /DB_XREF=gi:10834769 /UG=Hs.27258 calcyclin binding protein /FL=gb:AF275803.1	

210839_s_at		D45421	gb:D45421.1 /DEF=Human mRNA for phosphodiesterase I alpha, complete cds. /FEA=mRNA /PROD=phosphodiesterase I alpha /DB_XREF=gi:662289 /UG=Hs.174185 ectonucleotide pyrophosphatasephosphodiesterase 2 (autotaxin) /FL=gb:NM_006209.1 gb:D45421.1	
218143_s_at		NM_005697	gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mRNA /GEN=SCAMP2 /PROD=secretory carrier membrane protein 2 /DB_XREF=gi:5730030 /UG=Hs.238030 secretory carrier membrane protein 2 /FL=gb:BC001376.1 gb:BC004385.1 gb:AF005038.2 gb:NM_005697.2	

219973_at		NM_024590	gb:NM_024590.1 /DEF=Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /FEA=mRNA /GEN=FLJ23548 /PROD=hypothetical protein FLJ23548 /DB_XREF=gi:13375780 /UG=Hs.22895 hypothetical protein FLJ23548 /FL=gb:NM_024590.1	
203460_s_at		NM_007318	gb:NM_007318.1 /DEF=Homo sapiens presenilin 1 (Alzheimer disease 3) (PSEN1), transcript variant I-463, mRNA. /FEA=mRNA /GEN=PSEN1 /PROD=presenilin 1 isoform I-463 /DB_XREF=gi:7549812 /UG=Hs.3260 presenilin 1 (Alzheimer disease 3) /FL=gb:U40379.1 gb:L76517.1 gb:NM_007318.1	

201524_x_at		NM_003348	gb:NM_003348.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA. /FEA=mRNA /GEN=UBE2N /PROD=ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) /DB_XREF=gi:4507792 /UG=Hs.75355 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) /FL=gb:D83004.1 gb:BC000396.1 gb:BC003365.1 gb:NM_003348.1	
216005_at		BF434846	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]	

			gb:NM_014820.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 70 (yeast) homolog A (TOMM70A), mRNA. /FEA=mRNA /GEN=TOMM70A /PROD=translocase of outer mitochondrial membrane 70(yeast) homolog A /DB_XREF=gi:7662672 /UG=Hs.21198 translocase of outer mitochondrial membrane 70 (yeast) homolog A /FL=gb:BC003633.1 gb:AB018262.1 gb:NM_014820.1	
201519_at		NM_014820		
			gb:AB022663.1 /DEF=Homo sapiens HFB30 mRNA, complete cds. /FEA=mRNA /GEN=HFB30 /DB_XREF=gi:5019617 /UG=Hs.215857 ring finger protein 14 /FL=gb:AF060544.1 gb:NM_004290.1 gb:AB022663.1	
201824_at		AB022663		
219540_at	ZNF267	AU150728	zinc finger protein 267	



201807_at		NM_004896	gb:NM_004896.1 /DEF=Homo sapiens vacuolar protein sorting 26 (yeast homolog) (VPS26), mRNA. /FEA=mRNA /GEN=VPS26 /PROD=vacuolar protein sorting 26 (yeast homolog) /DB_XREF=gi:4758509 /UG=Hs.67052 vacuolar protein sorting 26 (yeast homolog) /FL=gb:AF054179.1 gb:NM_004896.1 gb:AF175266.1	
206858_s_at		NM_004503	gb:NM_004503.1 /DEF=Homo sapiens homeo box C6 (HOXC6), mRNA. /FEA=mRNA /GEN=HOXC6 /PROD=homeo box C6 /DB_XREF=gi:4758553 /UG=Hs.820 homeo box C6 /FL=gb:NM_004503.1	

210993_s_at		U54826	gb:U54826.1 /DEF=Human mad-related protein MADR1 mRNA, complete cds. /FEA=mRNA /PROD=mad-related protein MADR1 /DB_XREF=gi:1332713 /UG=Hs.79067 MAD (mothers against decapentaplegic, Drosophila) homolog 1 /FL=gb:U54826.1 gb:U59912.1	
209099_x_at		U73936	gb:U73936.1 /DEF=Homo sapiens Jagged 1 (HJ1) mRNA, complete cds. /FEA=mRNA /GEN=HJ1 /PROD=Jagged 1 /DB_XREF=gi:1695273 /UG=Hs.91143 jagged 1 (Alagille syndrome) /FL=gb:U61276.1 gb:U73936.1 gb:AF003837.1 gb:AF028593.1 gb:NM_000214.1	

210944_s_at		BC003169	gb:BC003169.1 /DEF=Homo sapiens, Similar to calpain 3, (p94), clone MGC:4403, mRNA, complete cds. /FEA=mRNA /PROD=Similar to calpain 3, (p94) /DB_XREF=gi:13111992 /UG=Hs.40300 calpain 3, (p94) /FL=gb:BC003169.1	
216941_s_at		AK026521	Consensus includes gb:AK026521.1 /DEF=Homo sapiens cDNA: FLJ22868 fis, clone KAT02340, highly similar to HUMTFSL1C Homo sapiens transcription factor SL1 mRNA. /FEA=mRNA /DB_XREF=gi:10439398 /UG=Hs.121044 TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kD	
36030_at	DKFZP586I2223	AL080214	intermediate filament-like MGC:2625	NM_015438; NM_080730; NM_080731
201736_s_at	TEB4	BF000409	similar to S. cerevisiae SSM4	
201752_s_at	ADD3	AI763123	adducin 3 (gamma)	

205554_s_at		NM_004944	gb:NM_004944.1 /DEF=Homo sapiens deoxyribonuclease I-like 3 (DNASE1L3), mRNA. /FEA=mRNA /GEN=DNASE1L3 /PROD=deoxyribonuclease I-like 3 /DB_XREF=gi:4826697 /UG=Hs.88646 deoxyribonuclease I-like 3 /FL=gb:U56814.1 gb:AF047354.1 gb:NM_004944.1	
213350_at	RPS11	BF680255	ribosomal protein S11	
202876_s_at		NM_002586	gb:NM_002586.1 /DEF=Homo sapiens pre-B-cell leukemia transcription factor 2 (PBX2), mRNA. /FEA=mRNA /GEN=PBX2 /PROD=pre-B-cell leukemia transcription factor 2 /DB_XREF=gi:4505624 /UG=Hs.93728 pre-B-cell leukemia transcription factor 2 /FL=gb:NM_002586.1	

214805_at		U79273	Consensus includes gb:U79273.1 /DEF=Human clone 23933 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710239 /UG=Hs.239483 Human clone 23933 mRNA sequence	
212535_at	MEF2A	AA142929	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	
221865_at	DKFZp547P234	BF969986	hypothetical protein DKFZp547P234	
218957_s_at		NM_025155	gb:NM_025155.1 /DEF=Homo sapiens hypothetical protein FLJ11848 (FLJ11848), mRNA. /FEA=mRNA /GEN=FLJ11848 /PROD=hypothetical protein FLJ11848 /DB_XREF=gi:13376750 /UG=Hs.289031 hypothetical protein FLJ11848 /FL=gb:NM_025155.1	

218124_at		NM_017750	gb:NM_017750.1 /DEF=Homo sapiens hypothetical protein FLJ20296 (FLJ20296), mRNA. /FEA=mRNA /GEN=FLJ20296 /PROD=hypothetical protein FLJ20296 /DB_XREF=gi:8923274 /UG=Hs.6603 hypothetical protein FLJ20296 /FL=gb:NM_017750.1	
205511_at		NM_017976	gb:NM_017976.1 /DEF=Homo sapiens hypothetical protein FLJ10038 (FLJ10038), mRNA. /FEA=mRNA /GEN=FLJ10038 /PROD=hypothetical protein FLJ10038 /DB_XREF=gi:8922197 /UG=Hs.181202 hypothetical protein FLJ10038 /FL=gb:NM_017976.1	

221617_at		AF077053	Consensus includes gb:AF077053.1 /DEF=Homo sapiens neuronal cell death-related protein mRNA, complete cds. /FEA=mRNA /PROD=neuronal cell death-related protein /DB_XREF=gi:4689153 /UG=Hs.171723 neuronal cell death-related protein /FL=gb:AF077053.1 gb:NM_015975.1 gb:AF220509.1	
221922_at	MCLC	AW195581	Mid-1-related chloride channel 1	
209317_at		AF008442	gb:AF008442.1 /DEF=Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds. /FEA=mRNA /PROD=RNA polymerase I subunit hRPA39 /DB_XREF=gi:2266928 /UG=Hs.5409 RNA polymerase I subunit /FL=gb:AF008442.1	

205711_x_at	NM_005174	gb:NM_005174.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), mRNA. /FEA=mRNA /GEN=ATP5C1 /PROD=ATP synthase, H+ transporting, mitochondrial F1complex, gamma polypeptide 1 /DB_XREF=gi:4885078 /UG=Hs.155433 ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 /FL=gb:D16563.1 gb:NM_005174.1
218937_at	NM_017810	gb:NM_017810.1 /DEF=Homo sapiens hypothetical protein FLJ20417 (FLJ20417), mRNA. /FEA=mRNA /GEN=FLJ20417 /PROD=hypothetical protein FLJ20417 /DB_XREF=gi:8923385 /UG=Hs.10710 hypothetical protein FLJ20417 /FL=gb:NM_017810.1



			Consensus includes gb:BF218922 /FEA=EST /DB_XREF=gi:11112418 /DB_XREF=est:601885091F1 /CLONE=IMAGE:4103447 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican)	
221731_x_at		J02814		
214695_at	NICE-4	AW051361	NICE-4 protein	
			Consensus includes gb:BE538424 /FEA=EST /DB_XREF=gi:9767069 /DB_XREF=est:601068256F1 /CLONE=IMAGE:3454693 /UG=Hs.288283 Homo sapiens cDNA: FLJ22355 fis, clone HRC06344	
221745_at		AK026008		
202656_s_at	TRIP-Br2	BG107456	transcriptional regulator interacting with the PHS-bromodomain 2	

209508_x_at		AF005774	gb:AF005774.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein (clarp) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=clarp /PROD=caspase-like apoptosis regulatory protein /DB_XREF=gi:2286144 /UG=Hs.195175 CASP8 and FADD- like apoptosis regulator /FL=gb:BC001602.1 gb:U97074.1 gb:AF010127.1 gb:AF005774.1 gb:AF009618.1 gb:U85059.1 gb:AF041458.1 gb:AF041460.1	
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202529_at		NM_002766	gb:NM_002766.1 /DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA. /FEA=mRNA /GEN=PRPSAP1 /PROD=phosphoribosyl pyrophosphatesynthetase-associated protein 1 /DB_XREF=gi:4506130 /UG=Hs.77498 phosphoribosyl pyrophosphate synthetase-associated protein 1 /FL=gb:D61391.1 gb:NM_002766.1	
213344_s_at	H2AFX	H51429	H2A histone family, member X	

209523_at		AK001618	Consensus includes gb:AK001618.1 /DEF=Homo sapiens cDNA FLJ10756 fis, clone NT2RP3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. /FEA=mRNA /DB_XREF=gi:7022983 /UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD /FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1	
202621_at		NM_001571	gb:NM_001571.1 /DEF=Homo sapiens interferon regulatory factor 3 (IRF3), mRNA. /FEA=mRNA /GEN=IRF3 /PROD=interferon regulatory factor 3 /DB_XREF=gi:4504724 /UG=Hs.75254 interferon regulatory factor 3 /FL=gb:NM_001571.1	

203169_at		NM_014785	gb:NM_014785.1 /DEF=Homo sapiens KIAA0258 gene product (KIAA0258), mRNA. /FEA=mRNA /GEN=KIAA0258 /PROD=KIAA0258 gene product /DB_XREF=gi:7662029 /UG=Hs.47313 KIAA0258 gene product /FL=gb:BC001725.1 gb:D87447.1 gb:NM_014785.1	
214193_s_at	DJ434O14.5	AI770084	novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7	
202211_at		BC005122	gb:BC005122.1 /DEF=Homo sapiens, ADP-ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. /FEA=mRNA /PROD=ADP-ribosylation factor GTPase activatingprotein 1 /DB_XREF=gi:13477296 /UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 /FL=gb:BC005122.1 gb:AF111847.1 gb:NM_014570.1	

202215_s_at		NM_014223	gb:NM_014223.2 /DEF=Homo sapiens nuclear transcription factor Y, gamma (NFYC), mRNA. /FEA=mRNA /GEN=NFYC /PROD=nuclear transcription factor Y, gamma /DB_XREF=gi:11496977 /UG=Hs.168157 nuclear transcription factor Y, gamma /FL=gb:NM_014223.2 gb:D85425.1 gb:BC005003.1 gb:D89986.1	
202165_at		NM_006241	Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:12333755 /DB_XREF=est:602287009T1 /CLONE=IMAGE:4375586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241.1	

203136_at	NM_006423	gb:NM_006423.1 /DEF=Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA. /FEA=mRNA /GEN=RABAC1 /PROD=Rab acceptor 1 (prenylated) /DB_XREF=gi:5453959 /UG=Hs.11417 Rab acceptor 1 (prenylated) /FL=gb:NM_006423.1 gb:AF112202.1
208003_s_at	NM_006599	gb:NM_006599.1 /DEF=Homo sapiens nuclear factor of activated T-cells 5, tonicity-resonsive (NFAT5), mRNA. /FEA=mRNA /GEN=NFAT5 /PROD=nuclear factor of activated T-cells 5,tonicity-resonsive /DB_XREF=gi:5729944 /UG=Hs.86998 nuclear factor of activated T-cells 5, tonicity-responsive /FL=gb:AB020634.1 gb:AF163836.1 gb:NM_006599.1

202113_s_at		AF043453	gb:AF043453.1 /DEF=Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. /FEA=mRNA /GEN=SNX2 /PROD=sorting nexin 2 /DB_XREF=gi:2827433 /UG=Hs.11183 sorting nexin 2 /FL=gb:BC003382.1 gb:AF043453.1 gb:AF065482.1 gb:NM_003100.1	
202069_s_at	BG1	AI826060	lipidosin	
213217_at	ADCY2	AU149572	adenylate cyclase 2 (brain)	
209620_s_at		AB005289	gb:AB005289.1 /DEF=Homo sapiens mRNA for ABC transporter 7 protein, complete cds. /FEA=mRNA /GEN=hABC7 /PROD=ABC transporter 7 protein /DB_XREF=gi:3228278 /UG=Hs.125856 ATP-binding cassette, sub-family B (MDRTAP), member 7 /FL=gb:AB005289.1 gb:AF038950.1 gb:AF133659.1 gb:NM_004299.2	



202979_s_at	NM_021212	gb:NM_021212.1 /DEF=Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA. /FEA=mRNA /GEN=ZF /PROD=HCF-binding transcription factor Zhangfei /DB_XREF=gi:10864024 /UG=Hs.29417 HCF-binding transcription factor Zhangfei /FL=gb:NM_021212.1 gb:AF039942.1
208073_x_at	NM_003316	gb:NM_003316.1 /DEF=Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA. /FEA=mRNA /GEN=TTC3 /PROD=tetratricopeptide repeat domain 3 /DB_XREF=gi:10835036 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:NM_003316.1 gb:D84295.1

208216_at		NM_001934	gb:NM_001934.1 /DEF=Homo sapiens distal-less homeobox 4 (DLX4), mRNA. /FEA=mRNA /GEN=DLX4 /PROD=distal-less homeobox 4 /DB_XREF=gi:4503342 /UG=Hs.172648 distal-less homeobox 4 /FL=gb:U73328.1 gb:NM_001934.1	
214934_at	ATP9B	AW411030	ATPase, Class II, type 9B	
214749_s_at		AK000818	Consensus includes gb:AK000818.1 /DEF=Homo sapiens cDNA FLJ20811 fis, clone ADSE01435. /FEA=mRNA /DB_XREF=gi:7021128 /UG=Hs.83530 hypothetical protein	

208424_s_at		NM_020313	gb:NM_020313.1 /DEF=Homo sapiens hypothetical protein (LOC57019), mRNA. /FEA=mRNA /GEN=LOC57019 /PROD=hypothetical protein /DB_XREF=gi:10092672 /UG=Hs.4900 hypothetical protein /FL=gb:NM_020313.1	
209610_s_at	SLC1A4	BF340083	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	
203046_s_at		NM_003920	gb:NM_003920.1 /DEF=Homo sapiens timeless (Drosophila) homolog (TIMELESS), mRNA. /FEA=mRNA /GEN=TIMELESS /PROD=timeless (Drosophila) homolog /DB_XREF=gi:4507506 /UG=Hs.118631 timeless (Drosophila) homolog /FL=gb:AF098162.1 gb:AB015597.1 gb:NM_003920.1	

219854_at		NM_021030	gb:NM_021030.1 /DEF=Homo sapiens zinc finger protein 14 (KOX 6) (ZNF14), mRNA. /FEA=mRNA /GEN=ZNF14 /PROD=zinc finger protein 14 (KOX 6) /DB_XREF=gi:11139306 /UG=Hs.197219 zinc finger protein 14 (KOX 6) /FL=gb:NM_021030.1 gb:AB021644.1	
212699_at	SCAMP5	BE222801	secretory carrier membrane protein 5	
222028_at	ZNF45	AI967981	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)	
214319_at		W58342	Homo sapiens cDNA FLJ34103 fis, clone FCBBF3007859, moderately similar to Human putative protein B2 mRNA	
213436_at	CNR1; CB1; CB-R; CB1A; CANN6; CB1K5	U73304	G protein-coupled receptor; Human CB1 cannabinoid receptor (CNR1) gene, complete cds.	NM_001840; NM_016083; NM_033181

208881_x_at	BC005247	gb:BC005247.1 /DEF=Homo sapiens, isopentenyl-diphosphate delta isomerase, clone MGC:12281, mRNA, complete cds. /FEA=mRNA /PROD=isopentenyl-diphosphate delta isomerase /DB_XREF=gi:13528899 /UG=Hs.76038 isopentenyl-diphosphate delta isomerase /FL=gb:BC005247.1
200886_s_at	NM_002629	gb:NM_002629.1 /DEF=Homo sapiens phosphoglycerate mutase 1 (brain) (PGAM1), mRNA. /FEA=mRNA /GEN=PGAM1 /PROD=phosphoglycerate mutase 1 (brain) /DB_XREF=gi:4505752 /UG=Hs.181013 phosphoglycerate mutase 1 (brain) /FL=gb:BC000455.1 gb:NM_002629.1 gb:J04173.1

212018_s_at		AK025446	Consensus includes gb:AK000822.1 /DEF=Homo sapiens cDNA FLJ20815 fis, clone ADSE01038, highly similar to AJ007398 Homo sapiens mRNA for PBK1 protein. /FEA=mRNA /DB_XREF=gi:7021134 /UG=Hs.85963 DKFZP564M182 protein	
200800_s_at		NM_005345	gb:NM_005345.3 /DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. /FEA=mRNA /GEN=HSPA1A /PROD=heat shock 70kD protein 1A /DB_XREF=gi:5579469 /UG=Hs.8997 heat shock 70kD protein 1A /FL=gb:BC002453.1 gb:NM_005345.3	
204186_s_at	PPID	AI014573	peptidylprolyl isomerase D (cyclophilin D)	

204180_s_at		NM_014007	Consensus includes gb:AI745225 /FEA=EST /DB_XREF=gi:5113513 /DB_XREF=est:wg10d12.x1 /CLONE=IMAGE:2364695 /UG=Hs.127649 KIAA0414 protein /FL=gb:NM_014007.1	
212060_at		AB002330	Consensus includes gb:AU152088 /FEA=EST /DB_XREF=gi:11013609 /DB_XREF=est:AU152088 /CLONE=NT2RP3000162 /UG=Hs.7976 KIAA0332 protein	
64418_at		AI472320	ESTs, Weakly similar to I38022 hypothetical protein - human [H.sapiens]	

200857_s_at		NM_006311	gb:NM_006311.1 /DEF=Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA. /FEA=mRNA /GEN=NCOR1 /PROD=nuclear receptor co-repressor 1 /DB_XREF=gi:5454137 /UG=Hs.144904 nuclear receptor co-repressor 1 /FL=gb:AF044209.1 gb:NM_006311.1	
217925_s_at		NM_022758	gb:NM_022758.1 /DEF=Homo sapiens hypothetical protein FLJ22195 (FLJ22195), mRNA. /FEA=mRNA /GEN=FLJ22195 /PROD=hypothetical protein FLJ22195 /DB_XREF=gi:12232426 /UG=Hs.25999 hypothetical protein FLJ22195 /FL=gb:NM_022758.1	
208883_at	DD5	U69567	progesterin induced protein	



217783_s_at	NM_016061	gb:NM_016061.1 /DEF=Homo sapiens CGI-127 protein (LOC51646), mRNA. /FEA=mRNA /GEN=LOC51646 /PROD=CGI-127 protein /DB_XREF=gi:7706340 /UG=Hs.184542 CGI-127 protein /FL=gb:BC000836.1 gb:AF151885.1 gb:NM_016061.1
201023_at	NM_005642	gb:NM_005642.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD (TAF2F), mRNA. /FEA=mRNA /GEN=TAF2F /PROD=TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD /DB_XREF=gi:5032148 /UG=Hs.155188 TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD /FL=gb:NM_005642.1 gb:U18062.1

205053_at		NM_000946	gb:NM_000946.1 /DEF=Homo sapiens primase, polypeptide 1 (49kD) (PRIM1), mRNA. /FEA=mRNA /GEN=PRIM1 /PROD=primase, polypeptide 1 (49kD) /DB_XREF=gi:4506050 /UG=Hs.82741 primase, polypeptide 1 (49kD) /FL=gb:BC005266.1 gb:NM_000946.1	
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204038_s_at		NM_001401	gb:NM_001401.1 /DEF=Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), mRNA. /FEA=mRNA /GEN=EDG2 /PROD=endothelial differentiation, lysophosphatidicacid G-protein-coupled receptor, 2 /DB_XREF=gi:4503456 /UG=Hs.75794 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1	
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207434_s_at		NM_021603	gb:NM_021603.1 /DEF=Homo sapiens FXYD domain-containing ion transport regulator 2 (FXYD2), transcript variant b, mRNA. /FEA=mRNA /GEN=FXYD2 /PROD=FXYD domain-containing ion transport regulator2, isoform 2 /DB_XREF=gi:11125763 /UG=Hs.19520 FXYD domain-containing ion transport regulator 2 /FL=gb:NM_021603.1 gb:BC005302.1	
200973_s_at		NM_005724	gb:NM_005724.1 /DEF=Homo sapiens tetraspan 3 (TSPAN-3), mRNA. /FEA=mRNA /GEN=TSPAN-3 /PROD=tetraspan 3 /DB_XREF=gi:5032200 /UG=Hs.100090 tetraspan 3 /FL=gb:BC000704.1 gb:BC004280.1 gb:AF054840.1 gb:NM_005724.1 gb:AF133423.1	

212008_at		D87684	Consensus includes gb:N29889 /FEA=EST /DB_XREF=gi:1148409 /DB_XREF=est:yy11e11.s1 /CLONE=IMAGE:270956 /UG=Hs.77495 UBX domain- containing 1	
51146_at	FLJ20477	AA203365	hypothetical protein FLJ20477	
219266_at		NM_021632	gb:NM_021632.1 /DEF=Homo sapiens zinc-finger protein ZBRK1 (ZBRK1), mRNA. /FEA=mRNA /GEN=ZBRK1 /PROD=zinc-finger protein ZBRK1 /DB_XREF=gi:11056003 /UG=Hs.130965 zinc-finger protein ZBRK1 /FL=gb:AF295096.1 gb:AF309561.1 gb:NM_021632.1	
204556_s_at	DZIP1	AL568422	zinc-finger protein DZIP1	
200630_x_at	SET	AV702810	SET translocation (myeloid leukemia- associated)	

			gb:NM_004544.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD) (NDUFA10), mRNA. /FEA=mRNA /GEN=NDUFA10 /PROD=NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 10 (42kD) /DB_XREF=gi:4758767 /UG=Hs.198271 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD) /FL=gb:BC003417.1 gb:AF087661.1 gb:NM_004544.1	
217860_at		NM_004544		
213650_at	GOLGIN-67	AW006438	golgin-67	

220287_at		NM_020249	gb:NM_020249.1 /DEF=Homo sapiens disintegrin metalloproteinase with thrombospondin repeats (ADAMTS9), mRNA. /FEA=mRNA /GEN=ADAMTS9 /PROD=a disintegrin and metalloproteinase with thrombospondin motifs-9 preproprotein /DB_XREF=gi:9910121 /UG=Hs.126855 disintegrin metalloproteinase with thrombospondin repeats /FL=gb:AF261918.1 gb:NM_020249.1	
208775_at		D89729	gb:D89729.1 /DEF=Homo sapiens mRNA for CRM1 protein, complete cds. /FEA=mRNA /PROD=CRM1 protein /DB_XREF=gi:2626839 /UG=Hs.79090 exportin 1 (CRM1, yeast, homolog) /FL=gb:D89729.1 gb:NM_003400.2	
213684_s_at	LIM	BF671400	LIM protein (similar to rat protein kinase C-binding enigma)	

212086_x_at	M13452	Consensus includes gb:AK026584.1 /DEF=Homo sapiens cDNA: FLJ22931 fis, clone KAT07501, highly similar to HSLAMAR Human mRNA for nuclear envelope protein lamin A precursor. /FEA=mRNA /DB_XREF=gi:10439468 /UG=Hs.77886 lamin AC
204489_s_at	NM_000610	gb:NM_000610.1 /DEF=Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), mRNA. /FEA=mRNA /GEN=CD44 /PROD=CD44 antigen (homing function and Indian bloodgroup system) /DB_XREF=gi:10835162 /UG=Hs.169610 CD44 antigen (homing function and Indian blood group system) /FL=gb:NM_000610.1 gb:U40373.1 gb:M59040.1 gb:M24915.1



208734_x_at		M28213	gb:M28213.1 /DEF=Homo sapiens GTP-binding protein (RAB2) mRNA, complete cds. /FEA=mRNA /GEN=RAB2 /PROD=GTP-binding protein /DB_XREF=gi:550061 /UG=Hs.78305 RAB2, member RAS oncogene family /FL=gb:NM_002865.1 gb:M28213.1	
213572_s_at	SERPINB1	AI554300	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	
200071_at	SPF30	BF224259	splicing factor 30, survival of motor neuron-related	
200060_s_at		BC001659	gb:BC001659.1 /DEF=Homo sapiens, RNA-binding protein S1, serine-rich domain, clone MGC:1125, mRNA, complete cds. /FEA=mRNA /PROD=RNA-binding protein S1, serine-rich domain /DB_XREF=gi:12804496 /UG=Hs.75104 RNA-binding protein S1, serine-rich domain /FL=gb:BC001659.1 gb:BC001838.1	

220261_s_at		NM_018106	gb:NM_018106.1 /DEF=Homo sapiens hypothetical protein FLJ10479 (FLJ10479), mRNA. /FEA=mRNA /GEN=FLJ10479 /PROD=hypothetical protein FLJ10479 /DB_XREF=gi:8922447 /UG=Hs.5268 hypothetical protein FLJ10479 /FL=gb:AL136674.1 gb:BC001239.1 gb:NM_018106.1	
200066_at		AF182645	gb:AF182645.1 /DEF=Homo sapiens chondrosarcoma-associated protein 2 (CSA2) mRNA, complete cds. /FEA=mRNA /GEN=CSA2 /PROD=chondrosarcoma-associated protein 2 /DB_XREF=gi:5901877 /UG=Hs.8024 IK cytokine, down-regulator of HLA II /FL=gb:NM_006083.2 gb:AF182645.1	

200754_x_at	NM_003016	gb:NM_003016.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 2 (SFRS2), mRNA. /FEA=mRNA /GEN=SFRS2 /PROD=splicing factor, arginineserine-rich 2 /DB_XREF=gi:4506898 /UG=Hs.73965 splicing factor, arginineserine-rich 2 /FL=gb:BC000339.1 gb:BC001303.1 gb:M90104.1 gb:NM_003016.1
218598_at	NM_021930	gb:NM_021930.1 /DEF=Homo sapiens hypothetical protein FLJ11785 (FLJ11785), mRNA. /FEA=mRNA /GEN=FLJ11785 /PROD=hypothetical protein FLJ11785 /DB_XREF=gi:11345465 /UG=Hs.44625 Rad50-interacting protein 1 /FL=gb:NM_021930.1 gb:AF317622.1

200744_s_at		NM_002074	Consensus includes gb:AI741124 /FEA=EST /DB_XREF=gi:5109412 /DB_XREF=est:wg19c04.x1 /CLONE=IMAGE:2365542 /UG=Hs.215595 guanine nucleotide binding protein (G protein), beta polypeptide 1 /FL=gb:NM_002074.1 gb:BC004186.1	
65472_at		AI161338	qb80a04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706382 3' similar to TR:O21123 O21123 CYTOCHROME OXIDASE I ;, mRNA sequence.	
200770_s_at		J03202	gb:J03202.1 /DEF=Human laminin B2 chain mRNA, complete cds. /FEA=mRNA /GEN=LAMB2 /DB_XREF=gi:186916 /UG=Hs.214982 laminin, gamma 1 (formerly LAMB2) /FL=gb:J03202.1 gb:NM_002293.2	
54632_at	FLJ21877	AI286226	hypothetical protein FLJ21877	

217798_at	CNOT2	AI123426	CCR4-NOT transcription complex, subunit 2	
204353_s_at		BC002923	gb:BC002923.1 /DEF=Homo sapiens, clone MGC:10280, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10280) /DB_XREF=gi:12804138 /UG=Hs.31968 DKFZP586D211 protein /FL=gb:BC002923.1 gb:NM_015450.1	
200704_at		AB034747	gb:AB034747.1 /DEF=Homo sapiens SIMPLE mRNA for small integral membrane protein of lysosomelate endosome, complete cds. /FEA=mRNA /GEN=SIMPLE /PROD=small integral membrane protein of lysosomelateendosome /DB_XREF=gi:12862475 /UG=Hs.76507 LPS-induced TNF-alpha factor /FL=gb:AB034747.1 gb:U77396.1 gb:AF010312.1 gb:NM_004862.1	

200693_at		NM_006826	gb:NM_006826.1 /DEF=Homo sapiens tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /FEA=mRNA /GEN=YWHAQ /PROD=tyrosine 3-monooxygenasetryptophan5-monooxygenase activation protein, theta polypeptide /DB_XREF=gi:5803226 /UG=Hs.74405 tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, theta polypeptide /FL=gb:NM_006826.1	
217795_s_at	MGC3222	W74580	hypothetical protein MGC3222	

208810_at		AF080569	gb:AF080569.1 /DEF=Homo sapiens DnaJ-like 2 protein (HSJ2) mRNA, complete cds. /FEA=mRNA /GEN=HSJ2 /PROD=DnaJ-like 2 protein /DB_XREF=gi:4322314 /UG=Hs.181195 DnaJ (Hsp40) homolog, subfamily B, member 6 /FL=gb:AL136707.1 gb:BC000177.2 gb:AB014888.1 gb:AF080569.1 gb:NM_005494.1 gb:AF075601.1 gb:AF060703.1 gb:AB015799.1	
200712_s_at	MAPRE1	AI633566	microtubule-associated protein, RP/EB family, member 1	

200713_s_at	NM_012325	gb:NM_012325.1 /DEF=Homo sapiens microtubule-associated protein, RPEB family, member 1 (MAPRE1), mRNA. /FEA=mRNA /GEN=MAPRE1 /PROD=microtubule-associated protein, RPEB family,member 1 /DB_XREF=gi:6912493 /UG=Hs.234279 microtubule-associated protein, RPEB family, member 1 /FL=gb:NM_012325.1 gb:U24166.1
211569_s_at	AF001903	gb:AF001903.1 /DEF=Human 3-hydroxyacyl-CoA dehydrogenase, isoform 2 mRNA, complete cds. /FEA=mRNA /PROD=3-hydroxyacyl-CoA dehydrogenase, isoform 2 /DB_XREF=gi:2078328 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:AF001903.1



207239_s_at		NM_006201	gb:NM_006201.1 /DEF=Homo sapiens PCTAIRE protein kinase 1 (PCTK1), mRNA. /FEA=mRNA /GEN=PCTK1 /PROD=PCTAIRE protein kinase 1 /DB_XREF=gi:5453859 /UG=Hs.171834 PCTAIRE protein kinase 1 /FL=gb:NM_006201.1	
208955_at		AB049113	gb:AB049113.1 /DEF=Homo sapiens DUT mRNA for dUTP pyrophosphatase, complete cds. /FEA=mRNA /GEN=DUT /PROD=dUTP pyrophosphatase /DB_XREF=gi:10257384 /UG=Hs.82113 dUTP pyrophosphatase /FL=gb:AB049113.1 gb:U31930.1 gb:U62891.1 gb:M89913.1 gb:NM_001948.1	

219599_at		NM_018507	gb:NM_018507.1 /DEF=Homo sapiens hypothetical protein PRO1843 (PRO1843), mRNA. /FEA=mRNA /GEN=PRO1843 /PROD=hypothetical protein PRO1843 /DB_XREF=gi:8924082 /UG=Hs.283330 hypothetical protein PRO1843 /FL=gb:AF119854.1 gb:NM_018507.1	
218532_s_at		NM_019000	gb:NM_019000.1 /DEF=Homo sapiens hypothetical protein (FLJ20152), mRNA. /FEA=mRNA /GEN=FLJ20152 /PROD=hypothetical protein /DB_XREF=gi:9506660 /UG=Hs.82273 hypothetical protein /FL=gb:NM_019000.1	

201210_at		NM_001356	gb:NM_001356.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 (DDX3), transcript variant 2, mRNA. /FEA=mRNA /GEN=DDX3 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 /DB_XREF=gi:13514812 /UG=Hs.147916 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 /FL=gb:NM_001356.2 gb:U50553.1 gb:AF000982.1 gb:AF061337.1	
218347_at		NM_018264	gb:NM_018264.1 /DEF=Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA. /FEA=mRNA /GEN=FLJ10900 /PROD=hypothetical protein FLJ10900 /DB_XREF=gi:8922751 /UG=Hs.16277 hypothetical protein FLJ10900 /FL=gb:NM_018264.1	

205100_at		NM_005110	gb:NM_005110.1 /DEF=Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA. /FEA=mRNA /GEN=GFPT2 /PROD=glutamine-fructose-6-phosphate transaminase 2 /DB_XREF=gi:4826741 /UG=Hs.30332 glutamine-fructose-6-phosphate transaminase 2 /FL=gb:BC000012.1 gb:AB016789.1 gb:NM_005110.1	
218696_at		NM_004836	gb:NM_004836.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA. /FEA=mRNA /GEN=EIF2AK3 /PROD=eukaryotic translation initiation factor 2-alpha kinase 3 /DB_XREF=gi:4758891 /UG=Hs.102506 eukaryotic translation initiation factor 2-alpha kinase 3 /FL=gb:AF110146.1 gb:NM_004836.1 gb:AF193339.1	

205091_x_at		NM_002907	gb:NM_002907.1 /DEF=Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), mRNA. /FEA=mRNA /GEN=RECQL /PROD=RecQ protein-like (DNA helicase Q1-like) /DB_XREF=gi:4506468 /UG=Hs.235069 RecQ protein-like (DNA helicase Q1-like) /FL=gb:NM_002907.1 gb:L36140.1	
201403_s_at		NM_004528	gb:NM_004528.1 /DEF=Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /FEA=mRNA /GEN=MGST3 /PROD=microsomal glutathione S-transferase 3 /DB_XREF=gi:4758713 /UG=Hs.111811 microsomal glutathione S-transferase 3 /FL=gb:BC000505.1 gb:BC003034.1 gb:AF026977.1 gb:NM_004528.1	

211296_x_at		AB009010	gb:AB009010.1 /DEF=Homo sapiens mRNA for polyubiquitin UbC, complete cds. /FEA=mRNA /GEN=UbC1 /PROD=polyubiquitin UbC /DB_XREF=gi:2647407 /UG=Hs.183704 ubiquitin C /FL=gb:BC000449.1 gb:AB009010.1	
201381_x_at		AF057356	gb:AF057356.1 /DEF=Homo sapiens calcyclin binding protein mRNA, complete cds. /FEA=mRNA /PROD=calcyclin binding protein /DB_XREF=gi:3063652 /UG=Hs.27258 calcyclin binding protein /FL=gb:AF314752.1 gb:AF057356.1 gb:NM_014412.1	
43544_at	TRAP95	AA314406	thyroid hormone receptor-associated protein, 95-kD subunit	
211509_s_at		AB015639	gb:AB015639.1 /DEF=Homo sapiens ASY mRNA, complete cds. /FEA=mRNA /GEN=ASY /DB_XREF=gi:5821139 /UG=Hs.65450 reticulon 4 /FL=gb:AB015639.1	

201190_s_at	PITPN	H15647	phosphatidylinositol transfer protein	
201218_at		NM_001329	Consensus includes gb:N23018 /FEA=EST /DB_XREF=gi:1137168 /DB_XREF=est:yx65d12.s1 /CLONE=IMAGE:266615 /UG=Hs.171391 C-terminal binding protein 2 /FL=gb:AF016507.1 gb:NM_001329.1	
201272_at		NM_001628	gb:NM_001628.1 /DEF=Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA. /FEA=mRNA /GEN=AKR1B1 /PROD=aldo-keto reductase family 1, member B1 (aldosereductase) /DB_XREF=gi:4502048 /UG=Hs.75313 aldo-keto reductase family 1, member B1 (aldose reductase) /FL=gb:BC000260.1 gb:BC005387.1 gb:J04795.1 gb:J05017.1 gb:J05474.1 gb:M34720.1 gb:NM_001628.1	

201245_s_at	FLJ20113	AL523776	hypothetical protein FLJ20113	
			Consensus includes gb:AL157398 /DEF=Human DNA sequence from clone RP11-56H7 on chromosome 10. Contains ESTs, STSs and GSSs. Contains the gene for the nebulette protein (NEBL, actin- binding Z-disc protein) /FEA=mRNA_1 /DB_XREF=gi:10045326 /UG=Hs.5025 nebulette /FL=gb:NM_006393.1	
203961_at		AL157398		
			gb:NM_018281.1 /DEF=Homo sapiens hypothetical protein FLJ10948 (FLJ10948), mRNA. /FEA=mRNA /GEN=FLJ10948 /PROD=hypothetical protein FLJ10948 /DB_XREF=gi:8922786 /UG=Hs.9670 hypothetical protein FLJ10948 /FL=gb:NM_018281.1	
218552_at		NM_018281		



218656_s_at		NM_005780	gb:NM_005780.1 /DEF=Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /FEA=mRNA /GEN=LHFP /PROD=lipoma HMGIC fusion partner /DB_XREF=gi:5031864 /UG=Hs.93765 lipoma HMGIC fusion partner /FL=gb:AF098807.1 gb:NM_005780.1	
213413_at		BG434174	ESTs, Weakly similar to PRO0478 protein [Homo sapiens] [H.sapiens]	
213916_at	ZNF20	AU154474	zinc finger protein 20 (KOX 13)	
218430_s_at		NM_022841	gb:NM_022841.1 /DEF=Homo sapiens hypothetical protein FLJ12994 (FLJ12994), mRNA. /FEA=mRNA /GEN=FLJ12994 /PROD=hypothetical protein FLJ12994 /DB_XREF=gi:12383091 /UG=Hs.126908 hypothetical protein FLJ12994 /FL=gb:NM_022841.1	

204879_at		NM_006474	gb:NM_006474.1 /DEF=Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, mRNA. /FEA=mRNA /GEN=T1A-2 /PROD=lung type-I cell membrane-associatedglycoprotein, isoform 2 precursor /DB_XREF=gi:5454097 /UG=Hs.135150 lung type-I cell membrane-associated glycoprotein /FL=gb:AF030428.1 gb:NM_006474.1	
213813_x_at		AI345238	ESTs, Highly similar to FRIL_HUMAN Ferritin light chain (Ferritin L subunit) [H.sapiens]	

205425_at		NM_005338	gb:NM_005338.3 /DEF=Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA. /FEA=mRNA /GEN=HIP1 /PROD=huntingtin interacting protein 1 /DB_XREF=gi:12545385 /UG=Hs.97206 huntingtin interacting protein 1 /FL=gb:NM_005338.3 gb:U79734.1	
214806_at		U90030	Consensus includes gb:U90030.1 /DEF=Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds. /FEA=mRNA /GEN=BICD /PROD=bicaudal-D /DB_XREF=gi:2745977 /UG=Hs.164975 Bicaudal D (Drosophila) homolog 1	

201691_s_at		NM_005079	gb:NM_005079.1 /DEF=Homo sapiens tumor protein D52 (TPD52), mRNA. /FEA=mRNA /GEN=TPD52 /PROD=tumor protein D52 /DB_XREF=gi:4827037 /UG=Hs.2384 tumor protein D52 /FL=gb:NM_005079.1 gb:U18914.1	
213753_x_at		BF541557	ESTs, Highly similar to IF5A_HUMAN Initiation factor 5A (eIF-5A) (eIF-4D) (Rev-binding factor) [H.sapiens]	
220596_at		NM_015590	gb:NM_015590.1 /DEF=Homo sapiens DKFZP434F1735 protein (DKFZP434F1735), mRNA. /FEA=mRNA /GEN=DKFZP434F1735 /PROD=DKFZP434F1735 protein /DB_XREF=gi:7661571 /UG=Hs.306189 DKFZP434F1735 protein /FL=gb:NM_015590.1	

206608_s_at		NM_020366	gb:NM_020366.1 /DEF=Homo sapiens retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1), mRNA. /FEA=mRNA /GEN=RPGRIP1 /PROD=retinitis pigmentosa GTPase regulatorinteracting protein 1 /DB_XREF=gi:9966834 /UG=Hs.131917 retinitis pigmentosa GTPase regulator interacting protein 1 /FL=gb:AF260257.1 gb:AF227257.1 gb:NM_020366.1
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220542_s_at	NM_016583	gb:NM_016583.1 /DEF=Homo sapiens LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein (LOC51297), mRNA. /FEA=mRNA /GEN=LOC51297 /PROD=LUNX protein; PLUNC (palate lung and nasalepithelium clone); tracheal epithelium enriched protein /DB_XREF=gi:7706118 /UG=Hs.211092 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein /FL=gb:AB024937.1 gb:NM_016583.1 gb:AF172993.1
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201655_s_at		M85289	gb:M85289.1 /DEF=Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds. /FEA=mRNA /GEN=HSPG2 /PROD=heparan sulfate proteoglycan /DB_XREF=gi:184426 /UG=Hs.211573 heparan sulfate proteoglycan 2 (perlecan) /FL=gb:M85289.1 gb:NM_005529.2	
221728_x_at		AK025198	Consensus includes gb:AA628440 /FEA=EST /DB_XREF=gi:2540827 /DB_XREF=est:af26f02.s1 /CLONE=IMAGE:1032795 /UG=Hs.83623 nuclear receptor subfamily 1, group I, member 3	

220241_at		NM_017905	gb:NM_017905.1 /DEF=Homo sapiens hypothetical protein FLJ20623 (FLJ20623), mRNA. /FEA=mRNA /GEN=FLJ20623 /PROD=hypothetical protein FLJ20623 /DB_XREF=gi:8923574 /UG=Hs.27337 hypothetical protein FLJ20623 /FL=gb:NM_017905.1	
219993_at		NM_022454	gb:NM_022454.1 /DEF=Homo sapiens hypothetical protein FLJ22252 similar to SRY-box containing gene 17 (FLJ22252), mRNA. /FEA=mRNA /GEN=FLJ22252 /PROD=hypothetical protein FLJ22252 similar to SRY-boxcontaining gene 17 /DB_XREF=gi:11967990 /UG=Hs.97984 hypothetical protein FLJ22252 similar to SRY-box containing gene 17 /FL=gb:NM_022454.1	



206003_at		NM_014645	gb:NM_014645.1 /DEF=Homo sapiens KIAA0635 gene product (KIAA0635), mRNA. /FEA=mRNA /GEN=KIAA0635 /PROD=KIAA0635 gene product /DB_XREF=gi:7662215 /UG=Hs.185091 KIAA0635 gene product /FL=gb:AB014535.1 gb:NM_014645.1	
209408_at		U63743	gb:U63743.1 /DEF=Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds. /FEA=mRNA /PROD=mitotic centromere-associated kinesin /DB_XREF=gi:1695881 /UG=Hs.69360 kinesin-like 6 (mitotic centromere-associated kinesin) /FL=gb:NM_006845.2 gb:U63743.1	
177_at	PLD1	U38545	phospholipase D1, phosphatidylcholine-specific	NM_002662

221335_x_at		NM_019108	gb:NM_019108.1 /DEF=Homo sapiens hypothetical protein F17127_1 (F17127_1), mRNA. /FEA=CDS /GEN=F17127_1 /PROD=hypothetical protein F17127_1 /DB_XREF=gi:10092658 /UG=Hs.10116 hypothetical protein F17127_1 /FL=gb:NM_019108.1	
205995_x_at		NM_014642	gb:NM_014642.1 /DEF=Homo sapiens KIAA0036 gene product (KIAA0036), mRNA. /FEA=mRNA /GEN=KIAA0036 /PROD=KIAA0036 gene product /DB_XREF=gi:7661875 /UG=Hs.169387 KIAA0036 gene product /FL=gb:D25278.1 gb:NM_014642.1	

205215_at		NM_007212	gb:NM_007212.1 /DEF=Homo sapiens ring finger protein 2 (RNF2), mRNA. /FEA=mRNA /GEN=RNF2 /PROD=ring finger protein 2 /DB_XREF=gi:6005746 /UG=Hs.124186 ring finger protein 2 /FL=gb:AF141327.1 gb:NM_007212.1	
201206_s_at		NM_004587	gb:NM_004587.1 /DEF=Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1), mRNA. /FEA=mRNA /GEN=RRBP1 /PROD=ribosome binding protein 1 /DB_XREF=gi:4759055 /UG=Hs.98614 ribosome binding protein 1 (dog 180kD homolog) /FL=gb:AF006751.1 gb:NM_004587.1	

218756_s_at		NM_024308	gb:NM_024308.1 /DEF=Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA. /FEA=mRNA /GEN=MGC4172 /PROD=hypothetical protein MGC4172 /DB_XREF=gi:13236541 /UG=Hs.8949 hypothetical protein MGC4172 /FL=gb:BC002731.1 gb:NM_024308.1	
204572_s_at		NM_006223	gb:NM_006223.1 /DEF=Homo sapiens protein (peptidyl-prolyl cistrans isomerase) NIMA-interacting, 4 (parvulin) (PIN4), mRNA. /FEA=mRNA /GEN=PIN4 /PROD=protein (peptidyl-prolyl cistrans isomerase)NIMA-interacting, 4 (parvulin) /DB_XREF=gi:5453901 /UG=Hs.11774 protein (peptidyl-prolyl cistrans isomerase) NIMA-interacting, 4 (parvulin) /FL=gb:BC005234.1 gb:AF143096.1 gb:AB009690.1 gb:NM_006223.1	

210117_at		AF311312	gb:AF311312.1 /DEF=Homo sapiens infertility-related sperm protein mRNA, complete cds. /FEA=mRNA /PROD=infertility-related sperm protein /DB_XREF=gi:10863767 /UG=Hs.153057 sperm associated antigen 1 /FL=gb:AF311312.1 gb:NM_003114.1	
204819_at		NM_004463	gb:NM_004463.1 /DEF=Homo sapiens faciogenital dysplasia (Aarskog-Scott syndrome) (FGD1), mRNA. /FEA=mRNA /GEN=FGD1 /PROD=faciogenital dysplasia protein /DB_XREF=gi:4758357 /UG=Hs.1572 faciogenital dysplasia (Aarskog-Scott syndrome) /FL=gb:NM_004463.1 gb:U11690.1	

			gb:NM_004346.1 /DEF=Homo sapiens caspase 3, apoptosis-related cysteine protease (CASP3), mRNA. /FEA=mRNA /GEN=CASP3 /PROD=caspase 3, apoptosis-related cysteine protease /DB_XREF=gi:4757911 /UG=Hs.74552 caspase 3, apoptosis-related cysteine protease /FL=gb:NM_004346.1 gb:U13737.1 gb:U13738.1 gb:U26943.1	
202763_at		NM_004346		
222341_x_at		AW973235	ESTs	
			Consensus includes gb:AL049261.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564E053 (from clone DKFZp564E053). /FEA=mRNA /DB_XREF=gi:4500009 /UG=Hs.133968 FGF receptor activating protein 1	
215293_s_at		AL049261		
203226_s_at	SAS	AL514076	sarcoma amplified sequence	

207780_at		NM_001340	gb:NM_001340.1 /DEF=Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /FEA=mRNA /GEN=CYLC2 /PROD=cylicin 2 /DB_XREF=gi:4557508 /UG=Hs.3232 cylicin, basic protein of sperm head cytoskeleton 2 /FL=gb:NM_001340.1	
208914_at		NM_015044	Consensus includes gb:BE646414 /FEA=EST /DB_XREF=gi:9970725 /DB_XREF=est:7e86d08.x1 /CLONE=IMAGE:3292047 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 /FL=gb:AF190863.1 gb:AF233522.1 gb:AF165531.1 gb:NM_015044.1	
214920_at		R33964	ESTs, Weakly similar to T45117 hU1-70K protein (286 AA) [imported] - human (fragment) [H.sapiens]	

214765_s_at		AK024677	Consensus includes gb:AK024677.1 /DEF=Homo sapiens cDNA: FLJ21024 fis, clone CAE06651, highly similar to HUMPLT Human LTR mRNA. /FEA=mRNA /DB_XREF=gi:10437016 /UG=Hs.264330 N-acylsphingosine amidohydrolase (acid ceramidase)- like	
201294_s_at		NM_015626	Consensus includes gb:N24643 /FEA=EST /DB_XREF=gi:1138793 /DB_XREF=est:yx89f11.s1 /CLONE=IMAGE:268941 /UG=Hs.187991 DKFZP564A122 protein /FL=gb:AF106684.1 gb:NM_015626.1	



205074_at		NM_003060	gb:NM_003060.1 /DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 5 (SLC22A5), mRNA. /FEA=mRNA /GEN=SLC22A5 /PROD=solute carrier family 22 (organic cation transporter), member 5 /DB_XREF=gi:4507004 /UG=Hs.15813 solute carrier family 22 (organic cation transporter), member 5 /FL=gb:AB015050.1 gb:AF057164.1 gb:NM_003060.1	
203119_at		NM_024098	gb:NM_024098.1 /DEF=Homo sapiens hypothetical protein MGC2574 (MGC2574), mRNA. /FEA=mRNA /GEN=MGC2574 /PROD=hypothetical protein MGC2574 /DB_XREF=gi:13129103 /UG=Hs.4253 hypothetical protein MGC2574 /FL=gb:BC001378.1 gb:NM_024098.1	

217212_s_at		Z84723	Human DNA sequence from phage LAW2 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains Interleukin 9 receptor pseudogene.	
201085_s_at	SON	AA664291	SON DNA binding protein	
214060_at	SSBP1	BE220360	single-stranded DNA binding protein	
217207_s_at		AK025267	Consensus includes gb:AK025267.1 /DEF=Homo sapiens cDNA: FLJ21614 fis, clone COL07391, highly similar to AB020625 Homo sapiens mRNA for butyrophilin like receptor. /FEA=mRNA /DB_XREF=gi:10437746 /UG=Hs.225949 butyrophilin-like 3	
208963_x_at	FADS1	BE540552	fatty acid desaturase 1	

201082_s_at		NM_004082	gb:NM_004082.2 /DEF=Homo sapiens dynactin 1 (p150, Glued (Drosophila) homolog) (DCTN1), transcript variant 1, mRNA. /FEA=mRNA /GEN=DCTN1 /PROD=dynactin 1, isoform 1 /DB_XREF=gi:13259509 /UG=Hs.74617 dynactin 1 (p150, Glued (Drosophila) homolog) /FL=gb:NM_023019.1 gb:NM_004082.2	
217253_at		L37198	Consensus includes gb:L37198.1 /DEF=Homo sapiens (clone B3B3E13) Huntingtons disease candidate region mRNA fragment. /FEA=mRNA /DB_XREF=gi:600519 /UG=Hs.233617 Homo sapiens (clone B3B3E13) Huntingtons disease candidate region mRNA fragment	

218766_s_at		NM_015836	gb:NM_015836.1 /DEF=Homo sapiens tryptophanyl tRNA synthetase 2 (mitochondrial) (WARS2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=WARS2 /PROD=tryptophanyl tRNA synthetase 2 (mitochondrial) /DB_XREF=gi:7710153 /UG=Hs.227274 tryptophanyl tRNA synthetase 2 (mitochondrial) /FL=gb:NM_015836.1	
209073_s_at		AF015040	gb:AF015040.1 /DEF=Homo sapiens NUMB protein (NUMB) mRNA, complete cds. /FEA=mRNA /GEN=NUMB /PROD=NUMB protein /DB_XREF=gi:4102704 /UG=Hs.78890 numb (Drosophila) homolog /FL=gb:AF015040.1 gb:AF108092.1 gb:AF171939.1	
37170_at	BIKE	AB015331	BMP-2 inducible kinase	NM_017593
52837_at	KIAA1644	AL047020	KIAA1644 protein	

209431_s_at		AF254083	gb:AF254083.1 /DEF=Homo sapiens zinc finger sarcoma gene long A isoform (ZSG) mRNA, complete cds. /FEA=mRNA /GEN=ZSG /PROD=zinc finger sarcoma gene long A isoform /DB_XREF=gi:9954374 /UG=Hs.27801 zinc finger protein 278 /FL=gb:NM_014323.1 gb:AF254083.1	
209994_s_at		AF016535	gb:AF016535.1 /DEF=Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds. /FEA=mRNA /GEN=mdr1 /PROD=P-glycoprotein /DB_XREF=gi:2353263 /UG=Hs.21330 ATP-binding cassette, sub-family B (MDRTAP), member 1 /FL=gb:M14758.1 gb:AF016535.1 gb:NM_000927.2	
216210_x_at	HRIHFB2122	AA046650	Tara-like protein	

207338_s_at		NM_003454	gb:NM_003454.1 /DEF=Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /FEA=mRNA /GEN=ZNF200 /PROD=zinc finger protein 200 /DB_XREF=gi:4508012 /UG=Hs.88219 zinc finger protein 200 /FL=gb:AF060866.1 gb:NM_003454.1	
218883_s_at		NM_024629	gb:NM_024629.1 /DEF=Homo sapiens hypothetical protein FLJ23468 (FLJ23468), mRNA. /FEA=mRNA /GEN=FLJ23468 /PROD=hypothetical protein FLJ23468 /DB_XREF=gi:13375855 /UG=Hs.38178 hypothetical protein FLJ23468 /FL=gb:NM_024629.1	

219354_at		NM_018316	gb:NM_018316.1 /DEF=Homo sapiens hypothetical protein FLJ11078 (FLJ11078), mRNA. /FEA=mRNA /GEN=FLJ11078 /PROD=hypothetical protein FLJ11078 /DB_XREF=gi:8922853 /UG=Hs.250632 hypothetical protein FLJ11078 /FL=gb:NM_018316.1	
215785_s_at		AL161999	Consensus includes gb:AL161999.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mRNA /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein	

209584_x_at		AF165520	gb:AF165520.1 /DEF=Homo sapiens phorbolin I protein (PBI) mRNA, complete cds. /FEA=mRNA /GEN=PBI /PROD=phorbolin I protein /DB_XREF=gi:9294746 /UG=Hs.8583 similar to APOBEC1 /FL=gb:AF165520.1	
214082_at		AW003516	ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precursor [Homo sapiens] [H.sapiens]	
211756_at		BC005961	gb:BC005961.1 /DEF=Homo sapiens, parathyroid hormone-like hormone, clone MGC:14611, mRNA, complete cds. /FEA=mRNA /PROD=parathyroid hormone-like hormone /DB_XREF=gi:13543620 /FL=gb:BC005961.1	
204762_s_at	GNAO1	BE670563	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	



			gb:NM_003810.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA. /FEA=mRNA /GEN=TNFSF10 /PROD=tumor necrosis factor (ligand) superfamily,member 10 /DB_XREF=gi:4507592 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 gb:NM_003810.1	
202688_at		NM_003810		
209163_at	CYB561	AL514271	cytochrome b-561	

213332_at		AL031290	Consensus includes gb:AL031290 /DEF=Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS /FEA=mRNA_1 /DB_XREF=gi:3550114 /UG=Hs.9654 similar to pregnancy-associated plasma protein A precursor	
219818_s_at		NM_018025	gb:NM_018025.1 /DEF=Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA. /FEA=mRNA /GEN=FLJ10206 /PROD=hypothetical protein FLJ10206 /DB_XREF=gi:8922282 /UG=Hs.55014 hypothetical protein FLJ10206 /FL=gb:NM_018025.1	

220019_s_at		NM_005774	gb:NM_005774.1 /DEF=Homo sapiens zinc finger protein 255 (ZNF255), mRNA. /FEA=mRNA /GEN=ZNF255 /PROD=zinc finger protein 255 /DB_XREF=gi:5031614 /UG=Hs.181696 zinc finger protein 255 /FL=gb:AF067164.1 gb:NM_005774.1	
216288_at		AU159276	AU159276 THYRO1 Homo sapiens cDNA clone THYRO1001262 3', mRNA sequence.	
219736_at		NM_018700	gb:NM_018700.1 /DEF=Homo sapiens zinc-binding protein Rbcc728 (Rbcc728), mRNA. /FEA=mRNA /GEN=Rbcc728 /PROD=zinc-binding protein Rbcc728 /DB_XREF=gi:8924237 /UG=Hs.121429 zinc-binding protein Rbcc728 /FL=gb:NM_018700.1	
203213_at	CDC2	AL524035	cell division cycle 2, G1 to S and G2 to M	

202791_s_at		AK022669	Consensus includes gb:AK022669.1 /DEF=Homo sapiens cDNA FLJ12607 fis, clone NT2RM4001489, highly similar to Homo sapiens mRNA for KIAA0685 protein. /FEA=mRNA /DB_XREF=gi:10434196 /UG=Hs.296406 KIAA0685 gene product /FL=gb:AB014585.1 gb:NM_014678.1	
215916_at		AL157418	Consensus includes gb:AL157418.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761K18121 (from clone DKFZp761K18121). /FEA=mRNA /DB_XREF=gi:7018439 /UG=Hs.112028 MisshapenNIK- related kinase	

221155_x_at		NM_018603	gb:NM_018603.1 /DEF=Homo sapiens hypothetical protein PRO1496 (PRO1496), mRNA. /FEA=mRNA /GEN=PRO1496 /PROD=hypothetical protein PRO1496 /DB_XREF=gi:8924053 /UG=Hs.283617 hypothetical protein PRO1496 /FL=gb:AF116665.1 gb:NM_018603.1	
52255_s_at	COL5A3	AI984221	collagen, type V, alpha 3	
216175_at		AK025276	Consensus includes gb:AK025276.1 /DEF=Homo sapiens cDNA: FLJ21623 fis, clone COL07915. /FEA=mRNA /DB_XREF=gi:10437759 /UG=Hs.306791 Homo sapiens cDNA: FLJ21623 fis, clone COL07915	

213105_s_at		AL031709	Consensus includes gb:AI799802 /FEA=EST /DB_XREF=gi:5365274 /DB_XREF=est:wc43d09.x1 /CLONE=IMAGE:2321393 /UG=Hs.134846 Human DNA sequence from clone 316G12 on chromosome 16. Contains the gene for C2 domain protein KIAA0734, the gene for a novel protein similar to predicted yeast, worm and archae-bacterial proteins, a novel gene and the 3 part of the gene for a novel prot	
200720_s_at	ACTR1A	AL532341	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	

208299_at		NM_021096	gb:NM_021096.1 /DEF=Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA. /FEA=mRNA /GEN=CACNA1I /PROD=calcium channel, voltage-dependent, alpha 1I subunit /DB_XREF=gi:10863882 /UG=Hs.125116 calcium channel, voltage-dependent, alpha 1I subunit /FL=gb:NM_021096.1 gb:AF129133.1	
205503_at		NM_005401	gb:NM_005401.1 /DEF=Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /FEA=mRNA /GEN=PTPN14 /PROD=protein tyrosine phosphatase, non-receptor type14 /DB_XREF=gi:4885566 /UG=Hs.159238 protein tyrosine phosphatase, non-receptor type 14 /FL=gb:NM_005401.1	
396_f_at	EPOR	X97671	erythropoietin receptor	NM_000121

221815_at		BE671816	Homo sapiens, Similar to hypothetical protein PRO2831, clone MGC:23813 IMAGE:4273837, mRNA, complete cds	
220777_at		NM_022113	gb:NM_022113.1 /DEF=Homo sapiens kinesin family member 13A (KIF13A), mRNA. /FEA=mRNA /GEN=KIF13A /PROD=kinesin family member 13A /DB_XREF=gi:11545828 /UG=Hs.146286 kinesin family member 13A /FL=gb:NM_022113.1	
212997_s_at	TLK2	AU119586	tousled-like kinase 2	



205288_at		NM_003672	gb:NM_003672.1 /DEF=Homo sapiens CDC14 (cell division cycle 14, S. cerevisiae) homolog A (CDC14A), mRNA. /FEA=mRNA /GEN=CDC14A /PROD=CDC14 (cell division cycle 14, S. cerevisiae)homolog A /DB_XREF=gi:4502696 /UG=Hs.65993 CDC14 (cell division cycle 14, S. cerevisiae) homolog A /FL=gb:AF000367.1 gb:NM_003672.1 gb:AF122013.1	
209457_at		U16996	gb:U16996.1 /DEF=Human protein tyrosine phosphatase mRNA, complete cds. /FEA=mRNA /PROD=protein tyrosine phosphatase /DB_XREF=gi:642012 /UG=Hs.2128 dual specificity phosphatase 5 /FL=gb:NM_004419.2 gb:U16996.1 gb:U15932.2	

207571_x_at		NM_004848	gb:NM_004848.1 /DEF=Homo sapiens basement membrane-induced gene (ICB-1), mRNA. /FEA=mRNA /GEN=ICB-1 /PROD=basement membrane-induced gene /DB_XREF=gi:4758579 /UG=Hs.10649 basement membrane-induced gene /FL=gb:AF044896.1 gb:NM_004848.1	
222034_at	GNB2L1	AA443762	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	
215651_at		AK026682	Consensus includes gb:AK026682.1 /DEF=Homo sapiens cDNA: FLJ23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo sapiens cDNA: FLJ23029 fis, clone LNG01883	

219470_x_at		NM_019084	gb:NM_019084.1 /DEF=Homo sapiens hypothetical protein FLJ10895 (FLJ10895), mRNA. /FEA=mRNA /GEN=FLJ10895 /PROD=hypothetical protein FLJ10895 /DB_XREF=gi:9506628 /UG=Hs.281348 hypothetical protein FLJ10895 /FL=gb:NM_019084.1	
208911_s_at		M34055	gb:M34055.1 /DEF=Human pyruvate dehydrogenase E1-beta subunit mRNA, complete cds. /FEA=mRNA /GEN=PDHB /DB_XREF=gi:190791 /UG=Hs.979 pyruvate dehydrogenase (lipoamide) beta /FL=gb:BC000439.1 gb:BC001924.1 gb:J03576.1 gb:M34479.1 gb:M54788.1 gb:M34055.1 gb:NM_000925.1	

203970_s_at		NM_003630	gb:NM_003630.1 /DEF=Homo sapiens peroxisomal biogenesis factor 3 (PEX3), mRNA. /FEA=mRNA /GEN=PEX3 /PROD=peroxisomal biogenesis factor 3 /DB_XREF=gi:4505726 /UG=Hs.7277 peroxisomal biogenesis factor 3 /FL=gb:NM_003630.1 gb:AB035307.1	
204000_at		NM_016194	gb:NM_016194.1 /DEF=Homo sapiens hypothetical protein (DKFZp586O1922), mRNA. /FEA=mRNA /GEN=DKFZp586O1922 /PROD=hypothetical protein /DB_XREF=gi:7705366 /UG=Hs.155090 hypothetical protein /FL=gb:AL117471.1 gb:NM_016194.1	
203906_at	KIAA0763	AI652645	KIAA0763 gene product	
213398_s_at	HCDI	AI347090	HCDI protein	

201117_s_at		NM_001873	gb:NM_001873.1 /DEF=Homo sapiens carboxypeptidase E (CPE), mRNA. /FEA=mRNA /GEN=CPE /PROD=carboxypeptidase E precursor /DB_XREF=gi:4503008 /UG=Hs.75360 carboxypeptidase E /FL=gb:NM_001873.1	
207394_at		NM_003438	gb:NM_003438.1 /DEF=Homo sapiens zinc finger protein 137 (clone pHZ-30) (ZNF137), mRNA. /FEA=mRNA /GEN=ZNF137 /PROD=zinc finger protein 137 (clone pHZ-30) /DB_XREF=gi:4507988 /UG=Hs.151689 zinc finger protein 137 (clone pHZ-30) /FL=gb:NM_003438.1 gb:U09414.1	

208922_s_at	BC004904	gb:BC004904.1 /DEF=Homo sapiens, nuclear RNA export factor 1, clone MGC:4612, mRNA, complete cds. /FEA=mRNA /PROD=nuclear RNA export factor 1 /DB_XREF=gi:13436184 /UG=Hs.323502 nuclear RNA export factor 1 /FL=gb:BC004904.1 gb:U80073.1 gb:AF126246.1 gb:AF112880.1 gb:NM_006362.1
211939_x_at	X74070	Consensus includes gb:X74070.1 /DEF=H.sapiens mRNA for transcription factor BTF 3. /FEA=mRNA /PROD=transcription factor BTF3 /DB_XREF=gi:395086 /UG=Hs.101025 basic transcription factor 3

200912_s_at		NM_001967	gb:NM_001967.2 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA. /FEA=mRNA /GEN=EIF4A2 /PROD=eukaryotic translation initiation factor 4A,isoform 2 /DB_XREF=gi:9945313 /UG=Hs.173912 eukaryotic translation initiation factor 4A, isoform 2 /FL=gb:D30655.1 gb:NM_001967.2	
208880_s_at		AB019219	gb:AB019219.1 /DEF=Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1Zer1 and Prp6. /FEA=mRNA /DB_XREF=gi:4164165 /UG=Hs.31334 putative mitochondrial outer membrane protein import receptor /FL=gb:BC001666.1 gb:AF026031.1 gb:AB019219.1 gb:NM_012469.1 gb:AF221842.1	

212037_at		Y09703	Consensus includes gb:BF508848 /FEA=EST /DB_XREF=gi:11592146 /DB_XREF=est:UI-H-BI4-aor-e-06-0- UI.s1 /CLONE=IMAGE:3085907 /UG=Hs.44499 pinin, desmosome associated protein	
205042_at		NM_005476	gb:NM_005476.2 /DEF=Homo sapiens UDP-N-acetylglucosamine-2- epimeraseN-acetylmannosamine kinase (GNE), mRNA. /FEA=mRNA /GEN=GNE /PROD=UDP-N- acetylglucosamine-2-epimeraseN- acetylmannosamine kinase /DB_XREF=gi:6382074 /UG=Hs.5920 UDP-N-acetylglucosamine-2- epimeraseN-acetylmannosamine kinase /FL=gb:AF051852.1 gb:AF155663.1 gb:NM_005476.2	



211959_at		L27560	Consensus includes gb:AW007532 /FEA=EST /DB_XREF=gi:5856310 /DB_XREF=est:ws52h07.x1 /CLONE=IMAGE:2500861 /UG=Hs.103391 Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA	
213982_s_at	KIAA0471	BG107203	KIAA0471 gene product	
203729_at		NM_001425	gb:NM_001425.1 /DEF=Homo sapiens epithelial membrane protein 3 (EMP3), mRNA. /FEA=mRNA /GEN=EMP3 /PROD=epithelial membrane protein 3 /DB_XREF=gi:4503562 /UG=Hs.9999 epithelial membrane protein 3 /FL=gb:U52101.1 gb:U87947.1 gb:NM_001425.1	

209007_s_at		AF267856	gb:AF267856.1 /DEF=Homo sapiens HT033 mRNA, complete cds. /FEA=mRNA /PROD=HT033 /DB_XREF=gi:12006038 /UG=Hs.8084 hypothetical protein dJ465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1	
207069_s_at		NM_005585	gb:NM_005585.1 /DEF=Homo sapiens MAD (mothers against decapentaplegic, Drosophila) homolog 6 (MADH6), mRNA. /FEA=mRNA /GEN=MADH6 /PROD=MAD (mothers against decapentaplegic,Drosophila) homolog 6 /DB_XREF=gi:5031898 /UG=Hs.153863 MAD (mothers against decapentaplegic, Drosophila) homolog 6 /FL=gb:U59914.1 gb:NM_005585.1	
39549_at	NPAS2	AI743090	neuronal PAS domain protein 2	

212328_at		AK027231	Consensus includes gb:AB029025.1 /DEF=Homo sapiens mRNA for KIAA1102 protein, partial cds. /FEA=mRNA /GEN=KIAA1102 /PROD=KIAA1102 protein /DB_XREF=gi:5689540 /UG=Hs.202949 KIAA1102 protein	
217225_x_at		AL512687	Consensus includes gb:AL512687.1 /DEF=Homo sapiens mRNA; cDNA DKFZp547A1913 (from clone DKFZp547A1913). /FEA=mRNA /GEN=DKFZp547A1913 /PROD=hypothetical protein /DB_XREF=gi:12224839 /UG=Hs.227823 pM5 protein	

201293_x_at	NM_021130	gb:NM_021130.1 /DEF=Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA. /FEA=mRNA /GEN=PPIA /PROD=peptidylprolyl isomerase A (cyclophilin A) /DB_XREF=gi:10863926 /UG=Hs.182937 peptidylprolyl isomerase A (cyclophilin A) /FL=gb:NM_021130.1 gb:BC000689.1 gb:BC005320.1
221046_s_at	NM_014170	gb:NM_014170.1 /DEF=Homo sapiens HSPC135 protein (HSPC135), mRNA. /FEA=mRNA /GEN=HSPC135 /PROD=HSPC135 protein /DB_XREF=gi:7661795 /UG=Hs.127496 HSPC135 protein /FL=gb:AF161484.1 gb:NM_014170.1

221104_s_at		NM_018376	gb:NM_018376.1 /DEF=Homo sapiens hypothetical protein FLJ11275 (FLJ11275), mRNA. /FEA=mRNA /GEN=FLJ11275 /PROD=hypothetical protein FLJ11275 /DB_XREF=gi:8922969 /UG=Hs.272248 hypothetical protein FLJ11275 /FL=gb:NM_018376.1	
209022_at		AK026678	Consensus includes gb:AK026678.1 /DEF=Homo sapiens cDNA: FLJ23025 fis, clone LNG01702, highly similar to HUMAUTOND Human autonomously replicating sequence (ARS) mRNA. /FEA=mRNA /DB_XREF=gi:10439584 /UG=Hs.8217 stromal antigen 2 /FL=gb:BC001765.1	
213918_s_at	IDN3	BF221673	IDN3 protein	

201173_x_at		NM_006600	gb:NM_006600.1 /DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. /FEA=mRNA /GEN=NUDC /PROD=nuclear distribution gene C (A.nidulans)homolog /DB_XREF=gi:5729952 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:BC002399.1 gb:BC003132.1 gb:AB019408.1 gb:AF130736.1 gb:AF125465.1 gb:AF100760.1 gb:NM_006600.1	
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203869_at		NM_022832	Consensus includes gb:AK024318.1 /DEF=Homo sapiens cDNA FLJ14256 fis, clone PLACE1000007, weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15). /FEA=mRNA /DB_XREF=gi:10436669 /UG=Hs.109268 hypothetical protein FLJ12552 /FL=gb:NM_022832.1	
201011_at		NM_002950	gb:NM_002950.1 /DEF=Homo sapiens ribophorin I (RPN1), mRNA. /FEA=mRNA /GEN=RPN1 /PROD=ribophorin I /DB_XREF=gi:4506674 /UG=Hs.2280 ribophorin I /FL=gb:NM_002950.1	
213951_s_at		BE964655	EST	
212289_at	KIAA0874	AW572909	KIAA0874 protein	
213931_at	ID2	AI819238	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	

213666_at		AK026589	Consensus includes gb:AK026589.1 /DEF=Homo sapiens cDNA: FLJ22936 fis, clone KAT07936. /FEA=mRNA /DB_XREF=gi:10439473 /UG=Hs.90998 KIAA0128 protein; sepin 2	
212887_at	SEC23A	AI753659	Sec23 homolog A (S. cerevisiae)	
200614_at		NM_004859	gb:NM_004859.1 /DEF=Homo sapiens clathrin, heavy polypeptide (Hc) (CLTC), mRNA. /FEA=mRNA /GEN=CLTC /PROD=clathrin heavy chain /DB_XREF=gi:4758011 /UG=Hs.178710 clathrin, heavy polypeptide (Hc) /FL=gb:D21260.1 gb:NM_004859.1	



207765_s_at		NM_025182	gb:NM_025182.1 /DEF=Homo sapiens hypothetical protein FLJ11560 (FLJ11560), mRNA. /FEA=mRNA /GEN=FLJ11560 /PROD=hypothetical protein FLJ11560 /DB_XREF=gi:13378154 /UG=Hs.301696 hypothetical protein FLJ11560 /FL=gb:NM_025182.1	
212944_at		AK024896	Consensus includes gb:AK024896.1 /DEF=Homo sapiens cDNA: FLJ21243 fis, clone COL01164. /FEA=mRNA /DB_XREF=gi:10437310 /UG=Hs.268016 Homo sapiens cDNA: FLJ21243 fis, clone COL01164	
213469_at		AV705244	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]	

218589_at		NM_005767	gb:NM_005767.1 /DEF=Homo sapiens purinergic receptor (family A group 5) (P2Y5), mRNA. /FEA=mRNA /GEN=P2Y5 /PROD=purinergic receptor (family A group 5) /DB_XREF=gi:5031968 /UG=Hs.189999 purinergic receptor (family A group 5) /FL=gb:AF000546.1 gb:NM_005767.1	
204524_at		NM_002613	gb:NM_002613.1 /DEF=Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1), mRNA. /FEA=mRNA /GEN=PDPK1 /PROD=3-phosphoinositide dependent protein kinase-1 /DB_XREF=gi:4505694 /UG=Hs.154729 3-phosphoinositide dependent protein kinase-1 /FL=gb:AF017995.1 gb:NM_002613.1	

200627_at		BC003005	gb:BC003005.1 /DEF=Homo sapiens, unactive progesterone receptor, 23 kD, clone MGC:4004, mRNA, complete cds. /FEA=mRNA /PROD=unactive progesterone receptor, 23 kD /DB_XREF=gi:12804292 /UG=Hs.278270 unactive progesterone receptor, 23 kD /FL=gb:BC003005.1 gb:L24804.1 gb:NM_006601.1	
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200640_at		NM_003406	gb:NM_003406.1 /DEF=Homo sapiens tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA. /FEA=mRNA /GEN=YWHAZ /PROD=tyrosine 3-monooxygenasetryptophan5-monooxygenase activation protein, zeta polypeptide /DB_XREF=gi:4507952 /UG=Hs.75103 tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, zeta polypeptide /FL=gb:BC003623.1 gb:M86400.1 gb:NM_003406.1 gb:U28964.1	
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204714_s_at		NM_000130	gb:NM_000130.2 /DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. /FEA=mRNA /GEN=F5 /PROD=coagulation factor V precursor /DB_XREF=gi:10518500 /UG=Hs.30054 coagulation factor V (proaccelerin, labile factor) /FL=gb:NM_000130.2 gb:M16967.1 gb:M14335.1	
217906_at		NM_014315	gb:NM_014315.1 /DEF=Homo sapiens host cell factor homolog (LCP), mRNA. /FEA=mRNA /GEN=LCP /PROD=host cell factor homolog /DB_XREF=gi:7657300 /UG=Hs.20597 host cell factor homolog /FL=gb:BC002335.1 gb:AF113131.1 gb:NM_014315.1 gb:AF244137.1	

218249_at		NM_022494	gb:NM_022494.1 /DEF=Homo sapiens hypothetical protein FLJ21952 (FLJ21952), mRNA. /FEA=mRNA /GEN=FLJ21952 /PROD=hypothetical protein FLJ21952 /DB_XREF=gi:11968052 /UG=Hs.22353 hypothetical protein FLJ21952 /FL=gb:NM_022494.1	
212158_at		J04621	Consensus includes gb:AL577322 /FEA=EST /DB_XREF=gi:12940338 /DB_XREF=est:AL577322 /CLONE=CS0DI085YI06 (3 prime) /UG=Hs.1501 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	

200594_x_at		NM_004501	gb:NM_004501.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), mRNA. /FEA=mRNA /GEN=HNRPU /PROD=heterogeneous nuclear ribonucleoprotein U(scaffold attachment factor A) /DB_XREF=gi:4758545 /UG=Hs.103804 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) /FL=gb:BC003367.1 gb:BC003621.1 gb:NM_004501.1	
204640_s_at		NM_003563	gb:NM_003563.1 /DEF=Homo sapiens speckle-type POZ protein (SPOP), mRNA. /FEA=mRNA /GEN=SPOP /PROD=speckle-type POZ protein /DB_XREF=gi:4507182 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC003385.1 gb:NM_003563.1	

218258_at		NM_015972	gb:NM_015972.1 /DEF=Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA. /FEA=mRNA /GEN=LOC51082 /PROD=RNA polymerase I 16 kDa subunit /DB_XREF=gi:7705739 /UG=Hs.106127 RNA polymerase I 16 kDa subunit /FL=gb:BC000889.1 gb:AF077044.1 gb:NM_015972.1	
218275_s_at		AP001745	Consensus includes gb:AP001745 /DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 /FEA=mRNA_3 /DB_XREF=gi:7768737 /UG=Hs.16007 chromosome 21 open reading frame 25	



218610_s_at		NM_018340	gb:NM_018340.1 /DEF=Homo sapiens hypothetical protein FLJ11151 (FLJ11151), mRNA. /FEA=mRNA /GEN=FLJ11151 /PROD=hypothetical protein FLJ11151 /DB_XREF=gi:8922900 /UG=Hs.14992 hypothetical protein FLJ11151 /FL=gb:NM_018340.1	
220525_s_at		NM_012103	gb:NM_012103.1 /DEF=Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA. /FEA=mRNA /GEN=AUP1 /PROD=ancient ubiquitous protein 1 /DB_XREF=gi:6912259 /UG=Hs.173736 ancient ubiquitous protein 1 /FL=gb:AF100754.1 gb:NM_012103.1	
65438_at	KIAA1609	AA195124	KIAA1609 protein	

204137_at		NM_003272	gb:NM_003272.1 /DEF=Homo sapiens transmembrane 7 superfamily member 1 (upregulated in kidney) (TM7SF1), mRNA. /FEA=mRNA /GEN=TM7SF1 /PROD=transmembrane 7 superfamily member 1(upregulated in kidney) /DB_XREF=gi:4507544 /UG=Hs.15791 transmembrane 7 superfamily member 1 (upregulated in kidney) /FL=gb:AF027826.1 gb:NM_003272.1	
212221_x_at		AL117536	Consensus includes gb:AV703259 /FEA=EST /DB_XREF=gi:10720588 /DB_XREF=est:AV703259 /CLONE=ADBCRE12 /UG=Hs.303154 popeye protein 3	

204354_at	NM_015450	gb:NM_015450.1 /DEF=Homo sapiens DKFZP586D211 protein (DKFZP586D211), mRNA. /FEA=mRNA /GEN=DKFZP586D211 /PROD=DKFZP586D211 protein /DB_XREF=gi:13123773 /UG=Hs.31968 DKFZP586D211 protein /FL=gb:BC002923.1 gb:NM_015450.1
208795_s_at	D55716	gb:D55716.1 /DEF=Human mRNA for P1cdc47, complete cds. /FEA=mRNA /GEN=P1cdc47 /PROD=P1cdc47 /DB_XREF=gi:1255616 /UG=Hs.77152 minichromosome maintenance deficient (S. cerevisiae) 7 /FL=gb:D55716.1

217835_x_at		NM_018840	gb:NM_018840.1 /DEF=Homo sapiens putative Rab5-interacting protein (LOC55969), mRNA. /FEA=mRNA /GEN=LOC55969 /PROD=putative Rab5-interacting protein /DB_XREF=gi:10047115 /UG=Hs.184062 putative Rab5-interacting protein /FL=gb:NM_018840.1 gb:AF274936.1 gb:AF112213.1	
218593_at		NM_018077	gb:NM_018077.1 /DEF=Homo sapiens hypothetical protein FLJ10377 (FLJ10377), mRNA. /FEA=mRNA /GEN=FLJ10377 /PROD=hypothetical protein FLJ10377 /DB_XREF=gi:8922387 /UG=Hs.274263 hypothetical protein FLJ10377 /FL=gb:NM_018077.1	

217808_s_at		NM_024117	gb:NM_024117.1 /DEF=Homo sapiens hypothetical protein MGC2745 (MGC2745), mRNA. /FEA=mRNA /GEN=MGC2745 /PROD=hypothetical protein MGC2745 /DB_XREF=gi:13129137 /UG=Hs.324178 hypothetical protein MGC2745 /FL=gb:BC002326.1 gb:BC003044.1 gb:NM_024117.1	
213062_at		AA643304	Homo sapiens, Similar to N-terminal Asn amidase, clone MGC:29626 IMAGE:4872717, mRNA, complete cds	
218875_s_at		NM_012177	gb:NM_012177.1 /DEF=Homo sapiens F-box only protein 5 (FBXO5), mRNA. /FEA=mRNA /GEN=FBXO5 /PROD=F-box only protein 5 /DB_XREF=gi:6912365 /UG=Hs.272027 F-box only protein 5 /FL=gb:AF129535.1 gb:NM_012177.1	
212684_at	ZNF3	AI752257	zinc finger protein 3 (A8-51)	

202365_at		BC004815	gb:BC004815.1 /DEF=Homo sapiens, clone MGC:5139, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:5139) /DB_XREF=gi:13435956 /UG=Hs.127610 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain /FL=gb:BC004815.1 gb:M26393.1 gb:NM_000017.1	
214328_s_at	HSPCA	R01140	heat shock 90kDa protein 1, alpha	
221667_s_at		AF133207	gb:AF133207.1 /DEF=Homo sapiens protein kinase (H11) mRNA, complete cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901654 /UG=Hs.111676 protein kinase H11; small stress protein-like protein HSP22 /FL=gb:AF133207.1	

202348_s_at		BC000674	gb:BC000674.1 /DEF=Homo sapiens, dystonia 1, torsion (autosomal dominant; torsin A), clone MGC:1558, mRNA, complete cds. /FEA=mRNA /PROD=dystonia 1, torsion (autosomal dominant; torsinA) /DB_XREF=gi:12653776 /UG=Hs.19261 dystonia 1, torsion (autosomal dominant; torsin A) /FL=gb:BC000674.1 gb:AF007871.1 gb:NM_000113.1	
221984_s_at	MGC3035	AL040896	hypothetical protein MGC3035	
202975_s_at	RHOBTB3	N21138	Rho-related BTB domain containing 3	

218448_at		NM_017896	gb:NM_017896.1 /DEF=Homo sapiens hypothetical protein FLJ20602 (FLJ20602), mRNA. /FEA=mRNA /GEN=FLJ20602 /PROD=hypothetical protein FLJ20602 /DB_XREF=gi:8923556 /UG=Hs.103808 hypothetical protein FLJ20602 /FL=gb:NM_017896.1	
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202168_at		NM_003187	gb:NM_003187.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD (TAF2G), mRNA. /FEA=mRNA /GEN=TAF2G /PROD=TATA box binding protein (TBP)-associatedfactor, RNA polymerase II, G, 32kD /DB_XREF=gi:4507350 /UG=Hs.60679 TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD /FL=gb:BC003400.1 gb:NM_003187.1 gb:U21858.1 gb:U25112.1 gb:U30504.1	
209227_at	N33	AU158251	Putative prostate cancer tumor suppressor	

209212_s_at	AB030824	<p>gb:AB030824.1 /DEF=Homo sapiens mRNA for transcription factor BTEB2, complete cds. /FEA=mRNA /GEN=bteb2 /PROD=transcription factor BTEB2 /DB_XREF=gi:8272417 /UG=Hs.84728 Kruppel-like factor 5 (intestinal) /FL=gb:D14520.1 gb:NM_001730.1 gb:AF132818.1 gb:AB030824.1 gb:AF287272.1</p>
218133_s_at	NM_021824	<p>gb:NM_021824.1 /DEF=Homo sapiens NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 (NIF3L1), mRNA. /FEA=mRNA /GEN=NIF3L1 /PROD=NIF3 (Ngg1 interacting factor 3, S.pombehomolog)-like 1 /DB_XREF=gi:11141898 /UG=Hs.21943 NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 /FL=gb:AF182416.1 gb:NM_021824.1 gb:AF060513.1 gb:AB038949.1</p>

212689_s_at		AA524505	Human putative zinc finger protein mRNA	
			gb:NM_006169.1 /DEF=Homo sapiens nicotinamide N-methyltransferase (NNMT), mRNA. /FEA=mRNA /GEN=NNMT /PROD=nicotinamide N-methyltransferase /DB_XREF=gi:5453789 /UG=Hs.76669 nicotinamide N-methyltransferase /FL=gb:BC000234.1 gb:U08021.1 gb:NM_006169.1	
202238_s_at		NM_006169		
			gb:BC000436.1 /DEF=Homo sapiens, endosulfine alpha, clone MGC:8394, mRNA, complete cds. /FEA=mRNA /PROD=endosulfine alpha /DB_XREF=gi:12653334 /UG=Hs.111680 endosulfine alpha /FL=gb:BC000436.1 gb:BC004461.1 gb:NM_004436.1 gb:AF157509.1	
202596_at		BC000436		
221806_s_at	FLJ10707	BF590997	hypothetical protein FLJ10707	

202775_s_at	NM_004592	gb:NM_004592.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8), mRNA. /FEA=mRNA /GEN=SFRS8 /PROD=splicing factor, arginineserine-rich 8(suppressor-of-white-apricot, Drosophila homolog) /DB_XREF=gi:4759101 /UG=Hs.84229 splicing factor, arginineserine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) /FL=gb:NM_004592.1 gb:U08377.1
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202501_at		NM_014268	gb:NM_014268.1 /DEF=Homo sapiens microtubule-associated protein, RPEB family, member 2 (MAPRE2), mRNA. /FEA=mRNA /GEN=MAPRE2 /PROD=microtubule-associated protein, RPEB family,member 2 /DB_XREF=gi:10346134 /UG=Hs.78335 microtubule-associated protein, RPEB family, member 2 /FL=gb:NM_014268.1	
209386_at	TM4SF1	AI346835	transmembrane 4 superfamily member 1	
208315_x_at		NM_003300	gb:NM_003300.1 /DEF=Homo sapiens TNF receptor-associated factor 3 (TRAF3), mRNA. /FEA=mRNA /GEN=TRAF3 /PROD=TNF receptor-associated factor 3 /DB_XREF=gi:4507678 /UG=Hs.297660 TNF receptor-associated factor 3 /FL=gb:NM_003300.1 gb:U21092.1	

209413_at		BC002431	gb:BC002431.1 /DEF=Homo sapiens, Similar to UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2, clone MGC:2008, mRNA, complete cds. /FEA=mRNA /PROD=Similar to UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 /DB_XREF=gi:12803236 /UG=Hs.206713 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 /FL=gb:BC002431.1 gb:AF038660.1 gb:NM_003780.1 gb:AB024434.1	
214700_x_at		AK000323	Consensus includes gb:AK000323.1 /DEF=Homo sapiens cDNA FLJ20316 fis, clone HEP07903, highly similar to U79263 Human clone 23760 mRNA. /FEA=mRNA /DB_XREF=gi:7020332 /UG=Hs.225841 DKFZP434D193 protein	
213318_s_at	APOM	BG028844	apolipoprotein M	

			Consensus includes gb:AW194730 /FEA=EST /DB_XREF=gi:6473630 /DB_XREF=est:xn43d11.x1 /CLONE=IMAGE:2696469 /UG=Hs.9075 serinethreonine kinase 17a (apoptosis-inducing) /FL=gb:AB011420.1 gb:NM_004760.1	
202693_s_at		NM_004760		
214919_s_at	FLJ20288	R39094	FLJ20288 protein	
221920_s_at	MSCP	BE677761	likely ortholog of mouse mitochondrial solute carrier protein	
218285_s_at		NM_020139	gb:NM_020139.1 /DEF=Homo sapiens oxidoreductase UCPA (LOC56898), mRNA. /FEA=mRNA /GEN=LOC56898 /PROD=oxidoreductase UCPA /DB_XREF=gi:10047131 /UG=Hs.124696 oxidoreductase UCPA /FL=gb:NM_020139.1 gb:AF164790.1	

202886_s_at	M65254	gb:M65254.1 /DEF=Protein phosphatase 2A 65 kDa regulatory subunit-beta mRNA, complete cds. /FEA=mRNA /GEN=SNRPEP1 /PROD=protein phosphatase-2A regulatory subunit-beta /DB_XREF=gi:189429 /UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FL=gb:NM_002716.1 gb:AF163473.1 gb:M65254.1 gb:AF087438.1	
218431_at	NM_022067	gb:NM_022067.1 /DEF=Homo sapiens hypothetical protein FLJ12707 (FLJ12707), mRNA. /FEA=mRNA /GEN=FLJ12707 /PROD=hypothetical protein FLJ12707 /DB_XREF=gi:11545778 /UG=Hs.16157 hypothetical protein FLJ12707 /FL=gb:NM_022067.1	



221669_s_at		BC001964	gb:BC001964.1 /DEF=Homo sapiens, acyl-Coenzyme A dehydrogenase family, member 8, clone MGC:4966, mRNA, complete cds. /FEA=mRNA /PROD=acyl-Coenzyme A dehydrogenase family, member 8 /DB_XREF=gi:12805020 /UG=Hs.14791 acyl-Coenzyme A dehydrogenase family, member 8 /FL=gb:BC001964.1	
205523_at		U43328	gb:U43328.1 /DEF=Human link protein mRNA, complete cds. /FEA=mRNA /PROD=link protein /DB_XREF=gi:1151008 /UG=Hs.2799 cartilage linking protein 1 /FL=gb:U43328.1 gb:NM_001884.1	

202439_s_at		NM_000202	gb:NM_000202.2 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2-sulfatase isoform a precursor /DB_XREF=gi:5360215 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:M58342.1 gb:NM_000202.2	
221693_s_at		AB049952	gb:AB049952.1 /DEF=Homo sapiens MRPS18a mRNA for mitochondrial ribosomal protein S18a, complete cds. /FEA=mRNA /GEN=MRPS18a /PROD=mitochondrial ribosomal protein S18a /DB_XREF=gi:13620904 /FL=gb:AB049952.1	

202436_s_at		NM_000104	Consensus includes gb:AU144855 /FEA=EST /DB_XREF=gi:11006376 /DB_XREF=est:AU144855 /CLONE=HEMBA1003161 /UG=Hs.154654 cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM_000104.2 gb:U03688.1	
202437_s_at		NM_000104	gb:NM_000104.2 /DEF=Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1), mRNA. /FEA=mRNA /GEN=CYP1B1 /PROD=cytochrome P450, subfamily I (dioxin-inducible),polypeptide 1 /DB_XREF=gi:13325059 /UG=Hs.154654 cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM_000104.2 gb:U03688.1	

218482_at		NM_020189	gb:NM_020189.1 /DEF=Homo sapiens DC6 protein (DC6), mRNA. /FEA=mRNA /GEN=DC6 /PROD=DC6 protein /DB_XREF=gi:9910185 /UG=Hs.283740 DC6 protein /FL=gb:AF201940.1 gb:AF173296.1 gb:NM_020189.1	
201713_s_at		D42063	gb:D42063.1 /DEF=Human mRNA for RanBP2 (Ran-binding protein 2), complete cds. /FEA=mRNA /PROD=RanBP2 (Ran-binding protein 2) /DB_XREF=gi:924266 /UG=Hs.199179 RAN binding protein 2 /FL=gb:NM_006267.2 gb:D42063.1	

203511_s_at		AF041432	gb:AF041432.1 /DEF=Homo sapiens bet3 (BET3) mRNA, complete cds. /FEA=mRNA /GEN=BET3 /PROD=bet3 /DB_XREF=gi:2791803 /UG=Hs.288013 similar to yeast BET3 (S. cerevisiae) /FL=gb:AF041432.1 gb:NM_014408.1	
212793_at	DAAM2	BF513244	dishevelled associated activator of morphogenesis 2	
206744_s_at		NM_014242	gb:NM_014242.1 /DEF=Homo sapiens zinc finger protein 237 (ZNF237), mRNA. /FEA=mRNA /GEN=ZNF237 /PROD=zinc finger protein 237 /DB_XREF=gi:7657706 /UG=Hs.124386 zinc finger protein 237 /FL=gb:NM_014242.1	
212756_s_at	KIAA0349	AI761518	KIAA0349 protein	
209149_s_at	TM9SF1	BE899402	transmembrane 9 superfamily member 1	

201779_s_at		AF070558	gb:AF070558.1 /DEF=Homo sapiens clone 24450 RING zinc finger protein RZF mRNA, complete cds. /FEA=mRNA /PROD=RING zinc finger protein RZF /DB_XREF=gi:3387924 /UG=Hs.6900 ring finger protein 13 /FL=gb:AF037204.1 gb:AF070558.1 gb:NM_007282.1	
201753_s_at		NM_019903	gb:NM_019903.1 /DEF=Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /FEA=mRNA /GEN=ADD3 /PROD=adducin 3, isoform b /DB_XREF=gi:9951926 /UG=Hs.324470 adducin 3 (gamma) /FL=gb:D67031.1 gb:NM_019903.1	
212796_s_at	KIAA1055	BF195608	KIAA1055 protein	

201443_s_at		AF248966	gb:AF248966.1 /DEF=Homo sapiens HT028 mRNA, complete cds. /FEA=mRNA /PROD=HT028 /DB_XREF=gi:12005668 /UG=Hs.183434 ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 /FL=gb:AF248966.1 gb:NM_005765.1	
203620_s_at		NM_014824	gb:NM_014824.1 /DEF=Homo sapiens KIAA0769 gene product (KIAA0769), mRNA. /FEA=mRNA /GEN=KIAA0769 /PROD=KIAA0769 gene product /DB_XREF=gi:7662295 /UG=Hs.19056 KIAA0769 gene product /FL=gb:AB018312.1 gb:NM_014824.1	

203599_s_at	NM_007187	gb:NM_007187.2 /DEF=Homo sapiens WW domain binding protein 4 (formin binding protein 21) (WBP4), mRNA. /FEA=mRNA /GEN=WBP4 /PROD=WW domain-containing binding protein 4 /DB_XREF=gi:9943844 /UG=Hs.28307 WW domain binding protein 4 (formin binding protein 21) /FL=gb:AF071185.1 gb:NM_007187.2
208625_s_at	AF104913	gb:AF104913.1 /DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic protein synthesis initiation factor /DB_XREF=gi:3941723 /UG=Hs.211568 eukaryotic translation initiation factor 4 gamma, 1 /FL=gb:AF104913.1



206766_at		AF112345	gb:AF112345.1 /DEF=Homo sapiens integrin alpha 10 subunit (ITGA10) mRNA, complete cds. /FEA=mRNA /GEN=ITGA10 /PROD=integrin alpha 10 subunit /DB_XREF=gi:6650627 /UG=Hs.158237 integrin, alpha 10 /FL=gb:AF074015.1 gb:NM_003637.2 gb:AF112345.1	
210962_s_at		AB019691	gb:AB019691.1 /DEF=Homo sapiens mRNA for Centrosome- and Golgi-localized PKN-associated protein (CG-NAP), complete cds. /FEA=mRNA /GEN=cg-nap /PROD=Centrosome- and Golgi-localized PKN-associated protein (CG-NAP) /DB_XREF=gi:5051742 /UG=Hs.58103 A kinase (PRKA) anchor protein (yotiao) 9 /FL=gb:AB019691.1	
34726_at	CACNB3	U07139	calcium channel, voltage-dependent, beta 3 subunit	
213101_s_at	ACTR3	Z78330	ARP3 actin-related protein 3 homolog (yeast)	
213015_at		BF448315	ESTs	

217995_at		NM_021199	gb:NM_021199.1 /DEF=Homo sapiens CGI-44 protein; sulfide dehydrogenase like (yeast) (CGI-44), mRNA. /FEA=mRNA /GEN=CGI-44 /PROD=CGI-44 protein; sulfide dehydrogenase like(yeast) /DB_XREF=gi:10864010 /UG=Hs.8185 CGI-44 protein; sulfide dehydrogenase like (yeast) /FL=gb:NM_021199.1 gb:AF151802.1 gb:AF118085.1	
210119_at		U73191	gb:U73191.1 /DEF=Human inward rectifier potassium channel (Kir1.3), complete cds. /FEA=mRNA /GEN=Kir1.3 /PROD=inward rectifier potassium channel /DB_XREF=gi:1765984 /UG=Hs.17287 potassium inwardly-rectifying channel, subfamily J, member 15 /FL=gb:U73191.1 gb:NM_002243.1	

219644_at		NM_016122	gb:NM_016122.1 /DEF=Homo sapiens NY-REN-58 antigen (LOC51134), mRNA. /FEA=mRNA /GEN=LOC51134 /PROD=NY-REN-58 antigen /DB_XREF=gi:7705838 /UG=Hs.56148 NY-REN-58 antigen /FL=gb:AF155115.1 gb:NM_016122.1	
219032_x_at		NM_014322	gb:NM_014322.1 /DEF=Homo sapiens opsin 3 (encephalopsin) (OPN3), mRNA. /FEA=mRNA /GEN=OPN3 /PROD=opsin 3 (encephalopsin) /DB_XREF=gi:7657070 /UG=Hs.279926 opsin 3 (encephalopsin) /FL=gb:AF140242.1 gb:NM_014322.1	

219064_at		NM_030569	gb:NM_030569.1 /DEF=Homo sapiens hypothetical protein MGC10848 (MGC10848), mRNA. /FEA=mRNA /GEN=MGC10848 /PROD=hypothetical protein MGC10848 /DB_XREF=gi:13386477 /UG=Hs.207443 hypothetical protein MGC10848 /FL=gb:BC004282.1 gb:NM_030569.1	
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219015_s_at		NM_018466	gb:NM_018466.1 /DEF=Homo sapiens uncharacterized hematopoietic stemprogenitor cells protein MDS031 (MDS031), mRNA. /FEA=mRNA /GEN=MDS031 /PROD=uncharacterized hematopoietic stemprogenitorcells protein MDS031 /DB_XREF=gi:8923933 /UG=Hs.110853 uncharacterized hematopoietic stemprogenitor cells protein MDS031 /FL=gb:BC005336.1 gb:AF220051.1 gb:NM_018466.1	
203181_x_at	SRPK2	AW149364	SFRS protein kinase 2	

202157_s_at		U69546	gb:U69546.1 /DEF=Homo sapiens RNA-binding protein BRUNOL3 (BRUNOL3) mRNA, complete cds. /FEA=mRNA /GEN=BRUNOL3 /PROD=RNA-binding protein BRUNOL3 /DB_XREF=gi:1568642 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1	
213253_at	SMC2L1	AU154486	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	
202022_at		NM_005165	gb:NM_005165.1 /DEF=Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA. /FEA=mRNA /GEN=ALDOC /PROD=aldolase C, fructose-bisphosphate /DB_XREF=gi:4885062 /UG=Hs.155247 aldolase C, fructose-bisphosphate /FL=gb:BC003613.1 gb:AF054987.1 gb:NM_005165.1	

206015_s_at		NM_014947	gb:NM_014947.1 /DEF=Homo sapiens KIAA1041 protein (KIAA1041), mRNA. /FEA=mRNA /GEN=KIAA1041 /PROD=KIAA1041 protein /DB_XREF=gi:7662455 /UG=Hs.26023 KIAA1041 protein /FL=gb:AB028964.1 gb:NM_014947.1	
203211_s_at		AK027038	Consensus includes gb:AK027038.1 /DEF=Homo sapiens cDNA: FLJ23385 fis, clone HEP16802. /FEA=mRNA /DB_XREF=gi:10440053 /UG=Hs.181326 KIAA1073 protein /FL=gb:AB028996.1 gb:NM_016156.1	
221509_at		AB014731	gb:AB014731.1 /DEF=Homo sapiens mRNA for SMAP-3, complete cds. /FEA=mRNA /GEN=smap-3 /PROD=SMAP-3 /DB_XREF=gi:12248760 /UG=Hs.22393 density-regulated protein /FL=gb:AB014731.1	

203375_s_at		NM_003291	gb:NM_003291.1 /DEF=Homo sapiens tripeptidyl peptidase II (TPP2), mRNA. /FEA=mRNA /GEN=TPP2 /PROD=tripeptidyl peptidase II /DB_XREF=gi:4507656 /UG=Hs.1117 tripeptidyl peptidase II /FL=gb:M73047.1 gb:NM_003291.1	
201859_at		NM_002727	gb:NM_002727.1 /DEF=Homo sapiens proteoglycan 1, secretory granule (PRG1), mRNA. /FEA=mRNA /GEN=PRG1 /PROD=proteoglycan 1, secretory granule /DB_XREF=gi:4506044 /UG=Hs.1908 proteoglycan 1, secretory granule /FL=gb:J03223.1 gb:NM_002727.1	
212737_at	GM2A	AL513583	GM2 ganglioside activator protein	



206414_s_at		NM_003887	gb:NM_003887.1 /DEF=Homo sapiens development and differentiation enhancing factor 2 (DDEF2), mRNA. /FEA=mRNA /GEN=DDEF2 /PROD=ADP-ribosylation factorarf-directed GTPaseactivating protein /DB_XREF=gi:4502248 /UG=Hs.12802 development and differentiation enhancing factor 2 /FL=gb:AB007860.1 gb:NM_003887.1	
212388_at		AB028980	Consensus includes gb:AB028980.1 /DEF=Homo sapiens mRNA for KIAA1057 protein, partial cds. /FEA=mRNA /GEN=KIAA1057 /PROD=KIAA1057 protein /DB_XREF=gi:5689450 /UG=Hs.7243 ubiquitin specific protease 24	

219080_s_at		NM_019857	gb:NM_019857.1 /DEF=Homo sapiens CTP synthase II (CTPS2), mRNA. /FEA=mRNA /GEN=CTPS2 /PROD=CTP synthase II /DB_XREF=gi:9789918 /UG=Hs.58553 CTP synthase II /FL=gb:AF226667.1 gb:NM_019857.1	
218515_at		NM_016631	gb:NM_016631.1 /DEF=Homo sapiens hypothetical protein (LOC51325), mRNA. /FEA=mRNA /GEN=LOC51325 /PROD=hypothetical protein /DB_XREF=gi:7706175 /UG=Hs.26461 hypothetical protein /FL=gb:AF208862.1 gb:NM_016631.1	

218324_s_at		NM_023071	gb:NM_023071.1 /DEF=Homo sapiens hypothetical protein FLJ13117 (FLJ13117), mRNA. /FEA=mRNA /GEN=FLJ13117 /PROD=hypothetical protein FLJ13117 /DB_XREF=gi:12751480 /UG=Hs.152982 hypothetical protein FLJ13117 /FL=gb:NM_023071.1	
201901_s_at		NM_003403	Consensus includes gb:Z14077.1 /DEF=H.sapiens mRNA for YY1NF-E1 protein. /FEA=mRNA /PROD=YY1 NF-E1 /DB_XREF=gi:38010 /UG=Hs.97496 YY1 transcription factor /FL=gb:M77698.1 gb:M76541.1 gb:NM_003403.2	

206342_x_at		NM_006123	gb:NM_006123.1 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 2, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2-sulfatase isoform b precursor /DB_XREF=gi:5360207 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:L40586.1 gb:NM_006123.1	
214150_x_at	ATP6V0E	BE043477	ATPase, H <sup>+</sup> transporting, lysosomal 9kDa, V0 subunit e	
209911_x_at		BC002842	gb:BC002842.1 /DEF=Homo sapiens, H2B histone family, member B, clone MGC:3802, mRNA, complete cds. /FEA=mRNA /PROD=H2B histone family, member B /DB_XREF=gi:12803984 /UG=Hs.180779 H2B histone family, member B /FL=gb:NM_021063.1 gb:BC002842.1	

205401_at		NM_003659	gb:NM_003659.1 /DEF=Homo sapiens alkylglycerone phosphate synthase (AGPS), mRNA. /FEA=mRNA /GEN=AGPS /PROD=alkylglycerone phosphate synthase precursor /DB_XREF=gi:4501992 /UG=Hs.22580 alkylglycerone phosphate synthase /FL=gb:NM_003659.1	
206571_s_at		NM_004834	gb:NM_004834.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA. /FEA=mRNA /GEN=MAP4K4 /PROD=mitogen-activated protein kinase kinase kinasekinase 4 /DB_XREF=gi:4758523 /UG=Hs.3628 mitogen-activated protein kinase kinase kinase kinase 4 /FL=gb:AF096300.1 gb:NM_004834.1	

214959_s_at		AF229253	Consensus includes gb:AF229253.1 /DEF=Homo sapiens clone FIF N1 fibroblast growth factor 2-interacting factor (API5) mRNA, partial cds.; alternatively spliced. /FEA=mRNA /GEN=API5 /PROD=fibroblast growth factor 2-interacting factor /DB_XREF=gi:12656082 /UG=Hs.227913 API5-like 1	
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218002_s_at	NM_004887	<p>gb:NM_004887.1 /DEF=Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK) (SCYB14), mRNA. /FEA=mRNA /GEN=SCYB14 /PROD=small inducible cytokine subfamily B(Cys-X-Cys), member 14 (BRAK) /DB_XREF=gi:4757869 /UG=Hs.24395 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK) /FL=gb:BC003513.1 gb:AF073957.1 gb:NM_004887.1 gb:AF144103.1 gb:AF106911.1</p>
220575_at	NM_024974	<p>gb:NM_024974.1 /DEF=Homo sapiens hypothetical protein FLJ11800 (FLJ11800), mRNA. /FEA=mRNA /GEN=FLJ11800 /PROD=hypothetical protein FLJ11800 /DB_XREF=gi:13376473 /UG=Hs.287456 hypothetical protein FLJ11800 /FL=gb:NM_024974.1</p>

211084_x_at	Z25429	gb:Z25429.1 /DEF=H.sapiens protein-serinethreonine kinase gene, complete CDS. /FEA=mRNA /PROD=protein-serinethreonine kinase /DB_XREF=gi:405736 /FL=gb:Z25429.1	
209339_at	U76248	gb:U76248.1 /DEF=Human hSIAH2 mRNA, complete cds. /FEA=mRNA /PROD=hSIAH2 /DB_XREF=gi:2673967 /UG=Hs.20191 seven in absentia (Drosophila) homolog 2 /FL=gb:U76248.1 gb:NM_005067.1	
210973_s_at	M63889	gb:M63889.1 /DEF=Human heparin-binding growth factor receptor (HBGF-R-alpha-a3) mRNA, complete cds. /FEA=mRNA /GEN=HBGF-R /PROD=heparin-binding growth factor receptor /DB_XREF=gi:183882 /UG=Hs.748 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) /FL=gb:M63889.1	



214697_s_at	ROD1	AW190873	ROD1 regulator of differentiation 1 (S. pombe)	
209229_s_at		BC002799	gb:BC002799.1 /DEF=Homo sapiens, KIAA1115 protein, clone MGC:3534, mRNA, complete cds. /FEA=mRNA /PROD=KIAA1115 protein /DB_XREF=gi:12803904 /UG=Hs.72172 KIAA1115 protein /FL=gb:BC002799.1	
217496_s_at	IDE	AA918442	insulin-degrading enzyme	
212046_x_at		X60188	Consensus includes gb:X60188.1 /DEF=Human ERK1 mRNA for protein serinethreonine kinase. /FEA=mRNA /GEN=ERK1 /PROD=protein serinethreonine kinase /DB_XREF=gi:31220 /UG=Hs.861 mitogen-activated protein kinase 3	

209587_at		U70370	gb:U70370.1 /DEF=Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds. /FEA=mRNA /GEN=Bft /PROD=hindlimb expressed homeobox protein backfoot /DB_XREF=gi:1870670 /UG=Hs.84136 paired-like homeodomain transcription factor 1 /FL=gb:BC003685.1 gb:U70370.1	
205431_s_at		NM_021073	gb:NM_021073.1 /DEF=Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA. /FEA=mRNA /GEN=BMP5 /PROD=bone morphogenetic protein 5 /DB_XREF=gi:10835090 /UG=Hs.1104 bone morphogenetic protein 5 /FL=gb:NM_021073.1 gb:M60314.1	

202075_s_at		NM_006227	gb:NM_006227.1 /DEF=Homo sapiens phospholipid transfer protein (PLTP), mRNA. /FEA=mRNA /GEN=PLTP /PROD=phospholipid transfer protein /DB_XREF=gi:5453913 /UG=Hs.283007 phospholipid transfer protein /FL=gb:L26232.1 gb:NM_006227.1	
215203_at		AW438464	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	
206685_at		NM_018985	gb:NM_018985.1 /DEF=Homo sapiens hypothetical protein (HCGIV.9), mRNA. /FEA=mRNA /GEN=HCGIV.9 /PROD=hypothetical protein /DB_XREF=gi:9506770 /UG=Hs.60856 hypothetical protein /FL=gb:NM_018985.1	

210493_s_at		BC001279	gb:BC001279.1 /DEF=Homo sapiens, Similar to KIAA0626 gene product, clone MGC:5129, mRNA, complete cds. /FEA=mRNA /PROD=Similar to KIAA0626 gene product /DB_XREF=gi:12654870 /UG=Hs.285318 Homo sapiens, Similar to KIAA0626 gene product, clone MGC:5129, mRNA, complete cds /FL=gb:BC001279.1	
215392_at		AU148154	AU148154 MAMMA1 Homo sapiens cDNA clone MAMMA1002744 3', mRNA sequence.	
210378_s_at		BC004118	gb:BC004118.1 /DEF=Homo sapiens, clone MGC:11170, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11170) /DB_XREF=gi:13278674 /UG=Hs.18528 Sjogrens syndrome nuclear autoantigen 1 /FL=gb:BC004118.1	

217608_at		AW408767	ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	
205211_s_at		NM_004292	gb:NM_004292.1 /DEF=Homo sapiens ras inhibitor (RIN1), mRNA. /FEA=mRNA /GEN=RIN1 /PROD=ras inhibitor /DB_XREF=gi:4759039 /UG=Hs.1030 ras inhibitor /FL=gb:L36463.1 gb:NM_004292.1	
214258_x_at	HTATIP	AA886971	HIV-1 Tat interactive protein, 60kDa	
204488_at		NM_014908	gb:NM_014908.1 /DEF=Homo sapiens KIAA1094 protein (KIAA1094), mRNA. /FEA=mRNA /GEN=KIAA1094 /PROD=KIAA1094 protein /DB_XREF=gi:7662481 /UG=Hs.161166 KIAA1094 protein /FL=gb:AB029017.1 gb:NM_014908.1	

218578_at		NM_024529	gb:NM_024529.1 /DEF=Homo sapiens hypothetical protein FLJ23316 (FLJ23316), mRNA. /FEA=mRNA /GEN=FLJ23316 /PROD=hypothetical protein FLJ23316 /DB_XREF=gi:13375677 /UG=Hs.5722 hypothetical protein FLJ23316 /FL=gb:AF312865.1 gb:NM_024529.1	
208916_at		AF105230	gb:AF105230.1 /DEF=Homo sapiens neutral amino acid transporter (SLC1A5) mRNA, complete cds. /FEA=mRNA /GEN=SLC1A5 /PROD=neutral amino acid transporter /DB_XREF=gi:4191561 /UG=Hs.183556 solute carrier family 1 (neutral amino acid transporter), member 5 /FL=gb:BC000062.1 gb:U53347.1 gb:AF102826.1 gb:AF105230.1 gb:AF105423.1 gb:NM_005628.1	

202687_s_at		U57059	gb:U57059.1 /DEF=Homo sapiens Apo-2 ligand mRNA, complete cds. /FEA=mRNA /PROD=Apo-2 ligand /DB_XREF=gi:1336207 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 gb:NM_003810.1	
201297_s_at		NM_018221	Consensus includes gb:AK023321.1 /DEF=Homo sapiens cDNA FLJ13259 fis, clone OVARC1000876, moderately similar to MOB1 PROTEIN. /FEA=mRNA /DB_XREF=gi:10435206 /UG=Hs.196437 hypothetical protein FLJ10788 /FL=gb:AB016839.1 gb:BC003398.1 gb:NM_018221.1	

207565_s_at		NM_001531	gb:NM_001531.1 /DEF=Homo sapiens major histocompatibility complex, class I-like sequence (HLALS), mRNA. /FEA=mRNA /GEN=HLALS /PROD=major histocompatibility complex, class I-like sequence /DB_XREF=gi:4504416 /UG=Hs.101840 major histocompatibility complex, class I-like sequence /FL=gb:NM_001531.1 gb:U22963.1	
220761_s_at		NM_016281	gb:NM_016281.1 /DEF=Homo sapiens STE20-like kinase (JIK), mRNA. /FEA=mRNA /GEN=JIK /PROD=STE20-like kinase /DB_XREF=gi:7705559 /UG=Hs.12040 STE20-like kinase /FL=gb:AF179867.1 gb:NM_016281.1	
221978_at	HLA-F	BE138825	major histocompatibility complex, class I, F	



221490_at		AL136733	gb:AL136733.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N1010 (from clone DKFZp434N1010); complete cds. /FEA=mRNA /GEN=DKFZp434N1010 /PROD=hypothetical protein /DB_XREF=gi:12052984 /UG=Hs.75425 ubiquitin associated protein /FL=gb:AL136733.1 gb:AF222043.2 gb:NM_016525.2	
213182_x_at	CDKN1C	R78668	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	
217704_x_at		AI820796	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	

209398_at		BC002649	gb:BC002649.1 /DEF=Homo sapiens, H1 histone family, member 2, clone MGC:3992, mRNA, complete cds. /FEA=mRNA /PROD=H1 histone family, member 2 /DB_XREF=gi:12803628 /UG=Hs.7644 H1 histone family, member 2 /FL=gb:BC002649.1 gb:NM_005319.1	
202254_at		AB007900	Consensus includes gb:AB007900.1 /DEF=Homo sapiens KIAA0440 mRNA, partial cds. /FEA=mRNA /GEN=KIAA0440 /DB_XREF=gi:2662160 /UG=Hs.172180 KIAA0440 protein /FL=gb:AF090990.1 gb:NM_015556.1	

203836_s_at		D84476	gb:D84476.1 /DEF=Homo sapiens mRNA for ASK1, complete cds. /FEA=mRNA /PROD=ASK1 /DB_XREF=gi:1805499 /UG=Hs.151988 mitogen-activated protein kinase kinase kinase 5 /FL=gb:U67156.1 gb:D84476.1 gb:NM_005923.2	
210837_s_at		AF012074	gb:AF012074.1 /DEF=Homo sapiens cAMP-specific phosphodiesterase PDE4D2 (PDE4D) mRNA, complete cds. /FEA=mRNA /GEN=PDE4D /PROD=cAMP-specific phosphodiesterase PDE4D2 /DB_XREF=gi:2735858 /UG=Hs.172081 phosphodiesterase 4D, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E3) /FL=gb:U50158.1 gb:AF012074.1	
213815_x_at	LOC58509	AI913329	NY-REN-24 antigen	

203498_at		NM_005822	gb:NM_005822.1 /DEF=Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein /DB_XREF=gi:5032234 /UG=Hs.156007 Down syndrome critical region gene 1-like 1 /FL=gb:D83407.1 gb:NM_005822.1	
220751_s_at		NM_016348	gb:NM_016348.1 /DEF=Homo sapiens chromosome 5 open reading frame 4 (C5ORF4), mRNA. /FEA=mRNA /GEN=C5ORF4 /PROD=putative tumor suppressor /DB_XREF=gi:7705942 /UG=Hs.10235 chromosome 5 open reading frame 4 /FL=gb:AF159165.1 gb:NM_016348.1	

219255_x_at	NM_018725	gb:NM_018725.1 /DEF=Homo sapiens IL-17B receptor (IL17BR), mRNA. /FEA=mRNA /GEN=IL17BR /PROD=IL-17B receptor /DB_XREF=gi:8923816 /UG=Hs.5470 IL-17B receptor /FL=gb:BC000980.1 gb:AF212365.1 gb:NM_018725.1 gb:AF208110.1
221073_s_at	NM_006092	gb:NM_006092.1 /DEF=Homo sapiens caspase recruitment domain 4 (NOD1), mRNA. /FEA=mRNA /GEN=NOD1 /PROD=caspase recruitment domain 4 /DB_XREF=gi:5174616 /UG=Hs.19405 caspase recruitment domain 4 /FL=gb:AF113925.1 gb:NM_006092.1

204116_at	NM_000206	gb:NM_000206.1 /DEF=Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA. /FEA=mRNA /GEN=IL2RG /PROD=interleukin 2 receptor, gamma chain, precursor /DB_XREF=gi:4557881 /UG=Hs.84 interleukin 2 receptor, gamma (severe combined immunodeficiency) /FL=gb:NM_000206.1
218953_s_at	NM_024028	gb:NM_024028.1 /DEF=Homo sapiens hypothetical protein MGC3265 (MGC3265), mRNA. /FEA=mRNA /GEN=MGC3265 /PROD=hypothetical protein MGC3265 /DB_XREF=gi:13128973 /UG=Hs.257111 hypothetical protein MGC3265 /FL=gb:BC000014.1 gb:NM_024028.1

213312_at		NM_020425	Consensus includes gb:NM_020425.1 /DEF=Homo sapiens hypothetical protein DKFZp586E1923 (DKFZP586E1923), mRNA. /FEA=CDS /GEN=DKFZP586E1923 /PROD=hypothetical protein DKFZp586E1923 /DB_XREF=gi:10092684 /UG=Hs.70769 hypothetical protein DKFZp586E1923 /FL=gb:NM_020425.1	
206928_at		NM_003431	gb:NM_003431.1 /DEF=Homo sapiens zinc finger protein 124 (HZF-16) (ZNF124), mRNA. /FEA=mRNA /GEN=ZNF124 /PROD=zinc finger protein 124 (HZF-16) /DB_XREF=gi:4507976 /UG=Hs.180248 zinc finger protein 124 (HZF-16) /FL=gb:NM_003431.1	

220898_at		NM_024972	gb:NM_024972.1 /DEF=Homo sapiens hypothetical protein FLJ11736 (FLJ11736), mRNA. /FEA=mRNA /GEN=FLJ11736 /PROD=hypothetical protein FLJ11736 /DB_XREF=gi:13376469 /UG=Hs.287448 hypothetical protein FLJ11736 /FL=gb:NM_024972.1	
202367_at		NM_001913	gb:NM_001913.1 /DEF=Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1), mRNA. /FEA=mRNA /GEN=CUTL1 /PROD=cut (Drosophila)-like 1 (CCAAT displacementprotein) /DB_XREF=gi:4503168 /UG=Hs.147049 cut (Drosophila)-like 1 (CCAAT displacement protein) /FL=gb:NM_001913.1 gb:L12579.1	



217120_s_at		AK023368	<p>Consensus includes gb:AK023368.1  /DEF=Homo sapiens cDNA  FLJ13306 fis, clone  OVARC1001417, highly similar to  Homo sapiens thyroid hormone  receptor-associated protein complex  component TRAP170 mRNA.  /FEA=mRNA  /DB_XREF=gi:10435273  /UG=Hs.21586 cofactor required for  Sp1 transcriptional activation,  subunit 2 (150kD)</p>	
206044_s_at		NM_004333	<p>gb:NM_004333.1 /DEF=Homo  sapiens v-raf murine sarcoma viral  oncogene homolog B1 (BRAF),  mRNA. /FEA=mRNA /GEN=BRAF  /PROD=v-raf murine sarcoma viral  oncogene homolog B1  /DB_XREF=gi:4757867 /UG=Hs.622  v-raf murine sarcoma viral  oncogene homolog B1  /FL=gb:M95712.1 gb:NM_004333.1</p>	

220453_at		NM_017765	gb:NM_017765.1 /DEF=Homo sapiens hypothetical protein FLJ20320 (FLJ20320), mRNA. /FEA=mRNA /GEN=FLJ20320 /PROD=hypothetical protein FLJ20320 /DB_XREF=gi:8923300 /UG=Hs.263081 hypothetical protein FLJ20320 /FL=gb:NM_017765.1	
201714_at		NM_001070	gb:NM_001070.1 /DEF=Homo sapiens tubulin, gamma 1 (TUBG1), mRNA. /FEA=mRNA /GEN=TUBG1 /PROD=tubulin, gamma 1 /DB_XREF=gi:4507730 /UG=Hs.21635 tubulin, gamma 1 /FL=gb:BC000619.1 gb:M61764.1 gb:NM_001070.1	

218816_at		NM_018214	gb:NM_018214.1 /DEF=Homo sapiens hypothetical protein FLJ10775 (FLJ10775), mRNA. /FEA=mRNA /GEN=FLJ10775 /PROD=hypothetical protein FLJ10775 /DB_XREF=gi:8922660 /UG=Hs.35091 hypothetical protein FLJ10775 /FL=gb:BC003193.1 gb:NM_018214.1	
213839_at		AW028110	ESTs	
203205_at		NM_014663	gb:NM_014663.1 /DEF=Homo sapiens KIAA0677 gene product (KIAA0677), mRNA. /FEA=mRNA /GEN=KIAA0677 /PROD=KIAA0677 gene product /DB_XREF=gi:7662245 /UG=Hs.155983 KIAA0677 gene product /FL=gb:BC002558.1 gb:AB014577.1 gb:NM_014663.1	

210330_at		U58331	gb:U58331.1 /DEF=Human placental delta sarcoglycan mRNA, complete cds. /FEA=mRNA /PROD=delta sarcoglycan /DB_XREF=gi:1695856 /UG=Hs.151899 sarcoglycan, delta (35kD dystrophin-associated glycoprotein) /FL=gb:U58331.1	
215506_s_at		AK021882	Consensus includes gb:AK021882.1 /DEF=Homo sapiens cDNA FLJ11820 fis, clone HEMBA1006445, highly similar to Homo sapiens putative tumor supressor NOEY2 mRNA. /FEA=mRNA /DB_XREF=gi:10433168 /UG=Hs.194695 ras homolog gene family, member I	

202409_at		X07868	Consensus includes gb:X07868 /DEF=Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF /FEA=mRNA_1 /DB_XREF=gi:32998 /UG=Hs.251664 insulin-like growth factor 2 (somatomedin A) /FL=gb:BC000531.1 gb:J03242.1 gb:M17426.1 gb:NM_000612.2	
216347_s_at		AK023188	Consensus includes gb:AK023188.1 /DEF=Homo sapiens cDNA FLJ13126 fis, clone NT2RP3002909, weakly similar to P53-BINDING PROTEIN 2. /FEA=mRNA /DB_XREF=gi:10435002 /UG=Hs.6162 KIAA0771 protein	

205527_s_at		NM_015487	gb:NM_015487.1 /DEF=Homo sapiens DKFZP434D174 protein (DKFZP434D174), mRNA. /FEA=mRNA /GEN=DKFZP434D174 /PROD=DKFZP434D174 protein /DB_XREF=gi:11094402 /UG=Hs.302421 DKFZP434D174 protein /FL=gb:NM_015487.1	
221430_s_at		NM_030963	gb:NM_030963.1 /DEF=Homo sapiens hypothetical protein DKFZp434O1427 (DKFZP434O1427), mRNA. /FEA=CDS /GEN=DKFZP434O1427 /PROD=hypothetical protein DKFZp434O1427 /DB_XREF=gi:13624336 /FL=gb:NM_030963.1	

204724_s_at		NM_001853	gb:NM_001853.1 /DEF=Homo sapiens collagen, type IX, alpha 3 (COL9A3), mRNA. /FEA=mRNA /GEN=COL9A3 /PROD=collagen, type IX, alpha 3 /DB_XREF=gi:4502966 /UG=Hs.53563 collagen, type IX, alpha 3 /FL=gb:L41162.1 gb:NM_001853.1	
204602_at		NM_012242	gb:NM_012242.1 /DEF=Homo sapiens dickkopf (Xenopus laevis) homolog 1 (DKK1), mRNA. /FEA=mRNA /GEN=DKK1 /PROD=dickkopf (Xenopus laevis) homolog 1 /DB_XREF=gi:7110718 /UG=Hs.40499 dickkopf (Xenopus laevis) homolog 1 /FL=gb:AF127563.1 gb:AF177394.1 gb:NM_012242.1	

204010_s_at		NM_004985	gb:NM_004985.1 /DEF=Homo sapiens v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog (KRAS2), mRNA. /FEA=mRNA /GEN=KRAS2 /PROD=v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogenehomolog /DB_XREF=gi:4826811 /UG=Hs.184050 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog /FL=gb:M54968.1 gb:NM_004985.1	
206279_at		NM_002760	gb:NM_002760.1 /DEF=Homo sapiens protein kinase, Y-linked (PRKY), mRNA. /FEA=mRNA /GEN=PRKY /PROD=protein kinase, Y-linked /DB_XREF=gi:10835064 /UG=Hs.56336 protein kinase, Y-linked /FL=gb:NM_002760.1	



219983_at		NM_020386	gb:NM_020386.1 /DEF=Homo sapiens H-REV107 protein-related protein (LOC57110), mRNA. /FEA=mRNA /GEN=LOC57110 /PROD=H-REV107 protein-related protein /DB_XREF=gi:9966858 /UG=Hs.36761 H-REV107 protein-related protein /FL=gb:AB030816.1 gb:NM_020386.1	
219954_s_at		NM_020973	gb:NM_020973.1 /DEF=Homo sapiens cytosolic beta-glucosidase (GLUC), mRNA. /FEA=mRNA /GEN=GLUC /PROD=cytosolic beta-glucosidase /DB_XREF=gi:13273312 /UG=Hs.146182 cytosolic beta-glucosidase /FL=gb:AB017913.1 gb:AF317840.1 gb:NM_020973.1	

219460_s_at		NM_017849	gb:NM_017849.1 /DEF=Homo sapiens hypothetical protein FLJ20507 (FLJ20507), mRNA. /FEA=mRNA /GEN=FLJ20507 /PROD=hypothetical protein FLJ20507 /DB_XREF=gi:8923465 /UG=Hs.202955 hypothetical protein FLJ20507 /FL=gb:NM_017849.1	
205394_at		NM_001274	gb:NM_001274.1 /DEF=Homo sapiens CHK1 (checkpoint, S.pombe) homolog (CHEK1), mRNA. /FEA=mRNA /GEN=CHK1 /PROD=CHK1 (checkpoint, S.pombe) homolog /DB_XREF=gi:4502802 /UG=Hs.20295 CHK1 (checkpoint, S.pombe) homolog /FL=gb:AF016582.1 gb:NM_001274.1	
214140_at	SLC25A16	AI827990	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	

209008_x_at	U76549	gb:U76549.1 /DEF=Human cytokeratin 8 mRNA, complete cds. /FEA=mRNA /PROD=cytokeratin 8 /DB_XREF=gi:1673574 /UG=Hs.242463 keratin 8 /FL=gb:BC000654.1 gb:U76549.1 gb:M34225.1 gb:M26324.1 gb:NM_002273.1
212948_at	AB020716	Consensus includes gb:AB020716.1 /DEF=Homo sapiens mRNA for KIAA0909 protein, partial cds. /FEA=mRNA /GEN=KIAA0909 /PROD=KIAA0909 protein /DB_XREF=gi:4240306 /UG=Hs.107362 KIAA0909 protein

210910_s_at		BC000487	gb:BC000487.1 /DEF=Homo sapiens, Similar to POM (POM121 rat homolog) and ZP3 fusion protein, clone MGC:8359, mRNA, complete cds. /FEA=mRNA /PROD=Similar to POM (POM121 rat homolog) and ZP3fusion protein /DB_XREF=gi:12653432 /UG=Hs.296380 POM (POM121 rat homolog) and ZP3 fusion protein /FL=gb:BC000487.1	
210715_s_at	/	AF027205	gb:AF027205.1 /DEF=Homo sapiens Kunitz-type protease inhibitor (kop) mRNA, complete cds. /FEA=mRNA /GEN=kop /PROD=Kunitz-type protease inhibitor /DB_XREF=gi:2598967 /UG=Hs.31439 serine protease inhibitor, Kunitz type, 2 /FL=gb:AF027205.1	

209006_s_at		AF247168	gb:AF247168.1 /DEF=Homo sapiens NPD014 (NPD014) mRNA, complete cds. /FEA=mRNA /GEN=NPD014 /PROD=NPD014 /DB_XREF=gi:12005626 /UG=Hs.8084 hypothetical protein dJ465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1	
219292_at		NM_018105	gb:NM_018105.1 /DEF=Homo sapiens hypothetical protein FLJ10477 (FLJ10477), mRNA. /FEA=mRNA /GEN=FLJ10477 /PROD=hypothetical protein FLJ10477 /DB_XREF=gi:8922445 /UG=Hs.7432 hypothetical protein FLJ10477 /FL=gb:NM_018105.1	

212232_at		AB023231	Consensus includes gb:AB023231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589677 /UG=Hs.6834 KIAA1014 protein	
208718_at		Z97056	Consensus includes gb:Z97056 /DEF=Human DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDEL (Lys-Asp-Glu-Leu) endoplasmic reticu... /FEA=mRNA_5 /DB_XREF=gi:2832593 /UG=Hs.6179 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 17 (72kD) /FL=gb:BC000595.1 gb:NM_006386.2 gb:U59321.1	

212145_at		D87453	Consensus includes gb:D87453.1 /DEF=Human mRNA for KIAA0264 gene, partial cds. /FEA=mRNA /GEN=KIAA0264 /DB_XREF=gi:1665794 /UG=Hs.122669 KIAA0264 protein	
208752_x_at	NAP1L1	AI888672	nucleosome assembly protein 1-like 1	
212077_at		AL583520	Homo sapiens OK/SW-cl.14 mRNA, complete cds	
212919_at	KIAA1096	AV715578	KIAA1096 protein	
211406_at		AF119875	gb:AF119875.1 /DEF=Homo sapiens PRO2309 mRNA, complete cds. /FEA=mRNA /PROD=PRO2309 /DB_XREF=gi:7770186 /UG=Hs.283037 HSPC039 protein /FL=gb:AF119875.1	

208787_at		BC003375	gb:BC003375.1 /DEF=Homo sapiens, mitochondrial ribosomal protein L3, clone MGC:5219, mRNA, complete cds. /FEA=mRNA /PROD=mitochondrial ribosomal protein L3 /DB_XREF=gi:13097224 /UG=Hs.79086 mitochondrial ribosomal protein L3 /FL=gb:BC003375.1 gb:NM_007208.1	
218362_s_at		NM_014953	gb:NM_014953.1 /DEF=Homo sapiens KIAA1008 protein (KIAA1008), mRNA. /FEA=mRNA /GEN=KIAA1008 /PROD=KIAA1008 protein /DB_XREF=gi:7662443 /UG=Hs.323346 KIAA1008 protein /FL=gb:AB023225.1 gb:NM_014953.1	



219377_at		NM_022751	gb:NM_022751.1 /DEF=Homo sapiens hypothetical protein FLJ21610 (FLJ21610), mRNA. /FEA=mRNA /GEN=FLJ21610 /PROD=hypothetical protein FLJ21610 /DB_XREF=gi:12232414 /UG=Hs.12727 hypothetical protein FLJ21610 /FL=gb:NM_022751.1	
208093_s_at		NM_030808	gb:NM_030808.1 /DEF=Homo sapiens LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA. /FEA=mRNA /GEN=NUDEL /PROD=LIS1-interacting protein NUDEL;endooligopeptidase A /DB_XREF=gi:13540599 /FL=gb:NM_030808.1	
212491_s_at	DNAJC8	AA843895	DnaJ (Hsp40) homolog, subfamily C, member 8	

213005_s_at		D79994	Consensus includes gb:D79994.1 /DEF=Human mRNA for KIAA0172 gene, partial cds. /FEA=mRNA /GEN=KIAA0172 /DB_XREF=gi:1136403 /UG=Hs.77546 KIAA0172 protein	
209632_at		L07590	Consensus includes gb:A1760130 /FEA=EST /DB_XREF=gi:5175797 /DB_XREF=est:wg58b07.x1 /CLONE=IMAGE:2369269 /UG=Hs.28219 protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 72), alpha isoform and (PR 130), beta isoform /FL=gb:L07590.1	

218356_at		NM_013393	gb:NM_013393.1 /DEF=Homo sapiens cell division protein FtsJ (FJH1), mRNA. /FEA=mRNA /GEN=FJH1 /PROD=cell division protein FtsJ /DB_XREF=gi:7019376 /UG=Hs.279877 cell division protein FtsJ /FL=gb:AF093415.1 gb:NM_013393.1	
212560_at	COX6B	AV728268	cytochrome c oxidase subunit VIb	
212628_at		AK023692	Consensus includes gb:BG292065 /FEA=EST /DB_XREF=gi:13050507 /DB_XREF=est:602386350F1 /CLONE=IMAGE:4515036 /UG=Hs.69171 protein kinase C-like 2	
209404_s_at		AF151867	gb:AF151867.1 /DEF=Homo sapiens CGI-109 protein mRNA, complete cds. /FEA=mRNA /PROD=CGI-109 protein /DB_XREF=gi:4929686 /UG=Hs.278391 CGI-109 protein /FL=gb:AF151867.1	

209444_at		BC001851	gb:BC001851.1 /DEF=Homo sapiens, Similar to RAP1, GTP-GDP dissociation stimulator 1, clone MGC:4525, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RAP1, GTP-GDP dissociation stimulator1 /DB_XREF=gi:12804812 /UG=Hs.7940 RAP1, GTP-GDP dissociation stimulator 1 /FL=gb:NM_021159.1 gb:BC001851.1 gb:BC001816.1 gb:AF215923.1 gb:AF237413.1	
209534_x_at	AKAP13	BF222823	A kinase (PRKA) anchor protein 13	

212499_s_at		AK025580	Consensus includes gb:AK025580.1 /DEF=Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence. /FEA=mRNA /DB_XREF=gi:10438139 /UG=Hs.81360 Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence	
209392_at		L35594	gb:L35594.1 /DEF=Human autotaxin mRNA, complete cds. /FEA=mRNA /PROD=autotaxin /DB_XREF=gi:537905 /UG=Hs.174185 ectonucleotide pyrophosphatasephosphodiesterase 2 (autotaxin) /FL=gb:L35594.1	

218379_at		NM_016090	gb:NM_016090.1 /DEF=Homo sapiens RNA binding motif protein 7 (RBM7), mRNA. /FEA=mRNA /GEN=RBM7 /PROD=RNA binding motif protein 7 /DB_XREF=gi:9994184 /UG=Hs.5887 RNA binding motif protein 7 /FL=gb:AF156098.1 gb:NM_016090.1	
218478_s_at		NM_017612	gb:NM_017612.1 /DEF=Homo sapiens hypothetical protein DKFZp434E2220 (DKFZp434E2220), mRNA. /FEA=mRNA /GEN=DKFZp434E2220 /PROD=hypothetical protein DKFZp434E2220 /DB_XREF=gi:8922133 /UG=Hs.37706 hypothetical protein DKFZp434E2220 /FL=gb:NM_017612.1	

218757_s_at		NM_023010	gb:NM_023010.1 /DEF=Homo sapiens similar to yeast Upf3, variant B (UPF3B), mRNA. /FEA=mRNA /GEN=UPF3B /PROD=similar to yeast Upf3, variant B /DB_XREF=gi:12711673 /UG=Hs.103832 similar to yeast Upf3, variant B /FL=gb:AY013251.1 gb:NM_023010.1	
210367_s_at		AF010316	gb:AF010316.1 /DEF=Homo sapiens Pig12 (PIG12) mRNA, complete cds. /FEA=mRNA /GEN=PIG12 /PROD=Pig12 /DB_XREF=gi:2415307 /UG=Hs.146688 prostaglandin E synthase /FL=gb:AF010316.1	

209814_at		BC004421	gb:BC004421.1 /DEF=Homo sapiens, nucleolar cysteine-rich protein, clone MGC:1452, mRNA, complete cds. /FEA=mRNA /PROD=nucleolar cysteine-rich protein /DB_XREF=gi:13325205 /UG=Hs.120766 nucleolar cysteine-rich protein /FL=gb:BC004421.1 gb:NM_014487.2	
218461_at		NM_016301	gb:NM_016301.1 /DEF=Homo sapiens protein x 0004 (LOC51184), mRNA. /FEA=mRNA /GEN=LOC51184 /PROD=protein x 0004 /DB_XREF=gi:9994188 /UG=Hs.284164 protein x 0004 /FL=gb:AF117229.1 gb:NM_016301.1	
212643_at	MISS	AI671747	likely ortholog of mouse MAPK-interacting and spindle-stabilizing protein	



219449_s_at		NM_017866	gb:NM_017866.1 /DEF=Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA. /FEA=mRNA /GEN=FLJ20533 /PROD=hypothetical protein FLJ20533 /DB_XREF=gi:8923499 /UG=Hs.106650 hypothetical protein FLJ20533 /FL=gb:BC002748.1 gb:NM_017866.1	
212757_s_at	CAMK2G	BF111268	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	
219092_s_at		NM_022755	gb:NM_022755.1 /DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. /FEA=mRNA /GEN=FLJ13163 /PROD=hypothetical protein FLJ13163 /DB_XREF=gi:12232422 /UG=Hs.16603 hypothetical protein FLJ13163 /FL=gb:NM_022755.1	

209894_at		U50748	gb:U50748.1 /DEF=Homo sapiens leptin receptor short form (db) mRNA, complete cds. /FEA=mRNA /GEN=db /PROD=leptin receptor /DB_XREF=gi:3236285 /UG=Hs.226627 leptin receptor /FL=gb:U50748.1	
210034_s_at	RPL5	AA582460	ribosomal protein L5	
201920_at		NM_005415	gb:NM_005415.2 /DEF=Homo sapiens solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA. /FEA=mRNA /GEN=SLC20A1 /PROD=solute carrier family 20 (phosphatetransporter), member 1 /DB_XREF=gi:7382462 /UG=Hs.78452 solute carrier family 20 (phosphate transporter), member 1 /FL=gb:L20859.1 gb:NM_005415.2	

			gb:NM_014914.1 /DEF=Homo sapiens KIAA1099 protein (KIAA1099), mRNA. /FEA=mRNA /GEN=KIAA1099 /PROD=KIAA1099 protein /DB_XREF=gi:7662483 /UG=Hs.159377 KIAA1099 protein /FL=gb:AB029022.1	
204066_s_at		NM_014914	gb:NM_014914.1	
222357_at		AW974823	ESTs	
201770_at		NM_004596	gb:NM_004596.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA. /FEA=mRNA /GEN=SNRPA /PROD=small nuclear ribonucleoprotein polypeptide A /DB_XREF=gi:4759155 /UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A /FL=gb:BC000405.1	
			gb:NM_004596.1	
215718_s_at	PHF3	AI949220	PHD finger protein 3	
213876_x_at	U2AF1RS2	AW089584	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2	

215452_x_at		AL031133	Consensus includes gb:AL031133 /DEF=Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains... /FEA=mRNA_2 /DB_XREF=gi:3676189 /UG=Hs.113293 Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, S	
203833_s_at	TGOLN2	BF061845	trans-golgi network protein 2	

203851_at		NM_002178	gb:NM_002178.1 /DEF=Homo sapiens insulin-like growth factor binding protein 6 (IGFBP6), mRNA. /FEA=mRNA /GEN=IGFBP6 /PROD=insulin-like growth factor binding protein 6 /DB_XREF=gi:11321592 /UG=Hs.274313 insulin-like growth factor binding protein 6 /FL=gb:NM_002178.1 gb:BC003507.1 gb:BC005007.1 gb:M62402.1	
201933_at		NM_002768	gb:NM_002768.1 /DEF=Homo sapiens procollagen (type III) N-endopeptidase (PCOLN3), mRNA. /FEA=mRNA /GEN=PCOLN3 /PROD=procollagen (type III) N-endopeptidase /DB_XREF=gi:4506138 /UG=Hs.183138 procollagen (type III) N-endopeptidase /FL=gb:U58048.1 gb:NM_002768.1 gb:AF281063.1	

201976_s_at		NM_012334	gb:NM_012334.1 /DEF=Homo sapiens myosin X (MYO10), mRNA. /FEA=mRNA /GEN=MYO10 /PROD=myosin X /DB_XREF=gi:11037056 /UG=Hs.61638 myosin X /FL=gb:NM_012334.1 gb:AF234532.1 gb:AF247457.2	
217994_x_at		NM_017871	gb:NM_017871.1 /DEF=Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA. /FEA=mRNA /GEN=FLJ20542 /PROD=hypothetical protein FLJ20542 /DB_XREF=gi:8923511 /UG=Hs.6449 hypothetical protein FLJ20542 /FL=gb:AL136813.1 gb:NM_017871.1	

218231_at		NM_017567	gb:NM_017567.1 /DEF=Homo sapiens N-Acetylglucosamine kinase (HSA242910), mRNA. /FEA=mRNA /GEN=HSA242910 /PROD=N-Acetylglucosamine kinase /DB_XREF=gi:8923736 /UG=Hs.7036 N-Acetylglucosamine kinase /FL=gb:BC001029.1 gb:BC005371.1 gb:NM_017567.1	
201711_x_at	RANBP2	AI681120	RAN binding protein 2	
32811_at	MYO1C	X98507	myosin IC	NM_033375
204256_at		NM_024090	gb:NM_024090.1 /DEF=Homo sapiens hypothetical protein MGC5487 (MGC5487), mRNA. /FEA=mRNA /GEN=MGC5487 /PROD=hypothetical protein MGC5487 /DB_XREF=gi:13129087 /UG=Hs.211556 hypothetical protein MGC5487 /FL=gb:NM_024090.1	
204571_x_at	PIN4	BE797213	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	

204211_x_at		NM_002759	gb:NM_002759.1 /DEF=Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /FEA=mRNA /GEN=PRKR /PROD=protein kinase, interferon-inducible doublestranded RNA dependent /DB_XREF=gi:4506102 /UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent /FL=gb:M35663.1 gb:M85294.1 gb:NM_002759.1	
214359_s_at	HSPCB	AI218219	heat shock 90kDa protein 1, beta	
214224_s_at	PIN4	BE674061	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	



203082_at		NM_014753	gb:NM_014753.1 /DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 /PROD=KIAA0187 gene product /DB_XREF=gi:7661979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 gb:NM_014753.1	
214172_x_at	RYK	BG032035	RYK receptor-like tyrosine kinase	
221599_at		BC002752	gb:BC002752.1 /DEF=Homo sapiens, Similar to PTD015 protein, clone MGC:3367, mRNA, complete cds. /FEA=mRNA /PROD=Similar to PTD015 protein /DB_XREF=gi:12803822 /UG=Hs.95870 PTD015 protein /FL=gb:BC002752.1	
203493_s_at	KIAA0092	AI123527	KIAA0092 gene product	

203721_s_at		NM_016001	gb:NM_016001.1 /DEF=Homo sapiens CGI-48 protein (LOC51096), mRNA. /FEA=mRNA /GEN=LOC51096 /PROD=CGI-48 protein /DB_XREF=gi:7705764 /UG=Hs.6153 CGI-48 protein /FL=gb:AF151806.1 gb:NM_016001.1	
215143_at		AL049437	Consensus includes gb:AL049437.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKFZp586E1120). /FEA=mRNA /DB_XREF=gi:4500220 /UG=Hs.100292 Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKFZp586E1120)	

202272_s_at		NM_015176	gb:NM_015176.1 /DEF=Homo sapiens KIAA0483 protein (KIAA0483), mRNA. /FEA=mRNA /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:7662157 /UG=Hs.64691 KIAA0483 protein /FL=gb:NM_015176.1	
203788_s_at	SEMA3C	AI962897	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	
221185_s_at		NM_025111	gb:NM_025111.1 /DEF=Homo sapiens hypothetical protein FLJ23571 (FLJ23571), mRNA. /FEA=mRNA /GEN=FLJ23571 /PROD=hypothetical protein FLJ23571 /DB_XREF=gi:13376682 /UG=Hs.288693 hypothetical protein FLJ23571 /FL=gb:NM_025111.1	
214801_at		W88821	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	

217792_at		NM_014426	gb:NM_014426.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mRNA /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657598 /UG=Hs.13794 sorting nexin 5 /FL=gb:BC000100.1 gb:AF121855.1 gb:NM_014426.1	
201025_at		NM_015904	Consensus includes gb:AB018284.1 /DEF=Homo sapiens mRNA for KIAA0741 protein, complete cds. /FEA=mRNA /GEN=KIAA0741 /PROD=KIAA0741 protein /DB_XREF=gi:3882202 /UG=Hs.158688 KIAA0741 gene product /FL=gb:AB018284.1 gb:AF078035.1 gb:NM_015904.1	
217717_s_at	GW128	BF246499	GW128 protein	

207135_at		NM_000621	gb:NM_000621.1 /DEF=Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /FEA=mRNA /GEN=HTR2A /PROD=5-hydroxytryptamine (serotonin) receptor 2A /DB_XREF=gi:10835174 /UG=Hs.298623 5-hydroxytryptamine (serotonin) receptor 2A /FL=gb:NM_000621.1	
217645_at		AW088547	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	
206818_s_at		NM_017649	gb:NM_017649.1 /DEF=Homo sapiens hypothetical protein FLJ20064 (FLJ20064), mRNA. /FEA=mRNA /GEN=FLJ20064 /PROD=hypothetical protein FLJ20064 /DB_XREF=gi:8923070 /UG=Hs.271221 hypothetical protein FLJ20064 /FL=gb:NM_017649.1	
61732_r_at	CMG1	AI610355	capillary morphogenesis protein 1	

205839_s_at		NM_004758	gb:NM_004758.1 /DEF=Homo sapiens peripheral benzodiazepine receptor-associated protein 1 (PRAX-1), mRNA. /FEA=mRNA /GEN=PRAX-1 /PROD=peripheral benzodiazepine receptor-associatedprotein 1 /DB_XREF=gi:4758955 /UG=Hs.112499 peripheral benzodiazepine receptor-associated protein 1 /FL=gb:AF039571.1 gb:NM_004758.1	
213164_at		AI867198	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]	

200803_s_at	AF033095	gb:AF033095.1 /DEF=Homo sapiens testis enhanced gene transcript protein (TEGT) mRNA, complete cds. /FEA=mRNA /GEN=TEGT /PROD=testis enhanced gene transcript protein /DB_XREF=gi:2645728 /UG=Hs.74637 testis enhanced gene transcript (BAX inhibitor 1) /FL=gb:BC000916.1 gb:AF033095.1 gb:NM_003217.1
217790_s_at	NM_007107	gb:NM_007107.1 /DEF=Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA. /FEA=mRNA /GEN=SSR3 /PROD=signal sequence receptor, gamma(translocon-associated protein gamma) /DB_XREF=gi:6005883 /UG=Hs.28707 signal sequence receptor, gamma (translocon-associated protein gamma) /FL=gb:AF110647.1 gb:NM_007107.1

213503_x_at	ANXA2	BE908217	annexin A2	
37549_g_at	B1	U87408	PTH-responsive osteosarcoma B1 protein	NM_014451
217042_at		AL096716	Consensus includes gb:AL096716.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564M1462 (from clone DKFZp564M1462); partial cds. /FEA=mRNA /GEN=DKFZp564M1462 /PROD=hypothetical protein /DB_XREF=gi:5419850 /UG=Hs.226007 DKFZP564M1462 protein	
201348_at		NM_002084	gb:NM_002084.2 /DEF=Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA. /FEA=mRNA /GEN=GPX3 /PROD=plasma glutathione peroxidase 3 precursor /DB_XREF=gi:6006000 /UG=Hs.172153 glutathione peroxidase 3 (plasma) /FL=gb:D00632.1 gb:NM_002084.2 gb:AF217787.1	



204675_at		NM_001047	gb:NM_001047.1 /DEF=Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA. /FEA=mRNA /GEN=SRD5A1 /PROD=steroid-5-alpha-reductase, alpha polypeptide 1(3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) /DB_XREF=gi:4507200 /UG=Hs.552 steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) /FL=gb:M32313.1 gb:AF052126.1 gb:NM_001047.1	
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207724_s_at		NM_014946	gb:NM_014946.2 /DEF=Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA. /FEA=mRNA /GEN=SPG4 /PROD=spastin /DB_XREF=gi:11875210 /UG=Hs.26334 spastic paraplegia 4 (autosomal dominant; spastin) /FL=gb:NM_014946.2	
201618_x_at		NM_003801	gb:NM_003801.2 /DEF=Homo sapiens anchor attachment protein 1 (Gaa1p, yeast) homolog (GPAA1), mRNA. /FEA=mRNA /GEN=GPAA1 /PROD=anchor attachment protein 1 /DB_XREF=gi:6031166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2	
204771_s_at	TTF1	AI632304	transcription termination factor, RNA polymerase I	

201601_x_at		NM_003641	gb:NM_003641.1 /DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA. /FEA=mRNA /GEN=IFITM1 /PROD=interferon induced transmembrane protein 1(9-27) /DB_XREF=gi:4504580 /UG=Hs.146360 interferon induced transmembrane protein 1 (9-27) /FL=gb:BC000897.1 gb:J04164.1 gb:NM_003641.1	
216870_x_at		AF264787	Consensus includes gb:AF264787.1 /DEF=Homo sapiens BCMS-upstream neighbor (BCMSUN) mRNA, partial sequence. /FEA=mRNA /DB_XREF=gi:11141510 /UG=Hs.43628 deleted in lymphocytic leukemia, 2	

217918_at		NM_014183	gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB_XREF=gi:7661821 /UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1 gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1 gb:AF165516.1	
201189_s_at		NM_002224	gb:NM_002224.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA. /FEA=mRNA /GEN=ITPR3 /PROD=inositol 1,4,5-triphosphate receptor, type 3 /DB_XREF=gi:4504794 /UG=Hs.77515 inositol 1,4,5-triphosphate receptor, type 3 /FL=gb:D26351.1 gb:NM_002224.1 gb:U01062.1	

205236_x_at		NM_003102	gb:NM_003102.1 /DEF=Homo sapiens superoxide dismutase 3, extracellular (SOD3), mRNA. /FEA=mRNA /GEN=SOD3 /PROD=superoxide dismutase 3, extracellular /DB_XREF=gi:4507150 /UG=Hs.2420 superoxide dismutase 3, extracellular /FL=gb:J02947.1 gb:NM_003102.1	
201162_at		NM_001553	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:L19182.1 gb:NM_001553.1	

200618_at		NM_006148	gb:NM_006148.1 /DEF=Homo sapiens LIM and SH3 protein 1 (LASP1), mRNA. /FEA=mRNA /GEN=LASP1 /PROD=LIM and SH3 protein 1 /DB_XREF=gi:5453709 /UG=Hs.75080 LIM and SH3 protein 1 /FL=gb:NM_006148.1	
205070_at		NM_019071	gb:NM_019071.1 /DEF=Homo sapiens inhibitor of growth family, member 3 (ING3), mRNA. /FEA=mRNA /GEN=ING3 /PROD=inhibitor of growth family, member 3 /DB_XREF=gi:9506658 /UG=Hs.143198 inhibitor of growth family, member 3 /FL=gb:AF074968.1 gb:AY007790.1 gb:NM_019071.1	

200654_at		J02783	gb:J02783.1 /DEF=Human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mRNA /GEN=P4HB /DB_XREF=gi:339646 /UG=Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM_000918.1	
217832_at		NM_006372	Consensus includes gb:BE672181 /FEA=EST /DB_XREF=gi:10032712 /DB_XREF=est:7b51c08.x1 /CLONE=IMAGE:3231758 /UG=Hs.155489 NS1-associated protein 1 /FL=gb:AF155568.1 gb:NM_006372.1	
214305_s_at	SF3B1	AW003030	splicing factor 3b, subunit 1, 155kDa	

200617_at		NM_014730	gb:NM_014730.1 /DEF=Homo sapiens KIAA0152 gene product (KIAA0152), mRNA. /FEA=mRNA /GEN=KIAA0152 /PROD=KIAA0152 gene product /DB_XREF=gi:7661947 /UG=Hs.181418 KIAA0152 gene product /FL=gb:BC000371.1 gb:D63486.1 gb:NM_014730.1	
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212268_at		NM_030666	Consensus includes gb:NM_030666.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 (SERPINB1), mRNA. /FEA=CDS /GEN=SERPINB1 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 1 /DB_XREF=gi:13489086 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 /FL=gb:NM_030666.1	
211779_x_at		BC006155	gb:BC006155.1 /DEF=Homo sapiens, clone MGC:13188, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13188) /DB_XREF=gi:13544040 /FL=gb:BC006155.1	

212264_s_at		D87450	Consensus includes gb:BE645850 /FEA=EST /DB_XREF=gi:9970161 /DB_XREF=est:7e77c03.x1 /CLONE=IMAGE:3288484 /UG=Hs.154978 KIAA0261 protein	
209869_at		AF284095	gb:AF284095.1 /DEF=Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds. /FEA=mRNA /PROD=alpha-2A adrenergic receptor /DB_XREF=gi:13447750 /UG=Hs.249159 adrenergic, alpha- 2A-, receptor /FL=gb:AF284095.1 gb:NM_000681.1	
211929_at		BE867771	Homo sapiens BX1 mRNA, partial cds	

201628_s_at		NM_006570	gb:NM_006570.1 /DEF=Homo sapiens Ras-related GTP-binding protein (RAGA), mRNA. /FEA=mRNA /GEN=RAGA /PROD=Ras-related GTP-binding protein /DB_XREF=gi:5729998 /UG=Hs.57304 Ras-related GTP-binding protein /FL=gb:U41654.1 gb:NM_006570.1	
212288_at		AB011126	Consensus includes gb:AB011126.1 /DEF=Homo sapiens mRNA for KIAA0554 protein, partial cds. /FEA=mRNA /GEN=KIAA0554 /PROD=KIAA0554 protein /DB_XREF=gi:3043631 /UG=Hs.301763 KIAA0554 protein	

201196_s_at		M21154	gb:M21154.1 /DEF=Human S-adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:178517 /UG=Hs.262476 S-adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1 gb:NM_001634.3	
209539_at		D25304	Consensus includes gb:D25304.1 /DEF=Human mRNA for KIAA0006 gene, partial cds. /FEA=mRNA /GEN=KIAA0006 /DB_XREF=gi:435445 /UG=Hs.79307 RacCdc42 guanine exchange factor (GEF) 6 /FL=gb:D13631.1	

214902_x_at		AL080232	Consensus includes gb:AL080232.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061). /FEA=mRNA /DB_XREF=gi:5262725 /UG=Hs.220696 Homo sapiens mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061)	
202560_s_at		NM_015607	gb:NM_015607.1 /DEF=Homo sapiens DKFZP547E1010 protein (DKFZP547E1010), mRNA. /FEA=mRNA /GEN=DKFZP547E1010 /PROD=DKFZP547E1010 protein /DB_XREF=gi:7661589 /UG=Hs.323817 DKFZP547E1010 protein /FL=gb:NM_015607.1	
201018_at	EIF1A	BE542684	eukaryotic translation initiation factor 1A	

203991_s_at		NM_021140	gb:NM_021140.1 /DEF=Homo sapiens ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (UTX), mRNA. /FEA=mRNA /GEN=UTX /PROD=ubiquitously transcribed tetratricopeptiderepeat gene, X chromosome /DB_XREF=gi:10863942 /UG=Hs.13980 ubiquitously transcribed tetratricopeptide repeat gene, X chromosome /FL=gb:NM_021140.1 gb:AF000992.1 gb:AF000993.1	
205191_at		NM_006915	gb:NM_006915.1 /DEF=Homo sapiens retinitis pigmentosa 2 (X-linked recessive) (RP2), mRNA. /FEA=mRNA /GEN=RP2 /PROD=XRP2 protein /DB_XREF=gi:5902059 /UG=Hs.44766 retinitis pigmentosa 2 (X-linked recessive) /FL=gb:NM_006915.1	

221498_at		BF939727	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	
208706_s_at		AL080102	Consensus includes gb:AK026933.1 /DEF=Homo sapiens cDNA: FLJ23280 fis, clone HEP07194. /FEA=mRNA /DB_XREF=gi:10439907 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1	
220173_at		NM_025057	gb:NM_025057.1 /DEF=Homo sapiens hypothetical protein FLJ23189 (FLJ23189), mRNA. /FEA=mRNA /GEN=FLJ23189 /PROD=hypothetical protein FLJ23189 /DB_XREF=gi:13376590 /UG=Hs.287733 hypothetical protein FLJ23189 /FL=gb:NM_025057.1	
208677_s_at	BSG	AL550657	basigin (OK blood group)	

220044_x_at	NM_016424	gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mRNA. /FEA=mRNA /GEN=LUC7A /PROD=cisplatin resistance-associated overexpressedprotein /DB_XREF=gi:7706534 /UG=Hs.3688 cisplatin resistance-associated overexpressed protein /FL=gb:NM_016424.1
203694_s_at	NM_003587	gb:NM_003587.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 (DDX16), mRNA. /FEA=mRNA /GEN=DDX16 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 /DB_XREF=gi:13787201 /UG=Hs.12797 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 /FL=gb:NM_003587.2 gb:AB011149.1 gb:AB001601.1



203315_at		BC000103	gb:BC000103.1 /DEF=Homo sapiens, NCK adaptor protein 2, clone MGC:1698, mRNA, complete cds. /FEA=mRNA /PROD=NCK adaptor protein 2 /DB_XREF=gi:12652708 /UG=Hs.101695 NCK adaptor protein 2 /FL=gb:BC000103.1 gb:AF043119.1 gb:AF047487.1 gb:NM_003581.1	
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204151_x_at		NM_001353	gb:NM_001353.2 /DEF=Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) (AKR1C1), mRNA. /FEA=mRNA /GEN=AKR1C1 /PROD=aldo-keto reductase family 1, member C1(dihydrodiol dehydrogenase 1; 20-alpha(3-alpha)-hydroxysteroid dehydrogenase) /DB_XREF=gi:5453542 /UG=Hs.306098 aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) /FL=gb:U05684.1 gb:NM_001353.2 gb:M86609.1	
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202065_s_at		NM_003626	Consensus includes gb:BG033593 /FEA=EST /DB_XREF=gi:12426042 /DB_XREF=est:602301717F1 /CLONE=IMAGE:4403212 /UG=Hs.183648 protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 /FL=gb:NM_003626.1 gb:U22816.1	
208250_s_at		NM_004406	gb:NM_004406.1 /DEF=Homo sapiens deleted in malignant brain tumors 1 (DMBT1), transcript variant 1, mRNA. /FEA=mRNA /GEN=DMBT1 /PROD=deleted in malignant brain tumors 1 isoform aprecursor /DB_XREF=gi:4758169 /UG=Hs.279611 deleted in malignant brain tumors 1 /FL=gb:NM_004406.1	

212956_at		AB020689	Consensus includes gb:AI348094 /FEA=EST /DB_XREF=gi:4085300 /DB_XREF=est:qp61g12.x1 /CLONE=IMAGE:1927558 /UG=Hs.90419 KIAA0882 protein	
39313_at	PRKWINK1	AB002342	protein kinase, lysine deficient 1	NM_018979
209943_at		AF176699	gb:AF176699.1 /DEF=Homo sapiens F-box protein FBL4 mRNA, complete cds. /FEA=mRNA /PROD=F-box protein FBL4 /DB_XREF=gi:6103636 /UG=Hs.49526 f-box and leucine- rich repeat protein 4 /FL=gb:AF176699.1 gb:AF199355.1 gb:NM_012160.1	
204754_at	HLF	AI810712	hepatic leukemia factor	

206467_x_at		NM_003823	gb:NM_003823.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B), mRNA. /FEA=mRNA /GEN=TNFRSF6B /PROD=decoy receptor 3 /DB_XREF=gi:4507584 /UG=Hs.278556 tumor necrosis factor receptor superfamily, member 6b, decoy /FL=gb:AF104419.1 gb:NM_003823.1 gb:AF134240.1 gb:AF217794.1	
823_at	CX3CL1	U84487	chemokine (C-X3-C motif) ligand 1	NM_002996

			gb:NM_013262.2 /DEF=Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA. /FEA=mRNA /GEN=MIR /PROD=myosin regulatory light chain interactingprotein /DB_XREF=gi:10880121 /UG=Hs.20072 myosin regulatory light chain interacting protein /FL=gb:AF187016.2	
220319_s_at		NM_013262	gb:NM_013262.2 gb:BC002860.1	
215854_at		AU146050	ESTs	
220272_at		NM_017637	gb:NM_017637.1 /DEF=Homo sapiens hypothetical protein FLJ20043 (FLJ20043), mRNA. /FEA=mRNA /GEN=FLJ20043 /PROD=hypothetical protein FLJ20043 /DB_XREF=gi:8923050 /UG=Hs.103853 hypothetical protein FLJ20043 /FL=gb:NM_017637.1	

216595_at		AL049983	Consensus includes gb:AL049983.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042). /FEA=mRNA /DB_XREF=gi:4884234 /UG=Hs.240136 Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042)	
207554_x_at		NM_001060	gb:NM_001060.1 /DEF=Homo sapiens thromboxane A2 receptor (TBXA2R), mRNA. /FEA=mRNA /GEN=TBXA2R /PROD=thromboxane A2 receptor /DB_XREF=gi:4507380 /UG=Hs.89887 thromboxane A2 receptor /FL=gb:NM_001060.1 gb:D38081.1 gb:U27325.1	
47560_at	FLJ11939	AI525402	hypothetical protein FLJ11939	

203797_at		AF039555	gb:AF039555.1 /DEF=Homo sapiens visinin-like protein 1 (VSNL1) mRNA, complete cds. /FEA=mRNA /GEN=VSNL1 /PROD=visinin-like protein 1 /DB_XREF=gi:4104813 /UG=Hs.2288 visinin-like 1 /FL=gb:AF039555.1 gb:NM_003385.1 gb:AB001104.1 gb:U14747.1	
219263_at		NM_024539	gb:NM_024539.1 /DEF=Homo sapiens hypothetical protein FLJ23516 (FLJ23516), mRNA. /FEA=mRNA /GEN=FLJ23516 /PROD=hypothetical protein FLJ23516 /DB_XREF=gi:13375696 /UG=Hs.9238 hypothetical protein FLJ23516 /FL=gb:NM_024539.1	



213393_at	U79290	Consensus includes gb:AI767210 /FEA=EST /DB_XREF=gi:5233719 /DB_XREF=est:wi94d05.x1 /CLONE=IMAGE:2400969 /UG=Hs.90449 Human clone 23908 mRNA sequence
202756_s_at	NM_002081	gb:NM_002081.1 /DEF=Homo sapiens glypican 1 (GPC1), mRNA. /FEA=mRNA /GEN=GPC1 /PROD=glypican 1 precursor /DB_XREF=gi:4504080 /UG=Hs.2699 glypican 1 /FL=gb:NM_002081.1

203337_x_at		NM_004763	gb:NM_004763.1 /DEF=Homo sapiens integrin cytoplasmic domain-associated protein 1 (ICAP-1A), transcript variant 1, mRNA. /FEA=mRNA /GEN=ICAP-1A /PROD=integrin cytoplasmic domain-associated protein1, isoform 1 /DB_XREF=gi:4758577 /UG=Hs.173274 integrin cytoplasmic domain-associated protein 1 /FL=gb:AF012023.1 gb:NM_004763.1	
214277_at	COX11	AI376724	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	
215695_s_at		U94357	Consensus includes gb:U94357.1 /DEF=Homo sapiens glycogenin-2 delta (glycogenin-2) mRNA, partial cds. /FEA=mRNA /GEN=glycogenin-2 /PROD=glycogenin-2 delta /DB_XREF=gi:2618756 /UG=Hs.58589 glycogenin 2	

201140_s_at		NM_004583	gb:NM_004583.1 /DEF=Homo sapiens RAB5C, member RAS oncogene family (RAB5C), mRNA. /FEA=mRNA /GEN=RAB5C /PROD=RAB5C, member RAS oncogene family /DB_XREF=gi:4759019 /UG=Hs.479 RAB5C, member RAS oncogene family /FL=gb:NM_004583.1 gb:U11293.1 gb:U18420.1 gb:AF141304.1	
213359_at	HNRPD	W74620	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	
218575_at		NM_022662	gb:NM_022662.1 /DEF=Homo sapiens meiotic checkpoint regulator (MCPR), mRNA. /FEA=mRNA /GEN=MCPR /PROD=meiotic checkpoint regulator /DB_XREF=gi:12056970 /UG=Hs.40137 anaphase-promoting complex 1; meiotic checkpoint regulator /FL=gb:NM_022662.1	

220399_at		NM_024796	gb:NM_024796.1 /DEF=Homo sapiens hypothetical protein FLJ22639 (FLJ22639), mRNA. /FEA=mRNA /GEN=FLJ22639 /PROD=hypothetical protein FLJ22639 /DB_XREF=gi:13376167 /UG=Hs.157184 hypothetical protein FLJ22639 /FL=gb:NM_024796.1	
207941_s_at		NM_004902	gb:NM_004902.1 /DEF=Homo sapiens splicing factor (CC1.3) (CC1.3), mRNA. /FEA=mRNA /GEN=CC1.3 /PROD=splicing factor (CC1.3) /DB_XREF=gi:4757925 /UG=Hs.145696 splicing factor (CC1.3) /FL=gb:L10910.1 gb:NM_004902.1	

207969_x_at		NM_020109	gb:NM_020109.1 /DEF=Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 5, mRNA. /FEA=mRNA /GEN=ACRV1 /PROD=acrosomal vesicle protein 1, isoform eprecursor /DB_XREF=gi:9955932 /UG=Hs.169222 acrosomal vesicle protein 1 /FL=gb:NM_020109.1	
216565_x_at	dJ781L3.1	AL121994	dJ781L3.1 (similar to IFITM3 (interferon induced transmembrane protein 3 (1-8U))) match: proteins: Sw:Q01628 Sw:Q01629 Tr:Q9R175 Tr:Q9R176 Sw:Q91499 Sw:P26376 Tr:O88728 Sw:P13164; Human DNA sequence from clone RP4-781L3 on chromosome 1p34.3-36.11 Contains a pseudogene similar to IFITM3 (interferon induced transmembrane protein 3 (1-8U)), STSs and GSSs, complete sequence.	

213083_at		AJ005866	Consensus includes gb:AJ005866.1 /DEF=Homo sapiens mRNA for putative Sqv-7-like protein, partial. /FEA=mRNA /PROD=Sqv-7-like protein /DB_XREF=gi:4008516 /UG=Hs.90078 nucleotide-sugar transporter similar to C. elegans sqv-7	
207332_s_at		NM_003234	gb:NM_003234.1 /DEF=Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /FEA=mRNA /GEN=TFRC /PROD=transferrin receptor (p90, CD71) /DB_XREF=gi:4507456 /UG=Hs.77356 transferrin receptor (p90, CD71) /FL=gb:NM_003234.1	
71933_at	WNT6	AI218134	wingless-type MMTV integration site family, member 6	

204875_s_at		NM_001500	gb:NM_001500.1 /DEF=Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /FEA=mRNA /GEN=GMDS /PROD=GDP-mannose 4,6-dehydratase /DB_XREF=gi:4504030 /UG=Hs.105435 GDP-mannose 4,6-dehydratase /FL=gb:BC000117.1 gb:AF042377.1 gb:NM_001500.1	
212062_at		AB014511	Consensus includes gb:AB014511.1 /DEF=Homo sapiens mRNA for KIAA0611 protein, partial cds. /FEA=mRNA /GEN=KIAA0611 /PROD=KIAA0611 protein /DB_XREF=gi:3327035 /UG=Hs.70604 ATPase, Class II, type 9A	
208772_at	FLJ20288	AU160676	FLJ20288 protein	
216399_s_at		AK025663	Consensus includes gb:AK025663.1 /DEF=Homo sapiens cDNA: FLJ22010 fis, clone HEP07134. /FEA=mRNA /DB_XREF=gi:10438253 /UG=Hs.285848 KIAA1454 protein	

212168_at		AB018308	Consensus includes gb:AL514547 /FEA=EST /DB_XREF=gi:12778041 /DB_XREF=est:AL514547 /CLONE=CL0BB004ZC07 (3 prime) /UG=Hs.180895 putative brain nuclearly-targeted protein	
216268_s_at		U77914	Consensus includes gb:U77914.1 /DEF=Human soluble protein Jagged mRNA, partial cds. /FEA=mRNA /PROD=soluble protein Jagged /DB_XREF=gi:1684889 /UG=Hs.91143 jagged 1 (Alagille syndrome)	
200009_at		NM_001494	gb:NM_001494.2 /DEF=Homo sapiens GDP dissociation inhibitor 2 (GDI2), mRNA. /FEA=mRNA /GEN=GDI2 /PROD=GDP dissociation inhibitor 2 /DB_XREF=gi:6598322 /UG=Hs.56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2	



218351_at		NM_017845	gb:NM_017845.1 /DEF=Homo sapiens hypothetical protein FLJ20502 (FLJ20502), mRNA. /FEA=mRNA /GEN=FLJ20502 /PROD=hypothetical protein FLJ20502 /DB_XREF=gi:8923457 /UG=Hs.23956 hypothetical protein FLJ20502 /FL=gb:AF182421.1 gb:NM_017845.1	
219378_at		NM_024561	gb:NM_024561.1 /DEF=Homo sapiens hypothetical protein FLJ22054 (FLJ22054), mRNA. /FEA=mRNA /GEN=FLJ22054 /PROD=hypothetical protein FLJ22054 /DB_XREF=gi:13375728 /UG=Hs.13277 hypothetical protein FLJ22054 /FL=gb:NM_024561.1	
201626_at	INSIG1	BE300521	insulin induced gene 1	
213300_at	KIAA0404	AW168132	KIAA0404 protein	
201160_s_at	CSDA	AL556190	cold shock domain protein A	

208328_s_at		NM_005587	gb:NM_005587.1 /DEF=Homo sapiens MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA. /FEA=mRNA /GEN=MEF2A /PROD=MADS box transcription enhancer factor 2,polypeptide A (myocyte enhancer factor 2A) /DB_XREF=gi:5031906 /UG=Hs.182280 MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) /FL=gb:NM_005587.1	
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219467_at		NM_017676	gb:NM_017676.1 /DEF=Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA. /FEA=mRNA /GEN=FLJ20125 /PROD=hypothetical protein FLJ20125 /DB_XREF=gi:8923123 /UG=Hs.24088 hypothetical protein FLJ20125 /FL=gb:NM_017676.1	
200920_s_at	BTG1	AL535380	B-cell translocation gene 1, anti-proliferative	
218631_at		NM_021732	gb:NM_021732.1 /DEF=Homo sapiens hypothetical protein PP5395 (PP5395), mRNA. /FEA=mRNA /GEN=PP5395 /PROD=hypothetical protein PP5395 /DB_XREF=gi:11119427 /UG=Hs.23918 hypothetical protein PP5395 /FL=gb:NM_021732.1 gb:AF241786.1 gb:BC000877.1	
208655_at	CCNI	BG530368	cyclin I	
208615_s_at	PTP4A2	BF795101	protein tyrosine phosphatase type IVA, member 2	

213366_x_at	ATP5C1	AV711183	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, gamma polypeptide 1	
208611_s_at		U83867	gb:U83867.1 /DEF=Human alpha II spectrin mRNA, complete cds. /FEA=mRNA /PROD=alpha II spectrin /DB_XREF=gi:1805279 /UG=Hs.77196 spectrin, alpha, non- erythrocytic 1 (alpha-fodrin) /FL=gb:J05243.1 gb:U83867.1 gb:NM_003127.1	
219443_at		NM_017714	gb:NM_017714.1 /DEF=Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA. /FEA=mRNA /GEN=FLJ20212 /PROD=hypothetical protein FLJ20212 /DB_XREF=gi:8923201 /UG=Hs.88367 hypothetical protein FLJ20212 /FL=gb:NM_017714.1	

213322_at		AL031778	Consensus includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine... /FEA=mRNA_2 /DB_XREF=gi:4153958 /UG=Hs.183056 Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine recepto	
217730_at		NM_022152	gb:NM_022152.1 /DEF=Homo sapiens PP1201 protein (PP1201), mRNA. /FEA=mRNA /GEN=PP1201 /PROD=PP1201 protein /DB_XREF=gi:11545897 /UG=Hs.184052 PP1201 protein /FL=gb:NM_022152.1	

212331_at		NM_005611	Consensus includes gb:X76061.1 /DEF=H.sapiens p130 mRNA for 130K protein. /FEA=mRNA /GEN=p130 /PROD=130K protein /DB_XREF=gi:416030 /UG=Hs.79362 retinoblastoma-like 2 (p130) /FL=gb:NM_005611.1	
213140_s_at		AB014593	Consensus includes gb:AB014593.1 /DEF=Homo sapiens mRNA for KIAA0693 protein, partial cds. /FEA=mRNA /GEN=KIAA0693 /PROD=KIAA0693 protein /DB_XREF=gi:3327199 /UG=Hs.154429 KIAA0693 protein	
213133_s_at		BE908931	ESTs, Highly similar to GCHUH glycine cleavage system protein H precursor - human [H.sapiens]	

200789_at	NM_001398	gb:NM_001398.1 /DEF=Homo sapiens enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA. /FEA=mRNA /GEN=ECH1 /PROD=peroxisomal enoyl-coenzyme A hydratase-likeprotein /DB_XREF=gi:4503446 /UG=Hs.196176 enoyl Coenzyme A hydratase 1, peroxisomal /FL=gb:NM_001398.1 gb:U16660.1
217168_s_at	AF217990	Consensus includes gb:AF217990.1 /DEF=Homo sapiens clone PP1722 unknown mRNA. /FEA=mRNA /PROD=unknown /DB_XREF=gi:10441910 /UG=Hs.146393 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1

211168_s_at		D86988	gb:D86988.1 /DEF=Human mRNA for KIAA0221 gene, complete cds. /FEA=mRNA /GEN=KIAA0221 /PROD=KIAA0221 /DB_XREF=gi:1944406 /UG=Hs.12719 regulator of nonsense transcripts 1 /FL=gb:D86988.1	
201200_at		NM_003851	gb:NM_003851.1 /DEF=Homo sapiens cellular repressor of E1A- stimulated genes (CREG), mRNA. /FEA=mRNA /GEN=CREG /PROD=cellular repressor of E1A- stimulated genes /DB_XREF=gi:4503036 /UG=Hs.5710 cellular repressor of E1A-stimulated genes /FL=gb:AF084523.1 gb:NM_003851.1	



211378_x_at		BC001224	gb:BC001224.1 /DEF=Homo sapiens, clone MGC:982, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:982) /DB_XREF=gi:12654762 /UG=Hs.267690 KIAA1228 protein /FL=gb:BC001224.1	
205911_at		NM_000316	gb:NM_000316.1 /DEF=Homo sapiens parathyroid hormone receptor 1 (PTH1R), mRNA. /FEA=mRNA /GEN=PTH1R /PROD=parathyroid hormone receptor 1 /DB_XREF=gi:4506270 /UG=Hs.1019 parathyroid hormone receptor 1 /FL=gb:L04308.1 gb:NM_000316.1 gb:U17418.1	

204908_s_at		NM_005178	gb:NM_005178.1 /DEF=Homo sapiens B-cell CLLlymphoma 3 (BCL3), mRNA. /FEA=mRNA /GEN=BCL3 /PROD=B-cell CLLlymphoma 3 /DB_XREF=gi:4885086 /UG=Hs.31210 B-cell CLLlymphoma 3 /FL=gb:M31732.1 gb:NM_005178.1	
202990_at		NM_002863	gb:NM_002863.1 /DEF=Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA. /FEA=mRNA /GEN=PYGL /PROD=phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) /DB_XREF=gi:4506352 /UG=Hs.771 phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) /FL=gb:M14636.1 gb:AF066858.1 gb:AF046785.1 gb:NM_002863.1	

202450_s_at		NM_000396	gb:NM_000396.1 /DEF=Homo sapiens cathepsin K (pseudodysostosis) (CTSK), mRNA. /FEA=mRNA /GEN=CTSK /PROD=cathepsin K (pseudodysostosis) /DB_XREF=gi:4503150 /UG=Hs.83942 cathepsin K (pseudodysostosis) /FL=gb:NM_000396.1 gb:U13665.1	
214790_at		AK001406	Consensus includes gb:AK001406.1 /DEF=Homo sapiens cDNA FLJ10544 fis, clone NT2RP2001601, highly similar to Homo sapiens mRNA for KIAA0797 protein. /FEA=mRNA /DB_XREF=gi:7022642 /UG=Hs.27197 SUMO-1-specific protease	

209695_at		BC003105	gb:BC003105.1 /DEF=Homo sapiens, Similar to protein tyrosine phosphatase type IVA, member 3, clone MGC:1950, mRNA, complete cds. /FEA=mRNA /PROD=Similar to protein tyrosine phosphatase typeIVA, member 3 /DB_XREF=gi:13111874 /UG=Hs.43666 protein tyrosine phosphatase type IVA, member 3 /FL=gb:BC003105.1	
212847_at	FUBP1	AL036840	far upstream element (FUSE) binding protein 1	
214022_s_at	IFITM1	AA749101	interferon induced transmembrane protein 1 (9-27)	
202393_s_at		NM_005655	gb:NM_005655.1 /DEF=Homo sapiens TGFB inducible early growth response (TIEG), mRNA. /FEA=mRNA /GEN=TIEG /PROD=TGFB inducible early growth response /DB_XREF=gi:5032176 /UG=Hs.82173 TGFB inducible early growth response /FL=gb:U21847.1 gb:NM_005655.1	

203786_s_at		NM_003287	gb:NM_003287.1 /DEF=Homo sapiens tumor protein D52-like 1 (TPD52L1), mRNA. /FEA=mRNA /GEN=TPD52L1 /PROD=tumor protein D52-like 1 /DB_XREF=gi:4507640 /UG=Hs.16611 tumor protein D52-like 1 /FL=gb:U44427.1 gb:NM_003287.1	
218152_at		NM_018200	gb:NM_018200.1 /DEF=Homo sapiens high-mobility group 20A (HMG20A), mRNA. /FEA=mRNA /GEN=HMG20A /PROD=high-mobility group 20A /DB_XREF=gi:8922632 /UG=Hs.69594 high-mobility group 20A /FL=gb:AF146222.1 gb:NM_018200.1	

221626_at		AL136548	gb:AL136548.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds. /FEA=mRNA /GEN=DKFZp761G18121 /PROD=hypothetical protein /DB_XREF=gi:12052731 /UG=Hs.260180 Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds /FL=gb:AL136548.1	
214582_at		NM_000753	Consensus includes gb:NM_000753.1 /DEF=Homo sapiens 2,3-cyclic nucleotide 3 phosphodiesterase (CNP), mRNA. /FEA=CDS /GEN=CNP /PROD=2,3-cyclic nucleotide 3 phosphodiesterase /DB_XREF=gi:4502924 /UG=Hs.150741 2,3-cyclic nucleotide 3 phosphodiesterase /FL=gb:NM_000753.1	
214657_s_at		AU134977	Human clone 137308 mRNA, partial cds	

218140_x_at		NM_021203	gb:NM_021203.1 /DEF=Homo sapiens APMCF1 protein (APMCF1), mRNA. /FEA=mRNA /GEN=APMCF1 /PROD=APMCF1 protein /DB_XREF=gi:10864014 /UG=Hs.12152 APMCF1 protein /FL=gb:NM_021203.1 gb:AF141882.1	
202843_at		NM_012328	gb:NM_012328.1 /DEF=Homo sapiens microvascular endothelial differentiation gene 1 (MDG1), mRNA. /FEA=mRNA /GEN=MDG1 /PROD=microvascular endothelial differentiation gene1 /DB_XREF=gi:9558754 /UG=Hs.6790 DnaJ (Hsp40) homolog, subfamily B, member 9 /FL=gb:AF083247.1 gb:AL080081.1 gb:AB026908.1 gb:NM_012328.1	
221480_at	HNRPD	BG180941	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	

202634_at	POLR2K	AL558030	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	
202667_s_at		NM_006979	gb:NM_006979.1 /DEF=Homo sapiens HLA class II region expressed gene KE4 (HKE4), mRNA. /FEA=mRNA /GEN=HKE4 /PROD=HLA class II region expressed gene KE4 /DB_XREF=gi:5901935 /UG=Hs.278721 HLA class II region expressed gene KE4 /FL=gb:D82060.1 gb:NM_006979.1	
202677_at		NM_002890	gb:NM_002890.1 /DEF=Homo sapiens RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA. /FEA=mRNA /GEN=RASA1 /PROD=RAS p21 protein activator 1, isoform 1 /DB_XREF=gi:4506430 /UG=Hs.758 RAS p21 protein activator (GTPase activating protein) 1 /FL=gb:M23379.1 gb:NM_002890.1	
212579_at	KIAA0650	AA868754	KIAA0650 protein	



			gb:NM_031207.1 /DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA. /FEA=CDS /GEN=HT036 /PROD=hypothetical protein HT036 /DB_XREF=gi:13654271 /FL=gb:NM_031207.1	
221435_x_at		NM_031207		
			gb:NM_014782.1 /DEF=Homo sapiens KIAA0512 gene product (KIAA0512), mRNA. /FEA=mRNA /GEN=KIAA0512 /PROD=KIAA0512 gene product /DB_XREF=gi:7662161 /UG=Hs.48924 KIAA0512 gene product; ALEX2 /FL=gb:AB011084.1 gb:NM_014782.1	
203404_at		NM_014782		
221778_at	KIAA1718	BE217882	KIAA1718 protein	

209430_at		AJ001017	Consensus includes gb:AJ001017.2 /DEF=Homo sapiens partial mRNA for TBP-associated factor 170 (TAFII170). /FEA=mRNA /GEN=TAFII170 /PROD=TBP associated factor /DB_XREF=gi:7018281 /UG=Hs.180930 TBP-associated factor 172 /FL=gb:AF038362.1	
210172_at		D26121	gb:D26121.1 /DEF=Human mRNA for ZFM1 protein alternatively spliced product, complete cds. /FEA=mRNA /PROD=ZFM1 protein, alternatively spliced product /DB_XREF=gi:785998 /UG=Hs.169303 Human mRNA for ZFM1 protein alternatively spliced product, complete cds /FL=gb:D26121.1	

201984_s_at		NM_005228	gb:NM_005228.1 /DEF=Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA. /FEA=mRNA /GEN=EGFR /PROD=epidermal growth factor receptor (avianerythroblastic leukemia viral (v-erb-b) oncogene homolog) /DB_XREF=gi:4885198 /UG=Hs.77432 epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) /FL=gb:NM_005228.1	
212434_at	HMGE	AL542571	GrpE-like protein cochaperone	

204345_at		NM_001856	gb:NM_001856.1 /DEF=Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA. /FEA=mRNA /GEN=COL16A1 /PROD=collagen, type XVI, alpha 1 /DB_XREF=gi:11386158 /UG=Hs.26208 collagen, type XVI, alpha 1 /FL=gb:NM_001856.1 gb:M92642.1
208829_at		AF029750	gb:AF029750.1 /DEF=Homo sapiens tapasin (NGS-17) mRNA, complete cds. /FEA=mRNA /GEN=NGS-17 /PROD=tapasin /DB_XREF=gi:2587057 /UG=Hs.179600 TAP binding protein (tapasin) /FL=gb:AF314222.1 gb:AF009510.1 gb:AF029750.1 gb:AB010639.1 gb:NM_003190.1

208863_s_at		M72709	gb:M72709.1 /DEF=Human alternative splicing factor mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:179073 /UG=Hs.73737 splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /FL=gb:M72709.1	
219034_at		NM_017851	gb:NM_017851.1 /DEF=Homo sapiens hypothetical protein FLJ20509 (FLJ20509), mRNA. /FEA=mRNA /GEN=FLJ20509 /PROD=hypothetical protein FLJ20509 /DB_XREF=gi:8923470 /UG=Hs.30634 hypothetical protein FLJ20509 /FL=gb:NM_017851.1	

204379_s_at		NM_000142	gb:NM_000142.2 /DEF=Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), transcript variant 1, mRNA. /FEA=mRNA /GEN=FGFR3 /PROD=fibroblast growth factor receptor 3, isoform 1precursor /DB_XREF=gi:13112046 /UG=Hs.1420 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) /FL=gb:NM_000142.2 gb:M58051.1	
201887_at		NM_001560	gb:NM_001560.1 /DEF=Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA. /FEA=mRNA /GEN=IL13RA1 /PROD=interleukin 13 receptor, alpha 1 /DB_XREF=gi:4504646 /UG=Hs.285115 interleukin 13 receptor, alpha 1 /FL=gb:NM_001560.1 gb:U81379.3	

209200_at	MEF2C	N22468	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	
218205_s_at		NM_017572	gb:NM_017572.1 /DEF=Homo sapiens G protein-coupled receptor kinase 7 (GPRK7), mRNA. /FEA=mRNA /GEN=GPRK7 /PROD=G protein-coupled receptor kinase 7 /DB_XREF=gi:9994196 /UG=Hs.261828 G protein-coupled receptor kinase 7 /FL=gb:AF237776.1 gb:AF125532.1 gb:NM_017572.1	
222279_at	HLA-F	AI669379	major histocompatibility complex, class I, F	
215191_at		AW836210	ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	

219073_s_at		NM_017784	gb:NM_017784.1 /DEF=Homo sapiens hypothetical protein FLJ20363 (FLJ20363), mRNA. /FEA=mRNA /GEN=FLJ20363 /PROD=hypothetical protein FLJ20363 /DB_XREF=gi:8923336 /UG=Hs.321622 hypothetical protein FLJ20363 /FL=gb:BC003168.1 gb:NM_017784.1	
208962_s_at	FADS1	BE540552	fatty acid desaturase 1	
218807_at		NM_006113	gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mRNA /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390 /UG=Hs.267659 vav 3 oncogene /FL=gb:AF067817.1 gb:AF118887.1 gb:NM_006113.2	



202225_at		NM_016823	Consensus includes gb:AW612311 /FEA=EST /DB_XREF=gi:7317497 /DB_XREF=est:hg95e07.x1 /CLONE=IMAGE:2953380 /UG=Hs.306088 v-crk avian sarcoma virus CT10 oncogene homolog /FL=gb:D10656.1 gb:NM_016823.1	
209896_s_at		AF119855	gb:AF119855.1 /DEF=Homo sapiens PRO1847 mRNA, complete cds. /FEA=mRNA /PROD=PRO1847 /DB_XREF=gi:7770146 /UG=Hs.285196 hypothetical protein PRO1847 /FL=gb:AF119855.1	
202103_at	BRD4	BF718610	bromodomain containing 4	
203791_at		NM_005509	gb:NM_005509.2 /DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA. /FEA=mRNA /GEN=DMXL1 /PROD=Dmx-like 1 /DB_XREF=gi:9961348 /UG=Hs.181042 Dmx-like 1 /FL=gb:NM_005509.2	

214130_s_at	PDE4DIP	AI821791	phosphodiesterase 4D interacting protein (myomegalin)	
212694_s_at		NM_000532	Consensus includes gb:NM_000532.1 /DEF=Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), nuclear gene encoding mitochondrial protein, mRNA. /FEA=CDS /GEN=PCCB /PROD=propionyl Coenzyme A carboxylase, betapolypeptide /DB_XREF=gi:4557043 /UG=Hs.63788 propionyl Coenzyme A carboxylase, beta polypeptide /FL=gb:NM_000532.1	
212183_at		AF191654	Consensus includes gb:AW511135 /FEA=EST /DB_XREF=gi:7149213 /DB_XREF=est:hd43g08.x1 /CLONE=IMAGE:2912318 /UG=Hs.92381 nudix (nucleoside diphosphate linked moiety X)-type motif 4	

217975_at		NM_016303	gb:NM_016303.1 /DEF=Homo sapiens pp21 homolog (LOC51186), mRNA. /FEA=mRNA /GEN=LOC51186 /PROD=pp21 homolog /DB_XREF=gi:10047099 /UG=Hs.15984 pp21 homolog /FL=gb:NM_016303.1 gb:AF125535.1	
217992_s_at		NM_024329	gb:NM_024329.1 /DEF=Homo sapiens hypothetical protein MGC4342 (MGC4342), mRNA. /FEA=mRNA /GEN=MGC4342 /PROD=hypothetical protein MGC4342 /DB_XREF=gi:13443015 /UG=Hs.301342 hypothetical protein MGC4342 /FL=gb:BC003033.1 gb:NM_024329.1	

218435_at		NM_013238	gb:NM_013238.1 /DEF=Homo sapiens DNAJ domain-containing (MCJ), mRNA. /FEA=mRNA /GEN=MCJ /PROD=DNAJ domain-containing /DB_XREF=gi:7019452 /UG=Hs.279884 DNAJ domain-containing /FL=gb:AF126743.1 gb:NM_013238.1	
218039_at		NM_016359	gb:NM_016359.1 /DEF=Homo sapiens clone HQ0310 PRO0310p1 (LOC51203), mRNA. /FEA=mRNA /GEN=LOC51203 /PROD=clone HQ0310 PRO0310p1 /DB_XREF=gi:7705950 /UG=Hs.279905 clone HQ0310 PRO0310p1 /FL=gb:AF305711.1 gb:BC001308.1 gb:AF290612.1 gb:AF090915.1 gb:NM_016359.1	
212861_at	MGC11308	BF690150	hypothetical protein MGC11308	

216484_x_at		L24521	Consensus includes gb:L24521.1 /DEF=Human transformation-related protein mRNA, 3 end. /FEA=mRNA /PROD=transformation-related protein /DB_XREF=gi:403459 /UG=Hs.300705 Human transformation-related protein mRNA, 3 end	
218101_s_at		NM_004549	gb:NM_004549.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) (NDUFC2), mRNA. /FEA=mRNA /GEN=NDUFC2 /PROD=NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) /DB_XREF=gi:4758783 /UG=Hs.193313 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) /FL=gb:AF087659.1 gb:AF070652.1 gb:NM_004549.1	

217947_at		NM_017801	gb:NM_017801.1 /DEF=Homo sapiens hypothetical protein FLJ20396 (FLJ20396), mRNA. /FEA=mRNA /GEN=FLJ20396 /PROD=hypothetical protein FLJ20396 /DB_XREF=gi:8923369 /UG=Hs.283685 hypothetical protein FLJ20396 /FL=gb:BC002797.1 gb:NM_017801.1	
217950_at		NM_015953	gb:NM_015953.1 /DEF=Homo sapiens CGI-25 protein (LOC51070), mRNA. /FEA=mRNA /GEN=LOC51070 /PROD=CGI-25 protein /DB_XREF=gi:7705715 /UG=Hs.7236 CGI-25 protein /FL=gb:AF132959.1 gb:NM_015953.1	
212639_x_at	K-ALPHA-1	AL581768	tubulin, alpha, ubiquitous	
213274_s_at	CTSB	BE875786	cathepsin B	
213278_at	MTMR9	AW014788	myotubularin related protein 9	

218049_s_at		NM_014078	gb:NM_014078.1 /DEF=Homo sapiens L13 protein (L13), mRNA. /FEA=mRNA /GEN=L13 /PROD=L13 protein /DB_XREF=gi:7662495 /UG=Hs.43946 L13 protein /FL=gb:AF112214.1 gb:NM_014078.1	
212490_at	DNAJC8	AA843895	DnaJ (Hsp40) homolog, subfamily C, member 8	
212791_at	FLJ38984	AL042729	hypothetical protein FLJ38984	
201163_s_at		NM_001553	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:L19182.1 gb:NM_001553.1	

209434_s_at		U00238	gb:U00238.1 /DEF=Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds. /FEA=mRNA /GEN=GPAT /PROD=glutamine PRPP amidotransferase /DB_XREF=gi:404860 /UG=Hs.311 phosphoribosyl pyrophosphate amidotransferase /FL=gb:U00238.1	
209393_s_at		AF047695	gb:AF047695.1 /DEF=Homo sapiens cap-binding protein 4EHP mRNA, complete cds. /FEA=mRNA /PROD=cap-binding protein 4EHP /DB_XREF=gi:3172338 /UG=Hs.19122 eukaryotic translation initiation factor 4E-like 3 /FL=gb:BC005392.1 gb:AF047695.1 gb:AF068117.1 gb:AF038957.1 gb:NM_004846.1	



219013_at		NM_022087	gb:NM_022087.1 /DEF=Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA. /FEA=mRNA /GEN=FLJ21634 /PROD=hypothetical protein FLJ21634 /DB_XREF=gi:11545800 /UG=Hs.97056 hypothetical protein FLJ21634 /FL=gb:NM_022087.1	
201202_at		NM_002592	gb:NM_002592.1 /DEF=Homo sapiens proliferating cell nuclear antigen (PCNA), mRNA. /FEA=mRNA /GEN=PCNA /PROD=proliferating cell nuclear antigen /DB_XREF=gi:4505640 /UG=Hs.78996 proliferating cell nuclear antigen /FL=gb:BC000491.1 gb:M15796.1 gb:NM_002592.1	

201205_at		AF006751	Consensus includes gb:AF006751.1 /DEF=Homo sapiens ES130 mRNA, complete cds. /FEA=mRNA /PROD=ES130 /DB_XREF=gi:3299884 /UG=Hs.98614 ribosome binding protein 1 (dog 180kD homolog) /FL=gb:AF006751.1 gb:NM_004587.1	
204017_at		NM_006855	gb:NM_006855.2 /DEF=Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 1, mRNA. /FEA=mRNA /GEN=KDEL3 /PROD=KDEL receptor 3, isoform a /DB_XREF=gi:8051612 /UG=Hs.250696 KDEL (Lys-Asp- Glu-Leu) endoplasmic reticulum protein retention receptor 3 /FL=gb:BC001277.1 gb:NM_006855.2	

209214_s_at	BC004817	gb:BC004817.1 /DEF=Homo sapiens, Ewing sarcoma breakpoint region 1, clone MGC:5432, mRNA, complete cds. /FEA=mRNA /PROD=Ewing sarcoma breakpoint region 1 /DB_XREF=gi:13435962 /UG=Hs.129953 Ewing sarcoma breakpoint region 1 /FL=gb:BC004817.1 gb:NM_005243.1
201059_at	NM_005231	gb:NM_005231.1 /DEF=Homo sapiens ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p8085 src substrate) (EMS1), mRNA. /FEA=mRNA /GEN=EMS1 /PROD=cortactin /DB_XREF=gi:4885204 /UG=Hs.119257 ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p8085 src substrate) /FL=gb:M98343.1 gb:NM_005231.1

56197_at	PLSCR3	AI783924	phospholipid scramblase 3	
203789_s_at		NM_006379	gb:NM_006379.1 /DEF=Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA. /FEA=mRNA /GEN=SEMA3C /PROD=sema domain, immunoglobulin domain (Ig), shortbasic domain, secreted, (semaphorin) 3C /DB_XREF=gi:5454047 /UG=Hs.171921 sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C /FL=gb:AB000220.1 gb:NM_006379.1	

203921_at	NM_004267	gb:NM_004267.1 /DEF=Homo sapiens carbohydrate (chondroitin 6keratan) sulfotransferase 2 (CHST2), mRNA. /FEA=mRNA /GEN=CHST2 /PROD=carbohydrate (chondroitin 6keratan)sulfotransferase 2 /DB_XREF=gi:4757983 /UG=Hs.8786 carbohydrate (chondroitin 6keratan) sulfotransferase 2 /FL=gb:AB021124.1 gb:AB014679.1 gb:AB014680.1 gb:AF083066.1 gb:NM_004267.1
209537_at	AF000416	gb:AF000416.1 /DEF=Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds. /FEA=mRNA /GEN=EXTL2 /PROD=EXT-like protein 2 /DB_XREF=gi:2895061 /UG=Hs.61152 exostoses (multiple)-like 2 /FL=gb:AB009284.1 gb:AF000416.1

207855_s_at		NM_015127	gb:NM_015127.1 /DEF=Homo sapiens KIAA0761 protein (KIAA0761), mRNA. /FEA=mRNA /GEN=KIAA0761 /PROD=KIAA0761 protein /DB_XREF=gi:13194194 /UG=Hs.93121 KIAA0761 protein /FL=gb:BC002939.1 gb:NM_015127.1	
205596_s_at		AY014180	gb:AY014180.1 /DEF=Homo sapiens E3 ubiquitin ligase Smurf2 mRNA, complete cds. /FEA=mRNA /PROD=E3 ubiquitin ligase Smurf2 /DB_XREF=gi:12408118 /UG=Hs.194477 E3 ubiquitin ligase SMURF2 /FL=gb:AF301463.1 gb:AF310676.1 gb:NM_022739.1 gb:AY014180.1	

219806_s_at		NM_020179	gb:NM_020179.1 /DEF=Homo sapiens FN5 protein (FN5), mRNA. /FEA=mRNA /GEN=FN5 /PROD=FN5 protein /DB_XREF=gi:9910225 /UG=Hs.259737 FN5 protein /FL=gb:AF197137.1 gb:NM_020179.1	
201874_at	FLJ21047	BF978611	hypothetical protein FLJ21047	
206580_s_at		NM_016938	gb:NM_016938.1 /DEF=Homo sapiens EGF-containing fibulin-like extracellular matrix protein 2 (EFEMP2), mRNA. /FEA=mRNA /GEN=EFEMP2 /PROD=EGF-containing fibulin-like extracellular matrixprotein 2 /DB_XREF=gi:8393298 /UG=Hs.6059 EGF-containing fibulin-like extracellular matrix protein 2 /FL=gb:AF093119.1 gb:AF109121.1 gb:NM_016938.1	

201739_at	NM_005627	gb:NM_005627.1 /DEF=Homo sapiens serumglucocorticoid regulated kinase (SGK), mRNA. /FEA=mRNA /GEN=SGK /PROD=serumglucocorticoid regulated kinase /DB_XREF=gi:5032090 /UG=Hs.296323 serumglucocorticoid regulated kinase /FL=gb:BC001263.1 gb:NM_005627.1 gb:AF153609.1
209509_s_at	BC000325	gb:BC000325.1 /DEF=Homo sapiens, clone MGC:8482, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:8482) /DB_XREF=gi:12653116 /UG=Hs.26433 dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase) /FL=gb:BC000325.1 gb:NM_001382.1



202289_s_at		NM_006997	gb:NM_006997.1 /DEF=Homo sapiens transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA. /FEA=mRNA /GEN=TACC2 /PROD=transforming, acidic coiled-coil containing protein 2 /DB_XREF=gi:11119413 /UG=Hs.272023 transforming, acidic coiled-coil containing protein 2 /FL=gb:AF095791.2 gb:NM_006997.1	
204216_s_at		NM_024824	gb:NM_024824.1 /DEF=Homo sapiens hypothetical protein FLJ11806 (FLJ11806), mRNA. /FEA=mRNA /GEN=FLJ11806 /PROD=hypothetical protein FLJ11806 /DB_XREF=gi:13376221 /UG=Hs.323443 hypothetical protein FLJ11806 /FL=gb:NM_024824.1	

201587_s_at	NM_001569	gb:NM_001569.2 /DEF=Homo sapiens interleukin-1 receptor-associated kinase 1 (IRAK1), mRNA. /FEA=mRNA /GEN=IRAK1 /PROD=interleukin-1 receptor-associated kinase 1 /DB_XREF=gi:4755143 /UG=Hs.182018 interleukin-1 receptor-associated kinase 1 /FL=gb:L76191.1 gb:NM_001569.2
208780_x_at	AF154847	gb:AF154847.1 /DEF=Homo sapiens 33 kDa Vamp-associated protein (VAMP) mRNA, complete cds. /FEA=mRNA /GEN=VAMP /PROD=33 kDa Vamp-associated protein /DB_XREF=gi:8099349 /UG=Hs.9006 VAMP (vesicle-associated membrane protein)-associated protein A (33kD) /FL=gb:BC002992.1 gb:AF057358.1 gb:AF044670.1 gb:AF086627.1 gb:NM_003574.1 gb:AF154847.1

208717_at	BC001669	gb:BC001669.1 /DEF=Homo sapiens, Similar to oxidase (cytochrome c) assembly 1-like, clone MGC:2171, mRNA, complete cds. /FEA=mRNA /PROD=Similar to oxidase (cytochrome c) assembly1-like /DB_XREF=gi:12804516 /UG=Hs.151134 oxidase (cytochrome c) assembly 1-like /FL=gb:BC001669.1 gb:NM_005015.1
200765_x_at	NM_001903	gb:NM_001903.1 /DEF=Homo sapiens catenin (cadherin-associated protein), alpha 1 (102kD) (CTNNA1), mRNA. /FEA=mRNA /GEN=CTNNA1 /PROD=catenin (cadherin-associated protein), alpha 1(102kD) /DB_XREF=gi:4503126 /UG=Hs.178452 catenin (cadherin-associated protein), alpha 1 (102kD) /FL=gb:L23805.1 gb:NM_001903.1

200782_at	NM_001154	gb:NM_001154.2 /DEF=Homo sapiens annexin A5 (ANXA5), mRNA. /FEA=mRNA /GEN=ANXA5 /PROD=annexin V /DB_XREF=gi:4809273 /UG=Hs.300711 annexin A5 /FL=gb:BC001429.1 gb:BC004993.1 gb:M18366.1 gb:J03745.1 gb:M21731.1 gb:M19384.1 gb:D00172.1 gb:NM_001154.2
202647_s_at	NM_002524	gb:NM_002524.2 /DEF=Homo sapiens neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS), mRNA. /FEA=mRNA /GEN=NRAS /PROD=neuroblastoma RAS viral (v-ras) oncogenehomolog /DB_XREF=gi:6006027 /UG=Hs.260523 neuroblastoma RAS viral (v-ras) oncogene homolog /FL=gb:BC005219.1 gb:NM_002524.2

200021_at		NM_005507	gb:NM_005507.1 /DEF=Homo sapiens cofilin 1 (non-muscle) (CFL1), mRNA. /FEA=mRNA /GEN=CFL1 /PROD=cofilin 1 (non-muscle) /DB_XREF=gi:5031634 /UG=Hs.180370 cofilin 1 (non-muscle) /FL=gb:NM_005507.1	
221761_at	ADSS	AA628948	adenylosuccinate synthase	
200710_at		NM_000018	gb:NM_000018.1 /DEF=Homo sapiens acyl-Coenzyme A dehydrogenase, very long chain (ACADVL), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACADVL /PROD=acyl-Coenzyme A dehydrogenase, very long chainprecursor /DB_XREF=gi:4557234 /UG=Hs.82208 acyl-Coenzyme A dehydrogenase, very long chain /FL=gb:D43682.1 gb:BC000399.1 gb:NM_000018.1	

211750_x_at		BC005946	gb:BC005946.1 /DEF=Homo sapiens, clone MGC:14580, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:14580) /DB_XREF=gi:13543588 /FL=gb:BC005946.1	
203031_s_at		NM_000375	gb:NM_000375.1 /DEF=Homo sapiens uroporphyrinogen III synthase (congenital erythropoietic porphyria) (UROS), mRNA. /FEA=mRNA /GEN=UROS /PROD=uroporphyrinogen III synthase /DB_XREF=gi:4557872 /UG=Hs.75593 uroporphyrinogen III synthase (congenital erythropoietic porphyria) /FL=gb:BC002573.1 gb:J03824.1 gb:NM_000375.1	
202681_at	USP4	AI346043	ubiquitin specific protease 4 (proto-oncogene)	
202906_s_at	NBS1	AI796269	Nijmegen breakage syndrome 1 (nibrin)	

200663_at		NM_001780	gb:NM_001780.1 /DEF=Homo sapiens CD63 antigen (melanoma 1 antigen) (CD63), mRNA. /FEA=mRNA /GEN=CD63 /PROD=CD63 antigen (melanoma 1 antigen) /DB_XREF=gi:4502678 /UG=Hs.76294 CD63 antigen (melanoma 1 antigen) /FL=gb:BC002349.1 gb:M59907.1 gb:NM_001780.1
211978_x_at	PPIA	AI708767	peptidylprolyl isomerase A (cyclophilin A)
211594_s_at		AB049636	gb:AB049636.1 /DEF=Homo sapiens MRPL9 mRNA for mitochondrial ribosomal protein L9 (L9mt), complete cds. /FEA=mRNA /GEN=MRPL9 /PROD=mitochondrial ribosomal protein L9 (L9mt) /DB_XREF=gi:13559362 /FL=gb:AB049636.1

202492_at		NM_024085	gb:NM_024085.1 /DEF=Homo sapiens hypothetical protein FLJ22169 (FLJ22169), mRNA. /FEA=mRNA /GEN=FLJ22169 /PROD=hypothetical protein FLJ22169 /DB_XREF=gi:13129081 /UG=Hs.323363 hypothetical protein FLJ22169 /FL=gb:BC001206.1 gb:NM_024085.1	
58994_at	FLJ20241	AI689402	hypothetical protein FLJ20241	
203534_at		NM_014462	gb:NM_014462.1 /DEF=Homo sapiens Lsm1 protein (LSM1), mRNA. /FEA=mRNA /GEN=LSM1 /PROD=Lsm1 protein /DB_XREF=gi:7657312 /UG=Hs.111783 Lsm1 protein /FL=gb:BC001767.1 gb:AF000177.1 gb:NM_014462.1	



200825_s_at		NM_006389	gb:NM_006389.2 /DEF=Homo sapiens oxygen regulated protein (150kD) (ORP150), mRNA. /FEA=mRNA /GEN=ORP150 /PROD=oxygen regulated protein precursor /DB_XREF=gi:13699861 /UG=Hs.277704 oxygen regulated protein (150kD) /FL=gb:NM_006389.2 gb:U65785.1	
208638_at	ATP6V1C2	BE910010	ATPase, H <sup>+</sup> transporting, lysosomal 42kDa, V1 subunit C isoform 2	
205257_s_at		NM_001635	gb:NM_001635.1 /DEF=Homo sapiens amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) (AMPH), mRNA. /FEA=mRNA /GEN=AMPH /PROD=amphiphysin /DB_XREF=gi:4502080 /UG=Hs.173034 amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen) /FL=gb:NM_001635.1 gb:U07616.1	

216557_x_at	A1VH3	U92706	Human rearranged immunoglobulin heavy chain (A1VH3) gene, partial cds.	
208989_s_at		AF179221	gb:AF179221.1 /DEF=Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds. /FEA=mRNA /GEN=LILINA /PROD=F-box protein Lilina /DB_XREF=gi:5917729 /UG=Hs.219614 f-box and leucine-rich repeat protein 11 /FL=gb:AF179221.1	
220842_at		NM_017651	gb:NM_017651.1 /DEF=Homo sapiens hypothetical protein FLJ20069 (FLJ20069), mRNA. /FEA=mRNA /GEN=FLJ20069 /PROD=hypothetical protein FLJ20069 /DB_XREF=gi:8923074 /UG=Hs.273294 hypothetical protein FLJ20069 /FL=gb:NM_017651.1	

201992_s_at		NM_004521	gb:NM_004521.1 /DEF=Homo sapiens kinesin family member 5B (KIF5B), mRNA. /FEA=mRNA /GEN=KIF5B /PROD=kinesin family member 5B /DB_XREF=gi:4758647 /UG=Hs.149436 kinesin family member 5B /FL=gb:NM_004521.1	
202027_at		NM_012264	gb:NM_012264.1 /DEF=Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA. /FEA=mRNA /GEN=C22ORF5 /PROD=chromosome 22 open reading frame 5 /DB_XREF=gi:7110634 /UG=Hs.182626 chromosome 22 open reading frame 5 /FL=gb:NM_012264.1	

205613_at		NM_016524	gb:NM_016524.1 /DEF=Homo sapiens BK protein (LOC51760), mRNA. /FEA=mRNA /GEN=LOC51760 /PROD=BK protein /DB_XREF=gi:7706558 /UG=Hs.26971 BK protein /FL=gb:BC004518.1 gb:AF220560.1 gb:NM_016524.1	
205935_at		NM_001451	gb:NM_001451.1 /DEF=Homo sapiens forkhead box F1 (FOXF1), mRNA. /FEA=mRNA /GEN=FOXF1 /PROD=forkhead box F1 /DB_XREF=gi:4503732 /UG=Hs.155591 forkhead box F1 /FL=gb:U13219.1 gb:NM_001451.1	

219532_at		NM_022726	gb:NM_022726.1 /DEF=Homo sapiens Stargardt disease 3 (autosomal dominant) (ELOVL4), mRNA. /FEA=mRNA /GEN=ELOVL4 /PROD=Stargardt disease 3 (autosomal dominant) /DB_XREF=gi:12232378 /UG=Hs.101915 Stargardt disease 3 (autosomal dominant) /FL=gb:AF277094.1 gb:NM_022726.1	
214284_s_at	FGF18	AA022949	fibroblast growth factor 18	

219340_s_at	AF123759	gb:AF123759.1 /DEF=Homo sapiens putative transmembrane protein (CLN8) mRNA, complete cds. /FEA=mRNA /GEN=CLN8 /PROD=putative transmembrane protein /DB_XREF=gi:6467264 /UG=Hs.127675 ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) /FL=gb:AF123757.1 gb:AF123759.1 gb:AF123760.1 gb:AF123761.1 gb:NM_018941.1
217770_at	NM_015937	gb:NM_015937.1 /DEF=Homo sapiens CGI-06 protein (LOC51604), mRNA. /FEA=mRNA /GEN=LOC51604 /PROD=CGI-06 protein /DB_XREF=gi:7706257 /UG=Hs.84038 CGI-06 protein /FL=gb:AF132940.1 gb:NM_015937.1

208978_at		U36190	gb:U36190.1 /DEF=Human cysteine-rich protein 2 (hCRP2) mRNA, complete cds. /FEA=mRNA /GEN=hCRP2 /PROD=cysteine-rich protein 2 /DB_XREF=gi:1399027 /UG=Hs.70327 cysteine-rich protein 2 /FL=gb:D42123.1 gb:BC000434.1 gb:BC001931.1 gb:U36190.1 gb:NM_001312.1	
204720_s_at	DNAJC6	AV729634	DnaJ (Hsp40) homolog, subfamily C, member 6	
214210_at	SLC25A17; PMP34	AL049764	match: proteins: Tr:O43808 Tr:O70579 Tr:O04200 Sw:P39953 Sw:P21245 Sw:Q00319 Sw:P40464 Tr:O22261 Tr:O13660; Human DNA sequence from clone RP3-362J20 on chromosome 22q13.1-13.31 Contains the 3' part of the gene for peroxisomal integral membrane protein, ESTs, STSs and GSSs, complete sequence.	NM_006358

202156_s_at	CUGBP2	N36839	CUG triplet repeat, RNA binding protein 2	
202158_s_at		NM_006561	gb:NM_006561.1 /DEF=Homo sapiens CUG triplet repeat, RNA-binding protein 2 (CUGBP2), mRNA. /FEA=mRNA /GEN=CUGBP2 /PROD=CUG triplet repeat, RNA-binding protein 2 /DB_XREF=gi:5729815 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1	
219779_at		NM_024721	gb:NM_024721.1 /DEF=Homo sapiens hypothetical protein FLJ20980 (FLJ20980), mRNA. /FEA=mRNA /GEN=FLJ20980 /PROD=hypothetical protein FLJ20980 /DB_XREF=gi:13376026 /UG=Hs.109314 hypothetical protein FLJ20980 /FL=gb:NM_024721.1	



203840_at		NM_003666	gb:NM_003666.1 /DEF=Homo sapiens basic leucine zipper nuclear factor 1 (JEM-1) (BLZF1), mRNA. /FEA=mRNA /GEN=BLZF1 /PROD=basic leucine zipper nuclear factor 1 (JEM-1) /DB_XREF=gi:4504804 /UG=Hs.158205 basic leucine zipper nuclear factor 1 (JEM-1) /FL=gb:U79751.1 gb:NM_003666.1	
217962_at		NM_018648	gb:NM_018648.1 /DEF=Homo sapiens nucleolar protein family A, member 3 (HACA small nucleolar RNPs) (NOLA3), mRNA. /FEA=mRNA /GEN=NOLA3 /PROD=nucleolar protein family A, member 3 (HACA small nucleolar RNPs) /DB_XREF=gi:8923941 /UG=Hs.14317 nucleolar protein family A, member 3 (HACA small nucleolar RNPs) /FL=gb:AB043104.1 gb:NM_018648.1	

214329_x_at	TNFSF10	AW474434	tumor necrosis factor (ligand) superfamily, member 10	
203946_s_at		U75667	gb:U75667.1 /DEF=Human arginase II mRNA, complete cds. /FEA=mRNA /PROD=arginase II /DB_XREF=gi:1763757 /UG=Hs.172851 arginase, type II /FL=gb:NM_001172.2 gb:BC001350.1 gb:D86724.1 gb:U75667.1 gb:U82256.1	
216942_s_at		D28586	Consensus includes gb:D28586.1 /DEF=Human mRNA for LFA- 3(delta D2), partial cds. /FEA=mRNA /PROD=LFA-3(delta D2) /DB_XREF=gi:466540 /UG=Hs.75626 CD58 antigen, (lymphocyte function-associated antigen 3)	

200611_s_at	AB010427	gb:AB010427.2 /DEF=Homo sapiens mRNA for NORI-1, complete cds. /FEA=mRNA /PROD=NORI-1 /DB_XREF=gi:5103672 /UG=Hs.85100 WD repeat domain 1 /FL=gb:BC000201.1 gb:BC002489.1 gb:AF020056.1 gb:AB010427.2 gb:NM_017491.1
222217_s_at	BC003654	Consensus includes gb:BC003654.1 /DEF=Homo sapiens, Similar to hypothetical protein MGC4365, clone IMAGE:3538020, mRNA, partial cds. /FEA=mRNA /PROD=Similar to hypothetical protein MGC4365 /DB_XREF=gi:13177768 /UG=Hs.109274 hypothetical protein MGC4365

215358_x_at		AK026980	Consensus includes gb:AK026980.1 /DEF=Homo sapiens cDNA: FLJ23327 fis, clone HEP12630, highly similar to HSZNF37 Homo sapiens ZNF37A mRNA for zinc finger protein. /FEA=mRNA /DB_XREF=gi:10439974 /UG=Hs.278064 Homo sapiens cDNA: FLJ23327 fis, clone HEP12630, highly similar to HSZNF37 Homo sapiens ZNF37A mRNA for zinc finger protein	
214725_at	FLJ40021	BE968773	hypothetical protein FLJ40021	

202787_s_at	U43784	gb:U43784.1 /DEF=Human mitogen activated protein kinase activated protein kinase-3 mRNA, complete cds. /FEA=mRNA /PROD=mitogen activated protein kinase activatedprotein kinase-3 /DB_XREF=gi:1256004 /UG=Hs.227789 mitogen-activated protein kinase-activated protein kinase 3 /FL=gb:U09578.1 gb:U43784.1 gb:BC001662.1 gb:NM_004635.1
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203759_at		NM_006278	<p>gb:NM_006278.1 /DEF=Homo sapiens sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase) (SIAT4C), mRNA. /FEA=mRNA /GEN=SIAT4C /PROD=sialyltransferase 4C (beta-galactosidasealpha-2,3-sialyltransferase) /DB_XREF=gi:5454057 /UG=Hs.75268 sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase) /FL=gb:L23767.1 gb:NM_006278.1</p>	
202009_at		NM_007284	<p>gb:NM_007284.1 /DEF=Homo sapiens protein tyrosine kinase 9-like (A6-related protein) (PTK9L), mRNA. /FEA=mRNA /GEN=PTK9L /PROD=protein tyrosine kinase 9-like (A6-relatedprotein) /DB_XREF=gi:6005845 /UG=Hs.6780 protein tyrosine kinase 9-like (A6-related protein) /FL=gb:BC000327.1 gb:BC003161.1 gb:NM_007284.1 gb:AL136773.1</p>	

212339_at		AB002336	Consensus includes gb:AL121895 /DEF=Human DNA sequence from clone RP11-234K24 on chromosome 20 Contains EPB41L1 gene encoding the erythrocyte membrane protein band 4.1-like protein (KIAA0338), a novel gene (CGI-23, DKFZP564N1363), a CpG island, ESTs, STSs and GSSs /FEA=mRNA_1 /DB_XREF=gi:9864397 /UG=Hs.26395 erythrocyte membrane protein band 4.1-like 1	
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219419_at		NM_024805	gb:NM_024805.1 /DEF=Homo sapiens hypothetical protein FLJ21172 (FLJ21172), mRNA. /FEA=mRNA /GEN=FLJ21172 /PROD=hypothetical protein FLJ21172 /DB_XREF=gi:13376184 /UG=Hs.164207 hypothetical protein FLJ21172 /FL=gb:NM_024805.1	
214435_x_at		NM_005402	Consensus includes gb:NM_005402.1 /DEF=Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA. /FEA=CDS /GEN=RALA /PROD=v-ral simian leukemia viral oncogene homolog A(ras related) /DB_XREF=gi:4885568 /UG=Hs.288757 v-ral simian leukemia viral oncogene homolog A (ras related) /FL=gb:M29893.1 gb:NM_005402.1	
213290_at	COL6A2	AL531750	collagen, type VI, alpha 2	

243_g_at	MAP4	M64571	microtubule-associated protein 4	NM_002375; NM_030884; NM_030885; NM_030983
202836_s_at		NM_006701	gb:NM_006701.1 /DEF=Homo sapiens similar to S. pombe dim1+ (DIM1), mRNA. /FEA=mRNA /GEN=DIM1 /PROD=similar to S. pombe dim1+ /DB_XREF=gi:5729801 /UG=Hs.5074 similar to S. pombe dim1+ /FL=gb:BC001046.1 gb:AF023611.1 gb:NM_006701.1 gb:AF146373.1	
205575_at		NM_006688	gb:NM_006688.1 /DEF=Homo sapiens C1q-related factor (CRF), mRNA. /FEA=mRNA /GEN=CRF /PROD=C1q-related factor /DB_XREF=gi:5729784 /UG=Hs.134012 C1q-related factor /FL=gb:AF095154.1 gb:NM_006688.1	
221840_at		AA775177	ESTs	
221844_x_at	XT3	AV756161	X transporter protein 3	

			gb:NM_002493.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) (NDUFB6), mRNA. /FEA=mRNA /GEN=NDUFB6 /PROD=NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 6 (17kD, B17) /DB_XREF=gi:4505364 /UG=Hs.109646 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17) /FL=gb:AF035840.1	
203613_s_at		NM_002493	gb:NM_002493.1 gb:AF067167.1	
			gb:NM_006810.1 /DEF=Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA. /FEA=mRNA /GEN=PDIR /PROD=for protein disulfide isomerase-related /DB_XREF=gi:5803120 /UG=Hs.76901 for protein disulfide isomerase-related /FL=gb:D49490.1	
203857_s_at		NM_006810	gb:NM_006810.1	
215438_x_at	GSPT1	BE906054	G1 to S phase transition 1	

201926_s_at	BC001288	gb:BC001288.1 /DEF=Homo sapiens, Similar to decay accelerating factor for complement (CD55, Cromer blood group system), clone MGC:5192, mRNA, complete cds. /FEA=mRNA /PROD=Similar to decay accelerating factor for complement (CD55, Cromer blood group system) /DB_XREF=gi:12654888 /UG=Hs.1369 decay accelerating factor for complement (CD55, Cromer blood group system) /FL=gb:NM_000574.1 gb:BC001288.1 gb:M31516.1
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205173_x_at		NM_001779	gb:NM_001779.1 /DEF=Homo sapiens CD58 antigen, (lymphocyte function-associated antigen 3) (CD58), mRNA. /FEA=mRNA /GEN=CD58 /PROD=CD58 antigen, (lymphocyte function-associated antigen 3) /DB_XREF=gi:4502676 /UG=Hs.75626 CD58 antigen, (lymphocyte function-associated antigen 3) /FL=gb:NM_001779.1	
215691_x_at	LOC51668	AV702994	HSPCO34 protein	

220446_s_at		NM_005769	gb:NM_005769.1 /DEF=Homo sapiens carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4 (CHST4), mRNA. /FEA=mRNA /GEN=CHST4 /PROD=carbohydrate (N-acetylglucosamine 6-O)sulfotransferase 4 /DB_XREF=gi:5031734 /UG=Hs.251383 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4 /FL=gb:AF131235.1 gb:NM_005769.1	
218243_at		NM_025158	gb:NM_025158.1 /DEF=Homo sapiens hypothetical protein FLJ22251 (FLJ22251), mRNA. /FEA=mRNA /GEN=FLJ22251 /PROD=hypothetical protein FLJ22251 /DB_XREF=gi:13376756 /UG=Hs.289064 hypothetical protein FLJ22251 /FL=gb:NM_025158.1	
213587_s_at	LOC155066	AI884867	vacuolar proton-ATPase subunit	

215283_at		U79248	Consensus includes gb:U79248.1 /DEF=Human clone 23826 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710195 /UG=Hs.12484 Human clone 23826 mRNA sequence	
219860_at		NM_025262	gb:NM_025262.1 /DEF=Homo sapiens G5C protein (G5C), mRNA. /FEA=mRNA /GEN=G5C /PROD=G5C protein /DB_XREF=gi:13376875 /UG=Hs.246845 G5C protein /FL=gb:NM_025262.1	
201124_at	ITGB5	AL048423	integrin, beta 5	
212502_at	FLJ14547	AV713053	hypothetical protein FLJ14547	

209365_s_at		U65932	gb:U65932.1 /DEF=Human extracellular matrix protein 1 (ECM1) mRNA, complete cds. /FEA=mRNA /GEN=ECM1 /PROD=extracellular matrix protein 1 /DB_XREF=gi:1488323 /UG=Hs.81071 extracellular matrix protein 1 /FL=gb:NM_004425.2 gb:U65932.1 gb:U68186.1	
218930_s_at		NM_018374	gb:NM_018374.1 /DEF=Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA. /FEA=mRNA /GEN=FLJ11273 /PROD=hypothetical protein FLJ11273 /DB_XREF=gi:8922965 /UG=Hs.3542 hypothetical protein FLJ11273 /FL=gb:NM_018374.1	



209054_s_at		AF083389	gb:AF083389.1 /DEF=Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product with complete exon 12, complete cds. /FEA=mRNA /GEN=WHSC1 /PROD=putative WHSC1 protein /DB_XREF=gi:4378016 /UG=Hs.110457 Wolf-Hirschhorn syndrome candidate 1 /FL=gb:AF083389.1	
201344_at		NM_003339	Consensus includes gb:BF196642 /FEA=EST /DB_XREF=gi:11084786 /DB_XREF=est:7m93c12.x1 /CLONE=IMAGE:3562750 /UG=Hs.108332 ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC45) /FL=gb:U39317.1 gb:NM_003339.1	
44111_at	VPS33B	AI672363	vacuolar protein sorting 33B (yeast)	

201090_x_at	NM_006082	gb:NM_006082.1 /DEF=Homo sapiens tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA. /FEA=mRNA /GEN=K-ALPHA-1 /PROD=tubulin, alpha, ubiquitous /DB_XREF=gi:5174476 /UG=Hs.278242 tubulin, alpha, ubiquitous /FL=gb:BC000696.1 gb:BC001128.1 gb:BC001209.1 gb:K00558.1 gb:AF081484.1 gb:NM_006082.1
201338_x_at	NM_002097	gb:NM_002097.1 /DEF=Homo sapiens general transcription factor IIIA (GTF3A), mRNA. /FEA=mRNA /GEN=GTF3A /PROD=general transcription factor IIIA /DB_XREF=gi:4753158 /UG=Hs.75113 general transcription factor IIIA /FL=gb:D32257.1 gb:NM_002097.1

200703_at		NM_003746	gb:NM_003746.1 /DEF=Homo sapiens dynein, cytoplasmic, light polypeptide (PIN), mRNA. /FEA=mRNA /GEN=PIN /PROD=dynein, cytoplasmic, light polypeptide /DB_XREF=gi:4505812 /UG=Hs.5120 dynein, cytoplasmic, light polypeptide /FL=gb:U32944.1 gb:NM_003746.1	
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200639_s_at	NM_003406	gb:NM_003406.1 /DEF=Homo sapiens tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA. /FEA=mRNA /GEN=YWHAZ /PROD=tyrosine 3-monooxygenasetryptophan5-monooxygenase activation protein, zeta polypeptide /DB_XREF=gi:4507952 /UG=Hs.75103 tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, zeta polypeptide /FL=gb:BC003623.1 gb:M86400.1 gb:NM_003406.1 gb:U28964.1	
212052_s_at	AB014576	Consensus includes gb:AB014576.1 /DEF=Homo sapiens mRNA for KIAA0676 protein, partial cds. /FEA=mRNA /GEN=KIAA0676 /PROD=KIAA0676 protein /DB_XREF=gi:3327165 /UG=Hs.155829 KIAA0676 protein	

212313_at		BC004344	Consensus includes gb:BC004344.1 /DEF=Homo sapiens, clone IMAGE:3633354, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3633354) /DB_XREF=gi:13279286 /UG=Hs.5019 Homo sapiens, clone IMAGE:3633354, mRNA, partial cds	
200660_at		NM_005620	gb:NM_005620.1 /DEF=Homo sapiens S100 calcium-binding protein A11 (calgizzarin) (S100A11), mRNA. /FEA=mRNA /GEN=S100A11 /PROD=S100 calcium-binding protein A11 /DB_XREF=gi:5032056 /UG=Hs.256290 S100 calcium- binding protein A11 (calgizzarin) /FL=gb:D49355.1 gb:BC001410.1 gb:D50374.1 gb:NM_005620.1 gb:D38583.1	

211072_x_at		BC006481	gb:BC006481.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:4387, mRNA, complete cds. /FEA=mRNA /PROD=tubulin alpha 1 /DB_XREF=gi:13623706 /FL=gb:BC006481.1	
217809_at		NM_014038	gb:NM_014038.1 /DEF=Homo sapiens HSPC028 protein (HSPC028), mRNA. /FEA=mRNA /GEN=HSPC028 /PROD=HSPC028 protein /DB_XREF=gi:7661743 /UG=Hs.5216 HSPC028 protein /FL=gb:AF110323.1 gb:BC003056.1 gb:AF083246.1 gb:NM_014038.1	
208398_s_at		NM_004865	gb:NM_004865.1 /DEF=Homo sapiens TBP-like 1 (TBPL1), mRNA. /FEA=mRNA /GEN=TBPL1 /PROD=TBP-like 1 /DB_XREF=gi:4759233 /UG=Hs.13993 TBP-like 1 /FL=gb:AF130312.1 gb:NM_004865.1	

207812_s_at		NM_015530	gb:NM_015530.1 /DEF=Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA. /FEA=mRNA /GEN=DKFZP434D156 /PROD=DKFZP434D156 protein /DB_XREF=gi:7661569 /UG=Hs.6880 DKFZP434D156 protein /FL=gb:NM_015530.1	
201622_at		NM_014390	gb:NM_014390.1 /DEF=Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA. /FEA=mRNA /GEN=p100 /PROD=EBNA-2 co-activator (100kD) /DB_XREF=gi:7657430 /UG=Hs.79093 EBNA-2 co-activator (100kD) /FL=gb:NM_014390.1 gb:U22055.1	

212959_s_at	AK001821	Consensus includes gb:AK001821.1 /DEF=Homo sapiens cDNA FLJ10959 fis, clone PLACE1000562. /FEA=mRNA /DB_XREF=gi:7023328 /UG=Hs.7041 hypothetical protein DKFZp762B226
216282_x_at	AJ224143	Consensus includes gb:AJ224143.1 /DEF=Homo sapiens mRNA variant alfa for RNA polymerase II subunit 3. /FEA=mRNA /GEN=RPB3 /PROD=RNA polymerase II subunit /DB_XREF=gi:2920708 /UG=Hs.79402 polymerase (RNA) II (DNA directed) polypeptide C (33kD)



208540_x_at		NM_021039	gb:NM_021039.1 /DEF=Homo sapiens S100 calcium-binding protein A14 (calgizzarin) (S100A14), mRNA. /FEA=CDS /GEN=S100A14 /PROD=S100 calcium-binding protein A14 (calgizzarin) /DB_XREF=gi:10567825 /UG=Hs.247697 S100 calcium-binding protein A14 (calgizzarin) /FL=gb:NM_021039.1	
201645_at		NM_002160	gb:NM_002160.1 /DEF=Homo sapiens hexabrachion (tenascin C, cytotactin) (HXB), mRNA. /FEA=mRNA /GEN=HXB /PROD=hexabrachion (tenascin C, cytotactin) /DB_XREF=gi:4504548 /UG=Hs.289114 hexabrachion (tenascin C, cytotactin) /FL=gb:M55618.1 gb:NM_002160.1	

212453_at		AB033105	Consensus includes gb:AB033105.1 /DEF=Homo sapiens mRNA for KIAA1279 protein, partial cds. /FEA=mRNA /GEN=KIAA1279 /PROD=KIAA1279 protein /DB_XREF=gi:6331321 /UG=Hs.172854 DKFZP586B0923 protein	
202657_s_at		NM_014755	gb:NM_014755.1 /DEF=Homo sapiens KIAA0127 gene product (KIAA0127), mRNA. /FEA=mRNA /GEN=KIAA0127 /PROD=KIAA0127 gene product /DB_XREF=gi:7661925 /UG=Hs.77293 KIAA0127 gene product /FL=gb:D50917.1 gb:NM_014755.1	
207842_s_at		NM_007359	gb:NM_007359.1 /DEF=Homo sapiens MLN51 protein (MLN51), mRNA. /FEA=mRNA /GEN=MLN51 /PROD=MLN51 protein /DB_XREF=gi:6678887 /UG=Hs.83422 MLN51 protein /FL=gb:NM_007359.1	

218331_s_at		NM_017782	gb:NM_017782.1 /DEF=Homo sapiens hypothetical protein FLJ20360 (FLJ20360), mRNA. /FEA=mRNA /GEN=FLJ20360 /PROD=hypothetical protein FLJ20360 /DB_XREF=gi:8923334 /UG=Hs.26434 hypothetical protein FLJ20360 /FL=gb:BC001759.1 gb:NM_017782.1	
218353_at		NM_025226	gb:NM_025226.1 /DEF=Homo sapiens MSTP032 protein (MSTP032), mRNA. /FEA=mRNA /GEN=MSTP032 /PROD=MSTP032 protein /DB_XREF=gi:13376831 /UG=Hs.274368 MSTP032 protein /FL=gb:AF113212.1 gb:NM_025226.1	
213326_at	VAMP1	AU150319	vesicle-associated membrane protein 1 (synaptobrevin 1)	

210282_at		AL136621	gb:AL136621.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564B162 (from clone DKFZp564B162); complete cds. /FEA=mRNA /GEN=DKFZp564B162 /PROD=hypothetical protein /DB_XREF=gi:12052767 /UG=Hs.109526 zinc finger protein 198 /FL=gb:AL136621.1	
211666_x_at		L22453	gb:L22453.1 /DEF=Homo sapiens HIV-1 TAR RNA binding protein (TARBP-b) mRNA, complete cds. /FEA=mRNA /GEN=TARBP-b /DB_XREF=gi:347963 /FL=gb:L22453.1	

201738_at		NM_005875	gb:NM_005875.1 /DEF=Homo sapiens translation factor sui1 homolog (GC20), mRNA. /FEA=mRNA /GEN=GC20 /PROD=translation factor sui1 homolog /DB_XREF=gi:5031710 /UG=Hs.21756 translation factor sui1 homolog /FL=gb:AF064607.1 gb:AF077052.1 gb:NM_005875.1 gb:AF263452.1	
203195_s_at		NM_005387	gb:NM_005387.2 /DEF=Homo sapiens nucleoporin 98kD (NUP98), mRNA. /FEA=mRNA /GEN=NUP98 /PROD=nucleoporin 98kD /DB_XREF=gi:11120677 /UG=Hs.112255 nucleoporin 98kD /FL=gb:NM_005387.2 gb:AF071076.1	

			gb:NM_012215.1 /DEF=Homo sapiens meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA. /FEA=mRNA /GEN=MGEA5 /PROD=meningioma expressed antigen 5 (hyaluronidase) /DB_XREF=gi:11024697 /UG=Hs.5734 meningioma expressed antigen 5 (hyaluronidase) /FL=gb:AF036144.2 gb:NM_012215.1	
200899_s_at		NM_012215		
			gb:NM_004733.2 /DEF=Homo sapiens acetyl-Coenzyme A transporter (ACATN), mRNA. /FEA=mRNA /GEN=ACATN /PROD=acetyl-Coenzyme A transporter /DB_XREF=gi:6042194 /UG=Hs.285176 acetyl-Coenzyme A transporter /FL=gb:D88152.1 gb:NM_004733.2	
203165_s_at		NM_004733		
209161_at	PRPF4	AI184802	PRP4 pre-mRNA processing factor 4 homolog (yeast)	

219433_at		NM_017745	gb:NM_017745.1 /DEF=Homo sapiens hypothetical protein FLJ20285 (FLJ20285), mRNA. /FEA=mRNA /GEN=FLJ20285 /PROD=hypothetical protein FLJ20285 /DB_XREF=gi:8923266 /UG=Hs.278732 hypothetical protein FLJ20285 /FL=gb:NM_017745.1	
217317_s_at		AB002391	Consensus includes gb:AB002391.2 /DEF=Homo sapiens mRNA for KIAA0393 protein, partial cds. /FEA=mRNA /GEN=KIAA0393 /PROD=KIAA0393 protein /DB_XREF=gi:6683696 /UG=Hs.266933 hect domain and RLD 2	

202795_x_at		NM_007032	gb:NM_007032.1 /DEF=Homo sapiens putative nuclear protein (HRIHFB2122), mRNA. /FEA=mRNA /GEN=HRIHFB2122 /PROD=putative nuclear protein /DB_XREF=gi:10334853 /UG=Hs.40342 putative nuclear protein /FL=gb:NM_007032.1	
212781_at		AK026954	Consensus includes gb:AK026954.1 /DEF=Homo sapiens cDNA: FLJ23301 fis, clone HEP11120. /FEA=mRNA /DB_XREF=gi:10439935 /UG=Hs.91065 hypothetical protein DKFZp761B2423	
213387_at		AB033066	Consensus includes gb:AB033066.1 /DEF=Homo sapiens mRNA for KIAA1240 protein, partial cds. /FEA=mRNA /GEN=KIAA1240 /PROD=KIAA1240 protein /DB_XREF=gi:6330790 /UG=Hs.62576 KIAA1240 protein	



201161_s_at		NM_003651	gb:NM_003651.1 /DEF=Homo sapiens cold shock domain protein A (CSDA), mRNA. /FEA=mRNA /GEN=CSDA /PROD=cold shock domain protein A /DB_XREF=gi:4503070 /UG=Hs.1139 cold shock domain protein A /FL=gb:NM_003651.1	
203962_s_at		NM_006393	gb:NM_006393.1 /DEF=Homo sapiens nebulette (NEBL), mRNA. /FEA=mRNA /GEN=NEBL /PROD=nebulette /DB_XREF=gi:5453757 /UG=Hs.5025 nebulette /FL=gb:NM_006393.1	
213878_at	RECQL	AI685944	RecQ protein-like (DNA helicase Q1-like)	

206323_x_at		NM_002547	gb:NM_002547.1 /DEF=Homo sapiens oligophrenin 1 (OPHN1), mRNA. /FEA=mRNA /GEN=OPHN1 /PROD=oligophrenin 1, Rho-GTPase acivating protein /DB_XREF=gi:4505506 /UG=Hs.128824 oligophrenin 1 /FL=gb:NM_002547.1	
218016_s_at		NM_018119	gb:NM_018119.1 /DEF=Homo sapiens hypothetical protein FLJ10509 (FLJ10509), mRNA. /FEA=mRNA /GEN=FLJ10509 /PROD=hypothetical protein FLJ10509 /DB_XREF=gi:8922476 /UG=Hs.274319 hypothetical protein FLJ10509 /FL=gb:BC000285.1 gb:NM_018119.1	

213546_at		AL050378	Consensus includes gb:AL050378.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone DKFZp586I1420); partial cds. /FEA=mRNA /GEN=DKFZp586I1420 /PROD=hypothetical protein /DB_XREF=gi:4914581 /UG=Hs.112423 Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone DKFZp586I1420); partial cds	
209293_x_at		U16153	gb:U16153.1 /DEF=Human Id-4H protein mRNA, complete cds. /FEA=mRNA /PROD=Id-4H protein /DB_XREF=gi:625095 /UG=Hs.34853 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein /FL=gb:NM_001546.1 gb:U16153.1 gb:U28368.1	

200064_at		AF275719	gb:AF275719.1 /DEF=Homo sapiens isolate Liv chaperone protein HSP90 beta (HSP90BETA) mRNA, complete cds. /FEA=mRNA /GEN=HSP90BETA /PROD=chaperone protein HSP90 beta /DB_XREF=gi:9082288 /UG=Hs.74335 heat shock 90kD protein 1, beta /FL=gb:BC004928.1 gb:M16660.1 gb:NM_007355.1 gb:AF275719.1	
200072_s_at		AF061832	gb:AF061832.1 /DEF=Homo sapiens M4 protein deletion mutant mRNA, complete cds. /FEA=mRNA /PROD=M4 protein deletion mutant /DB_XREF=gi:3126877 /UG=Hs.79024 heterogeneous nuclear ribonucleoprotein M /FL=gb:AF061832.1	

200643_at		NM_005336	gb:NM_005336.1 /DEF=Homo sapiens high density lipoprotein binding protein (vigilin) (HDLBP), mRNA. /FEA=mRNA /GEN=HDLBP /PROD=high density lipoprotein binding protein /DB_XREF=gi:4885408 /UG=Hs.177516 high density lipoprotein binding protein (vigilin) /FL=gb:BC001179.1 gb:M64098.1 gb:NM_005336.1	
201589_at		D80000	Consensus includes gb:D80000.1 /DEF=Human mRNA for KIAA0178 gene, partial cds. /FEA=mRNA /GEN=KIAA0178 /DB_XREF=gi:1136415 /UG=Hs.211602 SMC1 (structural maintenance of chromosomes 1, yeast)-like 1 /FL=gb:NM_006306.1	
41644_at	KIAA0790	AB018333	KIAA0790 protein	NM_015278
202568_s_at	MARK3	AI745639	MAP/microtubule affinity-regulating kinase 3	
221834_at	SIAH1	U70056	seven in absentia homolog 1 (Drosophila)	
47773_at	KIAA1332	AA836114	KIAA1332 protein	

202376_at		NM_001085	gb:NM_001085.2 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 (SERPINA3), mRNA. /FEA=mRNA /GEN=SERPINA3 /PROD=alpha-1-antichymotrypsin, precursor /DB_XREF=gi:9665246 /UG=Hs.234726 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 /FL=gb:BC003559.1 gb:K01500.1 gb:NM_001085.2	
222163_s_at	MGC5347	BE890973	hypothetical protein MGC5347	

210314_x_at	AF114013	gb:AF114013.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1gamma mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-related deathligand-1gamma /DB_XREF=gi:7328557 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF136294.1 gb:AF114013.1
205524_s_at	NM_001884	gb:NM_001884.1 /DEF=Homo sapiens cartilage linking protein 1 (CTRL1), mRNA. /FEA=mRNA /GEN=CTRL1 /PROD=cartilage linking protein 1 /DB_XREF=gi:4503052 /UG=Hs.2799 cartilage linking protein 1 /FL=gb:U43328.1 gb:NM_001884.1

204215_at		NM_024315	gb:NM_024315.1 /DEF=Homo sapiens hypothetical protein MGC4175 (MGC4175), mRNA. /FEA=mRNA /GEN=MGC4175 /PROD=hypothetical protein MGC4175 /DB_XREF=gi:13236556 /UG=Hs.322404 hypothetical protein MGC4175 /FL=gb:BC002837.1 gb:NM_024315.1	
220890_s_at		NM_016355	gb:NM_016355.1 /DEF=Homo sapiens hqp0256 protein (LOC51202), mRNA. /FEA=mRNA /GEN=LOC51202 /PROD=hqp0256 protein /DB_XREF=gi:10047107 /UG=Hs.284288 hqp0256 protein /FL=gb:NM_016355.1 gb:AF078843.1	



219717_at		NM_017741	gb:NM_017741.1 /DEF=Homo sapiens hypothetical protein FLJ20280 (FLJ20280), mRNA. /FEA=mRNA /GEN=FLJ20280 /PROD=hypothetical protein FLJ20280 /DB_XREF=gi:8923256 /UG=Hs.270134 hypothetical protein FLJ20280 /FL=gb:NM_017741.1	
213538_at	SON	AI936458	SON DNA binding protein	
205089_at		NM_003416	gb:NM_003416.1 /DEF=Homo sapiens zinc finger protein 7 (KOX 4, clone HF.16) (ZNF7), mRNA. /FEA=mRNA /GEN=ZNF7 /PROD=zinc finger protein 7 (KOX 4, clone HF.16) /DB_XREF=gi:4508034 /UG=Hs.2076 zinc finger protein 7 (KOX 4, clone HF.16) /FL=gb:M29580.1 gb:NM_003416.1	

208691_at		BC001188	gb:BC001188.1 /DEF=Homo sapiens, transferrin receptor (p90, CD71), clone MGC:3151, mRNA, complete cds. /FEA=mRNA /PROD=transferrin receptor (p90, CD71) /DB_XREF=gi:12654696 /UG=Hs.77356 transferrin receptor (p90, CD71) /FL=gb:BC001188.1 gb:M11507.1	
209170_s_at		AF016004	gb:AF016004.1 /DEF=Homo sapiens m6b1 mRNA, complete cds. /FEA=mRNA /GEN=m6b1 /DB_XREF=gi:3387766 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	
209167_at		AF016004	Consensus includes gb:AI419030 /FEA=EST /DB_XREF=gi:4264961 /DB_XREF=est:tf53b01.x1 /CLONE=IMAGE:2102953 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	

218134_s_at		NM_018047	gb:NM_018047.1 /DEF=Homo sapiens hypothetical protein FLJ10290 (FLJ10290), mRNA. /FEA=mRNA /GEN=FLJ10290 /PROD=hypothetical protein FLJ10290 /DB_XREF=gi:8922327 /UG=Hs.25516 hypothetical protein FLJ10290 /FL=gb:AL136933.1 gb:BC003402.1 gb:NM_018047.1	
203707_at		NM_005741	gb:NM_005741.1 /DEF=Homo sapiens zinc finger protein 263 (ZNF263), mRNA. /FEA=mRNA /GEN=ZNF263 /PROD=zinc finger protein 263 /DB_XREF=gi:5032240 /UG=Hs.182528 zinc finger protein 263 /FL=gb:D88827.1 gb:NM_005741.1	

218651_s_at		NM_018357	gb:NM_018357.1 /DEF=Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA. /FEA=mRNA /GEN=FLJ11196 /PROD=hypothetical protein FLJ11196 /DB_XREF=gi:8922933 /UG=Hs.6166 hypothetical protein FLJ11196 /FL=gb:NM_018357.1	
203313_s_at		NM_003244	gb:NM_003244.1 /DEF=Homo sapiens TG-interacting factor (TALE family homeobox) (TGIF), mRNA. /FEA=mRNA /GEN=TGIF /PROD=TG-interacting factor (TALE family homeobox) /DB_XREF=gi:4507472 /UG=Hs.90077 TG-interacting factor (TALE family homeobox) /FL=gb:BC000814.1 gb:NM_003244.1 gb:AF179900.1	

218429_s_at		NM_018381	gb:NM_018381.1 /DEF=Homo sapiens hypothetical protein FLJ11286 (FLJ11286), mRNA. /FEA=mRNA /GEN=FLJ11286 /PROD=hypothetical protein FLJ11286 /DB_XREF=gi:8922978 /UG=Hs.12151 hypothetical protein FLJ11286 /FL=gb:NM_018381.1	
206729_at		NM_001243	gb:NM_001243.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 8 (TNFRSF8), mRNA. /FEA=mRNA /GEN=TNFRSF8 /PROD=CD30 antigen (Ki-1 antigen) /DB_XREF=gi:4507588 /UG=Hs.1314 tumor necrosis factor receptor superfamily, member 8 /FL=gb:D86042.1 gb:M83554.1 gb:NM_001243.1	

215354_s_at		BC002875	Consensus includes gb:BC002875.1 /DEF=Homo sapiens, clone IMAGE:3940843, mRNA, partial cds. /FEA=mRNA /PROD=Unknown (protein for IMAGE:3940843) /DB_XREF=gi:12804044 /UG=Hs.274149 proline and glutamic acid rich nuclear protein	
207264_at		NM_016657	gb:NM_016657.1 /DEF=Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDEL3), transcript variant 2, mRNA. /FEA=mRNA /GEN=KDEL3 /PROD=KDEL receptor 3, isoform b /DB_XREF=gi:8051610 /UG=Hs.250696 KDEL (Lys-Asp- Glu-Leu) endoplasmic reticulum protein retention receptor 3 /FL=gb:NM_016657.1	

221123_x_at		NM_018660	gb:NM_018660.1 /DEF=Homo sapiens papillomavirus regulatory factor PRF-1 (LOC55893), mRNA. /FEA=mRNA /GEN=LOC55893 /PROD=papillomavirus regulatory factor PRF-1 /DB_XREF=gi:8923886 /UG=Hs.27410 papillomavirus regulatory factor PRF-1 /FL=gb:AF263928.1 gb:NM_018660.1	
206068_s_at	ACADL	AI367275	acyl-Coenzyme A dehydrogenase, long chain	
216048_s_at		AK023621	Consensus includes gb:AK023621.1 /DEF=Homo sapiens cDNA FLJ13559 fis, clone PLACE1007852, highly similar to Homo sapiens mRNA for KIAA0878 protein. /FEA=mRNA /DB_XREF=gi:10435602 /UG=Hs.188006 KIAA0878 protein	
212776_s_at	KIAA0657	AI978623	KIAA0657 protein	

201531_at		NM_003407	gb:NM_003407.1 /DEF=Homo sapiens zinc finger protein homologous to Zfp-36 in mouse (ZFP36), mRNA. /FEA=mRNA /GEN=ZFP36 /PROD=zinc finger protein homologous to Zfp-36 inmouse /DB_XREF=gi:4507960 /UG=Hs.1665 zinc finger protein homologous to Zfp-36 in mouse /FL=gb:M92843.1 gb:M63625.1 gb:NM_003407.1	
202747_s_at		NM_004867	gb:NM_004867.1 /DEF=Homo sapiens integral membrane protein 2A (ITM2A), mRNA. /FEA=mRNA /GEN=ITM2A /PROD=integral membrane protein 2A /DB_XREF=gi:4758223 /UG=Hs.17109 integral membrane protein 2A /FL=gb:AF038953.1 gb:NM_004867.1	
213006_at	CEBPD	AV655640	CCAAT/enhancer binding protein (C/EBP), delta	



209305_s_at		AF078077	gb:AF078077.1 /DEF=Homo sapiens growth arrest and DNA-damage-inducible protein GADD45beta mRNA, complete cds. /FEA=mRNA /PROD=growth arrest and DNA-damage-inducible proteinGADD45beta /DB_XREF=gi:3978391 /UG=Hs.110571 growth arrest and DNA-damage-inducible, beta /FL=gb:AF087853.1 gb:AF078077.1	
207574_s_at		NM_015675	gb:NM_015675.1 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. /FEA=mRNA /GEN=GADD45B /PROD=DKFZP566B133 protein /DB_XREF=gi:9945331 /UG=Hs.110571 growth arrest and DNA-damage-inducible, beta /FL=gb:AF090950.1 gb:NM_015675.1	
222041_at		BG235929	ESTs	

204377_s_at		NM_014703	gb:NM_014703.1 /DEF=Homo sapiens KIAA0800 gene product (KIAA0800), mRNA. /FEA=mRNA /GEN=KIAA0800 /PROD=KIAA0800 gene product /DB_XREF=gi:7662315 /UG=Hs.118738 KIAA0800 gene product /FL=gb:AB018343.1 gb:NM_014703.1	
217741_s_at	ZNF216	AW471220	zinc finger protein 216	
204563_at		NM_000655	gb:NM_000655.2 /DEF=Homo sapiens selectin L (lymphocyte adhesion molecule 1) (SELL), mRNA. /FEA=mRNA /GEN=SELL /PROD=selectin L /DB_XREF=gi:5713320 /UG=Hs.82848 selectin L (lymphocyte adhesion molecule 1) /FL=gb:M25280.1 gb:NM_000655.2	

204406_at		NM_002019	gb:NM_002019.1 /DEF=Homo sapiens fms-related tyrosine kinase 1 (vascular endothelial growth factorvascular permeability factor receptor) (FLT1), mRNA. /FEA=mRNA /GEN=FLT1 /PROD=fms-related tyrosine kinase 1 (vascularendothelial growth factorvascular permeability factorreceptor) /DB_XREF=gi:4503748 /UG=Hs.138671 fms-related tyrosine kinase 1 (vascular endothelial growth factorvascular permeability factor receptor) /FL=gb:AF063657.1 gb:NM_002019.1	
205976_at		NM_014929	gb:NM_014929.1 /DEF=Homo sapiens KIAA0971 protein (KIAA0971), mRNA. /FEA=mRNA /GEN=KIAA0971 /PROD=KIAA0971 protein /DB_XREF=gi:7662421 /UG=Hs.84429 KIAA0971 protein /FL=gb:AB023188.1 gb:NM_014929.1	

202315_s_at		NM_004327	gb:NM_004327.2 /DEF=Homo sapiens breakpoint cluster region (BCR), transcript variant 1, mRNA. /FEA=mRNA /GEN=BCR /PROD=breakpoint cluster region, isoform 1 /DB_XREF=gi:11038638 /UG=Hs.234799 breakpoint cluster region /FL=gb:NM_004327.2	
201896_s_at		BC001425	gb:BC001425.1 /DEF=Homo sapiens, Similar to differential display and activated by p53, clone MGC:1780, mRNA, complete cds. /FEA=mRNA /PROD=Similar to differential display and activated by p53 /DB_XREF=gi:12655140 /UG=Hs.77550 CDC28 protein kinase 1 /FL=gb:BC001425.1 gb:AF274941.1 gb:AF279897.1 gb:NM_001826.1	
206025_s_at	TNFAIP6	AW188198	tumor necrosis factor, alpha-induced protein 6	

64942_at		AI937160	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]	
211343_s_at		M33653	gb:M33653.1 /DEF=Human (clones HT-125,133) alpha-2 type IV collagen (COL4A2) mRNA, complete cds. /FEA=mRNA /GEN=COL4A2 /PROD=alpha-2 type IV collagen /DB_XREF=gi:180828 /UG=Hs.211933 collagen, type XIII, alpha 1 /FL=gb:M33653.1	
214119_s_at	FKBP1A	AI936769	FK506 binding protein 1A, 12kDa	
217772_s_at		NM_014342	gb:NM_014342.1 /DEF=Homo sapiens mitochondrial carrier homolog 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=MTCH2 /PROD=mitochondrial carrier homolog 2 /DB_XREF=gi:7657346 /UG=Hs.279609 mitochondrial carrier homolog 2 /FL=gb:BC000875.1 gb:AF085361.1 gb:AF176008.1 gb:NM_014342.1	

209222_s_at		BC000296	gb:BC000296.1 /DEF=Homo sapiens, Similar to KIAA0772 gene product, clone MGC:8342, mRNA, complete cds. /FEA=mRNA /PROD=Similar to KIAA0772 gene product /DB_XREF=gi:12653062 /UG=Hs.15519 KIAA0772 gene product /FL=gb:BC000296.1 gb:BC004455.1	
212252_at	CAMKK2	AA181179	calcium/calmodulin-dependent protein kinase kinase 2, beta	
206176_at		NM_001718	gb:NM_001718.2 /DEF=Homo sapiens bone morphogenetic protein 6 (BMP6), mRNA. /FEA=mRNA /GEN=BMP6 /PROD=bone morphogenetic protein 6 precursor /DB_XREF=gi:4809281 /UG=Hs.285671 bone morphogenetic protein 6 /FL=gb:M60315.1 gb:NM_001718.2	
213030_s_at	PLXNA2	AI688418	plexin A2	

208912_s_at		BC001362	gb:BC001362.1 /DEF=Homo sapiens, 2,3-cyclic nucleotide 3 phosphodiesterase, clone MGC:2262, mRNA, complete cds. /FEA=mRNA /PROD=2,3-cyclic nucleotide 3 phosphodiesterase /DB_XREF=gi:12655028 /UG=Hs.150741 2,3-cyclic nucleotide 3 phosphodiesterase /FL=gb:BC001362.1 gb:M19650.1	
220432_s_at		NM_016593	gb:NM_016593.1 /DEF=Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA. /FEA=mRNA /GEN=CYP39A1 /PROD=oxysterol 7alpha-hydroxylase /DB_XREF=gi:7706128 /UG=Hs.20766 oxysterol 7alpha-hydroxylase /FL=gb:AF237982.1 gb:NM_016593.1	

			gb:NM_006455.1 /DEF=Homo sapiens nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein (SC65), mRNA. /FEA=mRNA /GEN=SC65 /PROD=nucleolar autoantigen (55kD) similar to ratsynaptonemal complex protein /DB_XREF=gi:5454037 /UG=Hs.207251 nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein /FL=gb:BC001047.1 gb:U47621.1 gb:NM_006455.1	
204078_at		NM_006455		
221987_s_at	SRR	AI803633	serine racemase	
			gb:NM_018153.1 /DEF=Homo sapiens hypothetical protein FLJ10601 (FLJ10601), mRNA. /FEA=mRNA /GEN=FLJ10601 /PROD=hypothetical protein FLJ10601 /DB_XREF=gi:8922545 /UG=Hs.257174 hypothetical protein FLJ10601 /FL=gb:NM_018153.1	
220092_s_at		NM_018153		



			gb:L07515.1 /DEF=Human heterochromatin protein homologue (HP1) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:184310 /UG=Hs.89232 chromobox homolog 5 (Drosophila HP1 alpha) /FL=gb:L07515.1 gb:NM_012117.1	
209715_at		L07515		
213069_at	KIAA1237	AI148659	KIAA1237 protein	
			Consensus includes gb:AI357376 /FEA=EST /DB_XREF=gi:4108997 /DB_XREF=est:qy13a06.x1 /CLONE=IMAGE:2011858 /UG=Hs.12017 homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator	
212445_s_at		AB007899		
209197_at	SYT11	AA626780	synaptotagmin XI	



220603_s_at		NM_018349	gb:NM_018349.1 /DEF=Homo sapiens hypothetical protein FLJ11175 (FLJ11175), mRNA. /FEA=mRNA /GEN=FLJ11175 /PROD=hypothetical protein FLJ11175 /DB_XREF=gi:8922916 /UG=Hs.33368 hypothetical protein FLJ11175 /FL=gb:NM_018349.1	
218534_s_at		NM_018046	gb:NM_018046.1 /DEF=Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA. /FEA=mRNA /GEN=FLJ10283 /PROD=hypothetical protein FLJ10283 /DB_XREF=gi:8922325 /UG=Hs.284216 hypothetical protein FLJ10283 /FL=gb:NM_018046.1	
221833_at	SIAH1	U70056	seven in absentia homolog 1 (Drosophila)	

221508_at		AF181985	gb:AF181985.1 /DEF=Homo sapiens serinethreonine kinase (KDS) mRNA, complete cds. /FEA=mRNA /GEN=KDS /PROD=serinethreonine kinase /DB_XREF=gi:6708149 /UG=Hs.12040 STE20-like kinase /FL=gb:BC002756.1 gb:AF181985.1	
221691_x_at		AB042278	gb:AB042278.1 /DEF=Homo sapiens mRNA for nucleophosminB23.2, complete cds. /FEA=mRNA /PROD=nucleophosminB23.2 /DB_XREF=gi:13536990 /FL=gb:AB042278.1	

218098_at		NM_006420	Consensus includes gb:AL121903 /DEF=Human DNA sequence from clone RP1-155G6 on chromosome 20 Contains part of the gene for brefeldin A-inhibited guanine nucleotide-exchange protein 2, part of the gene for CSE1L (chromosome segregation 1 (yeast homolog)-like), ESTs, STSs, GSSs and a... /FEA=mRNA /DB_XREF=gi:7330682 /UG=Hs.118249 brefeldin A-inhibited guanine nucleotide-exchange protein 2 /FL=gb:AF084521.1 gb:NM_006420.1	
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220742_s_at		NM_018297	gb:NM_018297.1 /DEF=Homo sapiens hypothetical protein FLJ11005 (FLJ11005), mRNA. /FEA=mRNA /GEN=FLJ11005 /PROD=hypothetical protein FLJ11005 /DB_XREF=gi:8922817 /UG=Hs.63657 hypothetical protein FLJ11005 /FL=gb:NM_018297.1	
218127_at	NFYB	AI804118	nuclear transcription factor Y, beta	

218408_at		NM_012456	gb:NM_012456.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 10 (yeast) homolog (TIMM10), mRNA. /FEA=mRNA /GEN=TIMM10 /PROD=translocase of inner mitochondrial membrane 10(yeast) homolog /DB_XREF=gi:6912707 /UG=Hs.109571 translocase of inner mitochondrial membrane 10 (yeast) homolog /FL=gb:AF150089.1 gb:AF152354.1 gb:NM_012456.1	
217967_s_at		AF288391	gb:AF288391.1 /DEF=Homo sapiens C1orf24 mRNA, complete cds. /FEA=mRNA /PROD=C1orf24 /DB_XREF=gi:12620191 /UG=Hs.48778 niban protein /FL=gb:AB050477.1 gb:NM_022083.1 gb:AF288391.1	
34206_at	CENTD2	AB018325	centaurin, delta 2	NM_015242; NM_139181

218364_at		NM_017724	gb:NM_017724.1 /DEF=Homo sapiens leucine rich repeat (in FLII) interacting protein 2 (LRRFIP2), mRNA. /FEA=mRNA /GEN=LRRFIP2 /PROD=leucine rich repeat (in FLII) interactingprotein 2 /DB_XREF=gi:8923223 /UG=Hs.57672 leucine rich repeat (in FLII) interacting protein 2 /FL=gb:NM_017724.1	
219544_at		NM_024808	gb:NM_024808.1 /DEF=Homo sapiens hypothetical protein FLJ22624 (FLJ22624), mRNA. /FEA=mRNA /GEN=FLJ22624 /PROD=hypothetical protein FLJ22624 /DB_XREF=gi:13376190 /UG=Hs.166425 hypothetical protein FLJ22624 /FL=gb:NM_024808.1	



219037_at		NM_016052	gb:NM_016052.1 /DEF=Homo sapiens CGI-115 protein (LOC51018), mRNA. /FEA=mRNA /GEN=LOC51018 /PROD=CGI-115 protein /DB_XREF=gi:7705619 /UG=Hs.56043 CGI-115 protein /FL=gb:AF151873.1 gb:NM_016052.1	
219434_at		NM_018643	gb:NM_018643.1 /DEF=Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), mRNA. /FEA=mRNA /GEN=TREM1 /PROD=triggering receptor expressed on myeloid cells1 /DB_XREF=gi:8924261 /UG=Hs.283022 triggering receptor expressed on myeloid cells 1 /FL=gb:AF196329.1 gb:NM_018643.1 gb:AF287008.1	

218041_x_at	NM_018573	gb:NM_018573.1 /DEF=Homo sapiens hypothetical protein PRO1068 (PRO1068), mRNA. /FEA=mRNA /GEN=PRO1068 /PROD=hypothetical protein PRO1068 /DB_XREF=gi:8924006 /UG=Hs.321158 hypothetical protein PRO1068 /FL=gb:AF116620.1 gb:NM_018573.1
218313_s_at	NM_017423	gb:NM_017423.1 /DEF=Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA. /FEA=mRNA /GEN=GALNT7 /PROD=polypeptide N-acetylgalactosaminyltransferase 7 /DB_XREF=gi:8393408 /UG=Hs.246315 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) /FL=gb:NM_017423.1

212354_at	KIAA1077	AW043713	sulfatase FP	
212385_at		AK021980	Consensus includes gb:AU118026 /FEA=EST /DB_XREF=gi:10933043 /DB_XREF=est:AU118026 /CLONE=HEMBA1002729 /UG=Hs.289068 Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272	
212428_at		AB002366	Consensus includes gb:AW001101 /FEA=EST /DB_XREF=gi:5848017 /DB_XREF=est:wu24c05.x1 /CLONE=IMAGE:2520968 /UG=Hs.3852 KIAA0368 protein	
205917_at		NM_003417	gb:NM_003417.1 /DEF=Homo sapiens zinc finger protein 264 (ZNF264), mRNA. /FEA=mRNA /GEN=ZNF264 /PROD=zinc finger protein 264 /DB_XREF=gi:4585642 /UG=Hs.117077 zinc finger protein 264 /FL=gb:NM_003417.1	

206026_s_at	NM_007115	gb:NM_007115.1 /DEF=Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA. /FEA=mRNA /GEN=TNFAIP6 /PROD=tumor necrosis factor, alpha-induced protein 6 /DB_XREF=gi:6005905 /UG=Hs.29352 tumor necrosis factor, alpha-induced protein 6 /FL=gb:NM_007115.1
208025_s_at	NM_003483	gb:NM_003483.2 /DEF=Homo sapiens high-mobility group (nonhistone chromosomal) protein isoform I-C (HMGIC), mRNA. /FEA=mRNA /GEN=HMGIC /PROD=high-mobility group (nonhistone chromosomal)protein isoform I-C /DB_XREF=gi:6631086 /FL=gb:NM_003483.2

206284\_x\_at

212299_at		AL117502	Consensus includes gb:AL117502.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone DKFZp434D0935). /FEA=mRNA /DB_XREF=gi:5912009 /UG=Hs.7200 Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone DKFZp434D0935)	
204774_at		NM_014210	gb:NM_014210.1 /DEF=Homo sapiens ecotropic viral integration site 2A (EVI2A), mRNA. /FEA=mRNA /GEN=EVI2A /PROD=ecotropic viral integration site 2A /DB_XREF=gi:7657074 /UG=Hs.70499 ecotropic viral integration site 2A /FL=gb:NM_014210.1	

203939_at		NM_002526	gb:NM_002526.1 /DEF=Homo sapiens 5 nucleotidase (CD73) (NT5), mRNA. /FEA=mRNA /GEN=NT5 /PROD=5 nucleotidase /DB_XREF=gi:4505466 /UG=Hs.153952 5 nucleotidase (CD73) /FL=gb:NM_002526.1	
212725_s_at		N37081	ESTs	
212810_s_at	SLC1A4	BG032165	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	
212765_at	KIAA1078	AW593213	KIAA1078 protein	
205006_s_at		NM_004808	gb:NM_004808.1 /DEF=Homo sapiens N-myristoyltransferase 2 (NMT2), mRNA. /FEA=mRNA /GEN=NMT2 /PROD=glycylpeptide N-tetradecanoyltransferase 2 /DB_XREF=gi:4758815 /UG=Hs.122647 N-myristoyltransferase 2 /FL=gb:AF043325.1 gb:NM_004808.1	

209288_s_at	AL136842	<p>gb:AL136842.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434A0530 (from clone DKFZp434A0530); complete cds. /FEA=mRNA /GEN=DKFZp434A0530 /PROD=hypothetical protein /DB_XREF=gi:6807668 /UG=Hs.260024 Cdc42 effector protein 3 /FL=gb:AF094521.1 gb:AF104857.1 gb:NM_006449.1 gb:AF164118.1 gb:AL136842.1</p>
210058_at	BC000433	<p>gb:BC000433.1 /DEF=Homo sapiens, mitogen-activated protein kinase 13, clone MGC:8364, mRNA, complete cds. /FEA=mRNA /PROD=mitogen-activated protein kinase 13 /DB_XREF=gi:12653328 /UG=Hs.178695 mitogen-activated protein kinase 13 /FL=gb:BC000433.1 gb:BC001641.1 gb:BC004428.1 gb:AF004709.1 gb:AF015256.1 gb:U93232.1 gb:NM_002754.1 gb:AF092535.1 gb:AF100546.1</p>



209184_s_at	IRS2	BF700086	insulin receptor substrate 2	
			gb:AF114012.1 /DEF=Homo sapiens tumor necrosis factor-related death ligand-1beta mRNA, complete cds. /FEA=mRNA /PROD=tumor necrosis factor-related deathligand-1beta /DB_XREF=gi:7328555 /UG=Hs.54673 tumor necrosis factor (ligand) superfamily, member 13 /FL=gb:AF114012.1	
209500_x_at		AF114012		
209485_s_at	OSBPL1A	W19983	oxysterol binding protein-like 1A	
			gb:D43968.1 /DEF=Human AML1 mRNA for AML1b protein (alternatively spliced product), complete cds. /FEA=mRNA /GEN=AML1 /PROD=AML1b protein /DB_XREF=gi:966996 /UG=Hs.129914 runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) /FL=gb:L34598.1 gb:D43968.1	
209360_s_at		D43968		

209967_s_at	D14826	gb:D14826.1 /DEF=Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds. /FEA=mRNA /GEN=hCREM-2; hCREM-2; hCREM-2; hCREM-2 /PROD=hCREM 2beta-b protein; hCREM 2beta-a protein; hCREM 2alpha-b protein; hCREM 2alpha-a protein /DB_XREF=gi:532036 /UG=Hs.155924 cAMP responsive element modulator /FL=gb:AF069065.1 gb:D14826.1
212013_at	AF200348	Consensus includes gb:D86983.1 /DEF=Human mRNA for KIAA0230 gene, partial cds. /FEA=mRNA /GEN=KIAA0230 /DB_XREF=gi:1504039 /UG=Hs.118893 Melanoma associated gene

208896_at		BC003360	Consensus includes gb:X98743.1 /DEF=H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein). /FEA=mRNA /PROD=RNA helicase /DB_XREF=gi:1498228 /UG=Hs.100555 DEADH (Asp-Glu- Ala-AspHis) box polypeptide 18 (Myc-regulated) /FL=gb:BC001238.1 gb:BC003360.1	
212095_s_at		AL096842	Consensus includes gb:BE552421 /FEA=EST /DB_XREF=gi:9794113 /DB_XREF=est:hw26b02.x1 /CLONE=IMAGE:3184011 /UG=Hs.7946 KIAA1288 protein	

208708_x_at	AL080102	gb:AL080102.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564N1916 (from clone DKFZp564N1916); complete cds. /FEA=mRNA /GEN=DKFZp564N1916 /PROD=hypothetical protein /DB_XREF=gi:5262526 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1	
211615_s_at	M92439	gb:M92439.1 /DEF=Human leucine-rich protein mRNA, complete cds. /FEA=mRNA /PROD=leucine-rich protein; leucine-rich protein /DB_XREF=gi:177109 /FL=gb:M92439.1	
208952_s_at	BC003381	Consensus includes gb:AA811923 /FEA=EST /DB_XREF=gi:2881534 /DB_XREF=est:ob72f05.s1 /CLONE=IMAGE:1336929 /UG=Hs.78851 KIAA0217 protein /FL=gb:BC003381.1	

201960_s_at		NM_015057	gb:NM_015057.1 /DEF=Homo sapiens KIAA0916 protein (KIAA0916), mRNA. /FEA=mRNA /GEN=KIAA0916 /PROD=KIAA0916 protein /DB_XREF=gi:7662379 /UG=Hs.151411 KIAA0916 protein /FL=gb:AF075587.1 gb:AF083244.1 gb:NM_015057.1	
201473_at		NM_002229	gb:NM_002229.1 /DEF=Homo sapiens jun B proto-oncogene (JUNB), mRNA. /FEA=mRNA /GEN=JUNB /PROD=jun B proto-oncogene /DB_XREF=gi:4504808 /UG=Hs.198951 jun B proto-oncogene /FL=gb:BC004250.1 gb:NM_002229.1	

201324_at		NM_001423	gb:NM_001423.1 /DEF=Homo sapiens epithelial membrane protein 1 (EMP1), mRNA. /FEA=mRNA /GEN=EMP1 /PROD=epithelial membrane protein 1 /DB_XREF=gi:4503558 /UG=Hs.79368 epithelial membrane protein 1 /FL=gb:U77085.1 gb:U43916.1 gb:NM_001423.1	
201554_x_at		NM_004130	gb:NM_004130.1 /DEF=Homo sapiens glycogenin (GYG), mRNA. /FEA=mRNA /GEN=GYG /PROD=glycogenin /DB_XREF=gi:4758491 /UG=Hs.174071 glycogenin /FL=gb:U44131.1 gb:BC000033.1 gb:NM_004130.1 gb:U31525.1	
201502_s_at	NFKBIA	AI078167	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	

202406_s_at	NM_003252	gb:NM_003252.2 /DEF=Homo sapiens TIA1 cytotoxic granule-associated RNA-binding protein-like 1 (TIAL1), transcript variant 1, mRNA. /FEA=mRNA /GEN=TIAL1 /PROD=TIA1 cytotoxic granule-associated RNA-bindingprotein-like 1, isoform 1 /DB_XREF=gi:13435392 /UG=Hs.182741 TIA1 cytotoxic granule-associated RNA-binding protein-like 1 /FL=gb:NM_003252.2 gb:M96954.1
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202418_at		NM_020470	<p>gb:NM_020470.1 /DEF=Homo sapiens putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor) (54TM), mRNA. /FEA=mRNA /GEN=54TM /PROD=putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor) /DB_XREF=gi:9994168 /UG=Hs.5809 putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor) /FL=gb:BC001299.1 gb:AF004876.1 gb:NM_020470.1</p>	
214280_x_at		X79536	<p>Consensus includes gb:X79536.1 /DEF=H.sapiens mRNA for hnRNPcore protein A1. /FEA=mRNA /PROD=hnRNPcore protein A1 /DB_XREF=gi:496897 /UG=Hs.249495 heterogeneous nuclear ribonucleoprotein A1</p>	



202163_s_at		NM_004779	gb:NM_004779.1 /DEF=Homo sapiens CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA. /FEA=mRNA /GEN=CNOT8 /PROD=CCR4-NOT transcription complex, subunit 8 /DB_XREF=gi:4758945 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1	
217764_s_at		AF183421	gb:AF183421.1 /DEF=Homo sapiens small GTP-binding protein rab22b mRNA, complete cds. /FEA=mRNA /PROD=small GTP-binding protein rab22b /DB_XREF=gi:9963780 /UG=Hs.223025 RAB31, member RAS oncogene family /FL=gb:AF234995.1 gb:BC001148.1 gb:U59877.1 gb:U57091.1 gb:NM_006868.1 gb:AF183421.1	

217643_x_at		AA443771	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	
200872_at		NM_002966	gb:NM_002966.1 /DEF=Homo sapiens S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA. /FEA=mRNA /GEN=S100A10 /PROD=S100 calcium-binding protein A10 /DB_XREF=gi:4506760 /UG=Hs.119301 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) /FL=gb:M81457.1 gb:M38591.1 gb:NM_002966.1	
200844_s_at	AOP2	BE869583	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2)	

217836_s_at		NM_018253	gb:NM_018253.1 /DEF=Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA. /FEA=mRNA /GEN=FLJ10875 /PROD=hypothetical protein FLJ10875 /DB_XREF=gi:8922730 /UG=Hs.18851 hypothetical protein FLJ10875 /FL=gb:BC001655.1 gb:BC001843.1 gb:NM_018253.1	
217866_at		NM_024811	gb:NM_024811.1 /DEF=Homo sapiens hypothetical protein FLJ12529 (FLJ12529), mRNA. /FEA=mRNA /GEN=FLJ12529 /PROD=hypothetical protein FLJ12529 /DB_XREF=gi:13376196 /UG=Hs.169100 hypothetical protein FLJ12529 /FL=gb:NM_024811.1	

201194_at		NM_003009	gb:NM_003009.1 /DEF=Homo sapiens selenoprotein W, 1 (SEPW1), mRNA. /FEA=mRNA /GEN=SEPW1 /PROD=selenoprotein W, 1 /DB_XREF=gi:4506886 /UG=Hs.14231 selenoprotein W, 1 /FL=gb:U67171.1 gb:AF015283.1 gb:NM_003009.1	
215483_at		AK000270	Consensus includes gb:AK000270.1 /DEF=Homo sapiens cDNA FLJ20263 fis, clone COLF7804, highly similar to AJ131693 Homo sapiens mRNA for AKAP450 protein. /FEA=mRNA /DB_XREF=gi:7020239 /UG=Hs.164036 Homo sapiens AKAP350C mRNA sequence, alternatively spliced	
200890_s_at	SSR1	AI016620	signal sequence receptor, alpha (translocon-associated protein alpha)	

203150_at		NM_005833	gb:NM_005833.1 /DEF=Homo sapiens Rab9 effector p40 (RAB9P40), mRNA. /FEA=mRNA /GEN=RAB9P40 /PROD=Rab9 effector p40 /DB_XREF=gi:5032014 /UG=Hs.19012 Rab9 effector p40 /FL=gb:BC000503.1 gb:Z97074.1 gb:NM_005833.1	
203188_at		NM_006876	gb:NM_006876.1 /DEF=Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase (BETA3GNTI), mRNA. /FEA=mRNA /GEN=BETA3GNTI /PROD=i-beta-1,3-N-acetylglucosaminyltransferase /DB_XREF=gi:5802983 /UG=Hs.8526 i-beta-1,3-N-acetylglucosaminyltransferase /FL=gb:AF029893.1 gb:NM_006876.1	

203477_at		NM_001855	gb:NM_001855.1 /DEF=Homo sapiens collagen, type XV, alpha 1 (COL15A1), mRNA. /FEA=mRNA /GEN=COL15A1 /PROD=collagen, type XV, alpha 1 /DB_XREF=gi:4502940 /UG=Hs.83164 collagen, type XV, alpha 1 /FL=gb:NM_001855.1 gb:L25286.1	
213275_x_at	CTSB	BE875786	cathepsin B	
203411_s_at		NM_005572	gb:NM_005572.1 /DEF=Homo sapiens lamin AC (LMNA), mRNA. /FEA=mRNA /GEN=LMNA /PROD=lamin AC /DB_XREF=gi:5031874 /UG=Hs.77886 lamin AC /FL=gb:BC000511.1 gb:BC003162.1 gb:M13451.1 gb:NM_005572.1	

202595_s_at	AF161461	gb:AF161461.1 /DEF=Homo sapiens HSPC112 mRNA, complete cds. /FEA=mRNA /PROD=HSPC112 /DB_XREF=gi:6841445 /UG=Hs.11000 leptin receptor overlapping transcript-like 1 /FL=gb:BC000642.1 gb:AF063605.1 gb:AF161461.1 gb:NM_015344.1
221421_s_at	NM_030955	gb:NM_030955.1 /DEF=Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA. /FEA=CDS /GEN=ADAMTS12 /PROD=a disintegrin-like and metalloprotease(reprolysin type) with thrombospondin type 1 motif, 12 /DB_XREF=gi:13569927 /FL=gb:NM_030955.1

217765_at		NM_013392	gb:NM_013392.1 /DEF=Homo sapiens nuclear receptor binding protein (NRBP), mRNA. /FEA=mRNA /GEN=NRBP /PROD=nuclear receptor binding protein /DB_XREF=gi:7019332 /UG=Hs.272736 nuclear receptor binding protein /FL=gb:BC001221.1 gb:AF113249.1 gb:NM_013392.1	
213869_x_at	THY1	AA218868	Thy-1 cell surface antigen	
205256_at		NM_014830	gb:NM_014830.1 /DEF=Homo sapiens KIAA0352 gene product (KIAA0352), mRNA. /FEA=mRNA /GEN=KIAA0352 /PROD=KIAA0352 gene product /DB_XREF=gi:7662071 /UG=Hs.17262 KIAA0352 gene product /FL=gb:AB002350.1 gb:NM_014830.1	



206027_at		NM_002960	gb:NM_002960.1 /DEF=Homo sapiens S100 calcium-binding protein A3 (S100A3), mRNA. /FEA=mRNA /GEN=S100A3 /PROD=S100 calcium-binding protein A3 /DB_XREF=gi:4506762 /UG=Hs.2961 S100 calcium-binding protein A3 /FL=gb:NM_002960.1	
220391_at		NM_024784	gb:NM_024784.1 /DEF=Homo sapiens hypothetical protein FLJ23392 (FLJ23392), mRNA. /FEA=mRNA /GEN=FLJ23392 /PROD=hypothetical protein FLJ23392 /DB_XREF=gi:13376145 /UG=Hs.147554 hypothetical protein FLJ23392 /FL=gb:NM_024784.1	

209198_s_at		BC004291	gb:BC004291.1 /DEF=Homo sapiens, Similar to synaptotagmin 11, clone MGC:10881, mRNA, complete cds. /FEA=mRNA /PROD=Similar to synaptotagmin 11 /DB_XREF=gi:13279139 /UG=Hs.74554 KIAA0080 protein /FL=gb:BC004291.1	
219915_s_at		NM_018593	gb:NM_018593.1 /DEF=Homo sapiens hypothetical protein PRO0813 (PRO0813), mRNA. /FEA=mRNA /GEN=PRO0813 /PROD=hypothetical protein PRO0813 /DB_XREF=gi:8923980 /UG=Hs.270087 hypothetical protein PRO0813 /FL=gb:AF116652.1 gb:NM_018593.1	
214337_at	COPA	AI621079	coatomer protein complex, subunit alpha	

220979_s_at		NM_030965	gb:NM_030965.1 /DEF=Homo sapiens similar to sialyltransferase 7 ((alpha-N-acetylneuraminy1 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) E (MGC3184), mRNA. /FEA=mRNA /GEN=MGC3184 /PROD=similar to sialyltransferase 7((alpha-N-acetylneuraminy1,3-betagalactosyl-1,3)-N-acetyl galactosaminidealpha-2,6-sialyltransferase) E /DB_XREF=gi:13569937 /FL=gb:NM_030965.1	
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219321_at		NM_022474	gb:NM_022474.1 /DEF=Homo sapiens hypothetical protein FLJ12615 similar to membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 5) (FLJ12615), mRNA. /FEA=mRNA /GEN=FLJ12615 /PROD=hypothetical protein FLJ12615 similar to membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 5) /DB_XREF=gi:11968024 /UG=Hs.306219 hypothetical protein FLJ12615 similar to membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 5) /FL=gb:NM_022474.1	
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207275_s_at		NM_001995	gb:NM_001995.1 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=FACL1 /PROD=long-chain fatty-acid-coenzyme A ligase 1 /DB_XREF=gi:4503650 /UG=Hs.278333 fatty-acid-Coenzyme A ligase, long-chain 1 /FL=gb:L09229.1 gb:NM_001995.1	
207753_at		NM_020657	gb:NM_020657.1 /DEF=Homo sapiens zinc finger protein 304 (ZNF304), mRNA. /FEA=mRNA /GEN=ZNF304 /PROD=zinc finger protein 304 /DB_XREF=gi:10190695 /UG=Hs.287374 zinc finger protein 304 /FL=gb:NM_020657.1	
202438_x_at	IDS	BF346014	iduronate 2-sulfatase (Hunter syndrome)	

205200_at		NM_003278	gb:NM_003278.1 /DEF=Homo sapiens tetranectin (plasminogen-binding protein) (TNA), mRNA. /FEA=mRNA /GEN=TNA /PROD=tetranectin (plasminogen-binding protein) /DB_XREF=gi:4507556 /UG=Hs.65424 tetranectin (plasminogen-binding protein) /FL=gb:NM_003278.1	
214838_at		AL035297	Consensus includes gb:AL035297.1 /DEF=H.sapiens gene from PAC 747L4. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:4200248 /UG=Hs.119254 H.sapiens gene from PAC 747L4	

205406_s_at		NM_017425	gb:NM_017425.1 /DEF=Homo sapiens sperm autoantigenic protein 17 (SPA17), mRNA. /FEA=mRNA /GEN=SPA17 /PROD=sperm autoantigenic protein 17 /DB_XREF=gi:8394342 /UG=Hs.286233 sperm autoantigenic protein 17 /FL=gb:NM_017425.1	
78330_at	ZNF335	AA845577	zinc finger protein 335	
202604_x_at		NM_001110	gb:NM_001110.1 /DEF=Homo sapiens a disintegrin and metalloproteinase domain 10 (ADAM10), mRNA. /FEA=mRNA /GEN=ADAM10 /PROD=a disintegrin and metalloprotease domain 10 /DB_XREF=gi:4557250 /UG=Hs.172028 a disintegrin and metalloproteinase domain 10 /FL=gb:AF009615.1 gb:NM_001110.1	
209047_at	AQP1	AL518391	aquaporin 1 (channel-forming integral protein, 28kDa)	

205651_x_at		NM_007023	gb:NM_007023.1 /DEF=Homo sapiens cAMP-regulated guanine nucleotide exchange factor II (CAMP-GEFII), mRNA. /FEA=mRNA /GEN=CAMP-GEFII /PROD=cAMP-regulated guanine nucleotide exchangefactor II /DB_XREF=gi:5901913 /UG=Hs.91971 cAMP-regulated guanine nucleotide exchange factor II /FL=gb:U78516.1 gb:NM_007023.1	
202802_at		NM_001930	gb:NM_001930.2 /DEF=Homo sapiens deoxyhypusine synthase (DHPS), transcript variant 1, mRNA. /FEA=mRNA /GEN=DHPS /PROD=deoxyhypusine synthase isoform a /DB_XREF=gi:7108341 /UG=Hs.79064 deoxyhypusine synthase /FL=gb:U40579.1 gb:BC000333.1 gb:U32178.1 gb:U79262.1 gb:NM_001930.2 gb:L39068.1	



208623_s_at		J05021	gb:J05021.1 /DEF=Human cytovillin 2 (VIL2) mRNA, complete cds. /FEA=mRNA /GEN=VIL2 /DB_XREF=gi:340216 /UG=Hs.155191 villin 2 (ezrin) /FL=gb:J05021.1 gb:AL162086.1 gb:Nm_003379.2	
219620_x_at		NM_017723	gb:Nm_017723.1 /DEF=Homo sapiens hypothetical protein FLJ20245 (FLJ20245), mRNA. /FEA=mRNA /GEN=FLJ20245 /PROD=hypothetical protein FLJ20245 /DB_XREF=gi:8923220 /UG=Hs.169758 hypothetical protein FLJ20245 /FL=gb:Nm_017723.1	

204451_at		NM_003505	gb:NM_003505.1 /DEF=Homo sapiens frizzled (Drosophila) homolog 1 (FZD1), mRNA. /FEA=mRNA /GEN=FZD1 /PROD=frizzled 1 /DB_XREF=gi:4503824 /UG=Hs.94234 frizzled (Drosophila) homolog 1 /FL=gb:AB017363.1 gb:NM_003505.1 gb:AF072872.1	
209621_s_at		AF002280	gb:AF002280.1 /DEF=Homo sapiens alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds. /FEA=mRNA /PROD=alpha-actinin-2 associated LIM protein /DB_XREF=gi:3138919 /UG=Hs.135281 alpha-actinin-2-associated LIM protein /FL=gb:AF039018.1 gb:AF002280.1 gb:NM_014476.1	

201826_s_at		NM_016002	gb:NM_016002.1 /DEF=Homo sapiens CGI-49 protein (LOC51097), mRNA. /FEA=mRNA /GEN=LOC51097 /PROD=CGI-49 protein /DB_XREF=gi:7705766 /UG=Hs.238126 CGI-49 protein /FL=gb:AF151807.1 gb:NM_016002.1	
209057_x_at		AB007892	gb:AB007892.1 /DEF=Homo sapiens KIAA0432 mRNA, complete cds. /FEA=mRNA /GEN=KIAA0432 /DB_XREF=gi:2887434 /UG=Hs.155174 CDC5 (cell division cycle 5, S. pombe, homolog)-like /FL=gb:NM_001253.1 gb:U86753.1 gb:AB007892.1	

218149_s_at		NM_017606	gb:NM_017606.1 /DEF=Homo sapiens hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA. /FEA=mRNA /GEN=DKFZp434K1210 /PROD=hypothetical protein DKFZp434K1210 /DB_XREF=gi:8922146 /UG=Hs.32352 hypothetical protein DKFZp434K1210 /FL=gb:NM_017606.1	
202609_at		NM_004447	gb:NM_004447.1 /DEF=Homo sapiens epidermal growth factor receptor pathway substrate 8 (EPS8), mRNA. /FEA=mRNA /GEN=EPS8 /PROD=epidermal growth factor receptor pathwaysubstrate 8 /DB_XREF=gi:4758295 /UG=Hs.2132 epidermal growth factor receptor pathway substrate 8 /FL=gb:NM_004447.1 gb:U12535.1	
214004_s_at	GSA7	AI806207	ubiquitin activating enzyme E1-like protein	
213909_at		AU147799	ESTs	

202481_at		NM_004753	gb:NM_004753.1 /DEF=Homo sapiens short-chain dehydrogenasereductase 1 (SDR1), mRNA. /FEA=mRNA /GEN=SDR1 /PROD=short-chain dehydrogenasereductase 1 /DB_XREF=gi:4759083 /UG=Hs.17144 short-chain dehydrogenasereductase 1 /FL=gb:BC002730.1 gb:AF061741.1 gb:NM_004753.1	
202739_s_at		NM_000293	gb:NM_000293.1 /DEF=Homo sapiens phosphorylase kinase, beta (PHKB), mRNA. /FEA=mRNA /GEN=PHKB /PROD=phosphorylase kinase, beta /DB_XREF=gi:4505782 /UG=Hs.78060 phosphorylase kinase, beta /FL=gb:NM_000293.1	

202733_at		NM_004199	gb:NM_004199.1 /DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II (P4HA2), mRNA. /FEA=mRNA /GEN=P4HA2 /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptidII /DB_XREF=gi:4758867 /UG=Hs.3622 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II /FL=gb:U90441.1 gb:NM_004199.1
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221730_at		NM_000393	Consensus includes gb:NM_000393.1 /DEF=Homo sapiens collagen, type V, alpha 2 (COL5A2), mRNA. /FEA=CDS /GEN=COL5A2 /PROD=collagen, type V, alpha 2 /DB_XREF=gi:4502958 /UG=Hs.82985 collagen, type V, alpha 2 /FL=gb:NM_000393.1	
202746_at	ITM2A; E25A	AL021786	Human DNA sequence from clone RP4-696H22 on chromosome Xq21.1-21.2, complete sequence.	NM_004867
221737_at		NM_007353	Consensus includes gb:AK024696.1 /DEF=Homo sapiens cDNA: FLJ21043 fis, clone CAE11633. /FEA=mRNA /DB_XREF=gi:10437043 /UG=Hs.182874 guanine nucleotide binding protein (G protein) alpha 12 /FL=gb:L01694.1 gb:NM_007353.1	
221773_at		AW575374	ESTs, Highly similar to A48765 G protein-coupled receptor kinase (EC 2.7.1.-) 6 - human [H.sapiens]	

213902_at	ASAH1	AI379338	N-acylsphingosine amidohydrolase (acid ceramidase) 1	
202321_at		AW299507	ESTs, Weakly similar to A53959 thromboxane A-2 receptor, endothelial - human [H.sapiens]	
221988_at		AA463853	ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precursor [Homo sapiens] [H.sapiens]	
202220_at		NM_014949	gb:NM_014949.1 /DEF=Homo sapiens KIAA0907 protein (KIAA0907), mRNA. /FEA=mRNA /GEN=KIAA0907 /PROD=KIAA0907 protein /DB_XREF=gi:7662371 /UG=Hs.24656 KIAA0907 protein /FL=gb:AB020714.1 gb:NM_014949.1	



202164_s_at	AF180476	gb:AF180476.1 /DEF=Homo sapiens CALIFp (CALIF) mRNA, complete cds. /FEA=mRNA /GEN=CALIF /PROD=CALIFp /DB_XREF=gi:6856208 /UG=Hs.26703 CCR4-NOT transcription complex, subunit 8 /FL=gb:AF053318.1 gb:NM_004779.1 gb:AL122045.1 gb:AF180476.1
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222024_s_at		AK022014	Consensus includes gb:AK022014.1 /DEF=Homo sapiens cDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA. /FEA=mRNA /DB_XREF=gi:10433327 /UG=Hs.306619 Homo sapiens cDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA	
214252_s_at	CLN5	AV700514	ceroid-lipofuscinosis, neuronal 5	
214093_s_at	FUBP1	AA156865	far upstream element (FUSE) binding protein 1	
221897_at	MGC16175	AA205660	hypothetical protein MGC16175	

218136_s_at		NM_018579	gb:NM_018579.1 /DEF=Homo sapiens mitochondrial solute carrier (LOC51312), mRNA. /FEA=mRNA /GEN=LOC51312 /PROD=hypothetical protein PRO1278 /DB_XREF=gi:8924027 /UG=Hs.300496 mitochondrial solute carrier /FL=gb:AF155660.1 gb:AF116630.1 gb:NM_018579.1	
214106_s_at	GMDS	AI762113	GDP-mannose 4,6-dehydratase	
218139_s_at		NM_018229	gb:NM_018229.1 /DEF=Homo sapiens hypothetical protein FLJ10813 (FLJ10813), mRNA. /FEA=mRNA /GEN=FLJ10813 /PROD=hypothetical protein FLJ10813 /DB_XREF=gi:8922687 /UG=Hs.106210 hypothetical protein FLJ10813 /FL=gb:AL136685.1 gb:NM_018229.1	

202404_s_at		NM_000089	gb:NM_000089.1 /DEF=Homo sapiens collagen, type I, alpha 2 (COL1A2), mRNA. /FEA=mRNA /GEN=COL1A2 /PROD=collagen, type I, alpha 2 /DB_XREF=gi:4502946 /UG=Hs.179573 collagen, type I, alpha 2 /FL=gb:J03464.1 gb:NM_000089.1	
203325_s_at	COL5A1	AI130969	collagen, type V, alpha 1	
218257_s_at		NM_020120	gb:NM_020120.1 /DEF=Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA. /FEA=mRNA /GEN=HUGT1 /PROD=UDP-glucose:glycoprotein glucosyltransferase 1 /DB_XREF=gi:9910279 /UG=Hs.105794 UDP-glucose:glycoprotein glucosyltransferase 1 /FL=gb:AF227905.1 gb:NM_020120.1	

203395_s_at		NM_005524	gb:NM_005524.2 /DEF=Homo sapiens hairy (Drosophila)-homolog (HRY), mRNA. /FEA=mRNA /GEN=HRY /PROD=hairy (Drosophila)-homolog /DB_XREF=gi:8400709 /UG=Hs.250666 hairy (Drosophila)-homolog /FL=gb:AF264785.1 gb:NM_005524.2	
203380_x_at		NM_006925	gb:NM_006925.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 5 (SFRS5), mRNA. /FEA=mRNA /GEN=SFRS5 /PROD=splicing factor, arginineserine-rich 5 /DB_XREF=gi:5902077 /UG=Hs.166975 splicing factor, arginineserine-rich 5 /FL=gb:U30827.1 gb:NM_006925.1	

213524_s_at	NM_015714	Consensus includes gb:NM_015714.1 /DEF=Homo sapiens putative lymphocyte G0G1 switch gene (G0S2), mRNA. /FEA=CDS /GEN=G0S2 /PROD=putative lymphocyte G0G1 switch gene /DB_XREF=gi:7657103 /UG=Hs.95910 putative lymphocyte G0G1 switch gene /FL=gb:NM_015714.1
221517_s_at	AF105421	gb:AF105421.1 /DEF=Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds. /FEA=mRNA /GEN=DRIP80 /PROD=vitamin D3 receptor interacting protein /DB_XREF=gi:4838128 /UG=Hs.22630 cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) /FL=gb:AF105421.1

			gb:NM_002767.1 /DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2), mRNA. /FEA=mRNA /GEN=PRPSAP2 /PROD=phosphoribosyl pyrophosphatesynthetase-associated protein 2 /DB_XREF=gi:4506132 /UG=Hs.13339 phosphoribosyl pyrophosphate synthetase-associated protein 2 /FL=gb:AB007851.1 gb:NM_002767.1	
203537_at		NM_002767		
213455_at	LOC92689	W87466	hypothetical protein BC001096	
213392_at	MGC35048	AW070229	hypothetical protein MGC35048	
221718_s_at		M90360	gb:M90360.1 /DEF=Human type II cAMP-dependent protein kinase (Ht31) mRNA, complete cds. /FEA=CDS /GEN=Ht31 /PROD=protein kinase /DB_XREF=gi:184434 /FL=gb:M90360.1	

202887_s_at		NM_019058	gb:NM_019058.1 /DEF=Homo sapiens hypothetical protein (FLJ20500), mRNA. /FEA=mRNA /GEN=FLJ20500 /PROD=hypothetical protein /DB_XREF=gi:9506686 /UG=Hs.111244 hypothetical protein /FL=gb:AL136668.1 gb:NM_019058.1	
202814_s_at	HIS1	AW193511	HMBA-inducible	
221729_at		NM_000393	Consensus includes gb:AL575735 /FEA=EST /DB_XREF=gi:12937190 /DB_XREF=est:AL575735 /CLONE=CS0DI070YK23 (3 prime) /UG=Hs.82985 collagen, type V, alpha 2 /FL=gb:NM_000393.1	
202403_s_at	COL1A2	AA788711	collagen, type I, alpha 2	



202998_s_at		NM_002318	gb:NM_002318.1 /DEF=Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA. /FEA=mRNA /GEN=LOXL2 /PROD=lysyl oxidase-like 2 /DB_XREF=gi:4505010 /UG=Hs.83354 lysyl oxidase-like 2 /FL=gb:BC000594.1 gb:U89942.1 gb:NM_002318.1 gb:AF117949.1	
213627_at	MAGED2	AI924630	melanoma antigen, family D, 2	
202912_at		NM_001124	gb:NM_001124.1 /DEF=Homo sapiens adrenomedullin (ADM), mRNA. /FEA=mRNA /GEN=ADM /PROD=adrenomedullin /DB_XREF=gi:4501944 /UG=Hs.394 adrenomedullin /FL=gb:NM_001124.1 gb:D14874.1	
213653_at	M6A	AW069290	putative methyltransferase	

201126_s_at		NM_002406	gb:NM_002406.2 /DEF=Homo sapiens mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA. /FEA=mRNA /GEN=MGAT1 /PROD=mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase /DB_XREF=gi:6031182 /UG=Hs.151513 mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase /FL=gb:M55621.1 gb:NM_002406.2	
200995_at		AL137335	Consensus includes gb:AI741392 /FEA=EST /DB_XREF=gi:5109680 /DB_XREF=est:wg27b08.x1 /CLONE=IMAGE:2366295 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1	

217043_s_at		U95822	Consensus includes gb:U95822.1 /DEF=Human putative transmembrane GTPase mRNA, partial cds. /FEA=mRNA /GEN=fzo /PROD=putative transmembrane GTPase /DB_XREF=gi:2252803 /UG=Hs.197877 hypothetical protein FLJ20693	
218032_at		AF070673	gb:AF070673.1 /DEF=Homo sapiens stannin mRNA, complete cds. /FEA=mRNA /PROD=stannin /DB_XREF=gi:3978241 /UG=Hs.76691 stannin /FL=gb:AF030196.1 gb:AF070673.1 gb:NM_003498.1 gb:AL161976.1	
201328_at	ETS2	AL575509	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	

201185_at		NM_002775	gb:NM_002775.1 /DEF=Homo sapiens protease, serine, 11 (IGF binding) (PRSS11), mRNA. /FEA=mRNA /GEN=PRSS11 /PROD=protease, serine, 11 (IGF binding) /DB_XREF=gi:4506140 /UG=Hs.75111 protease, serine, 11 (IGF binding) /FL=gb:D87258.1 gb:NM_002775.1	
201152_s_at		NM_021038	Consensus includes gb:N31913 /FEA=EST /DB_XREF=gi:1152312 /DB_XREF=est:yy21f10.s1 /CLONE=IMAGE:271915 /UG=Hs.28578 muscleblind (Drosophila)-like /FL=gb:NM_021038.1 gb:AB007888.1	
201204_s_at	RRBP1	AI921320	ribosome binding protein 1 homolog 180kDa (dog)	

217771_at		NM_016548	gb:NM_016548.1 /DEF=Homo sapiens golgi membrane protein GP73 (LOC51280), mRNA. /FEA=mRNA /GEN=LOC51280 /PROD=golgi membrane protein GP73 /DB_XREF=gi:7706084 /UG=Hs.182793 golgi membrane protein GP73 /FL=gb:BC001740.1 gb:AF236056.1 gb:NM_016548.1	
200762_at		NM_001386	gb:NM_001386.1 /DEF=Homo sapiens dihydropyrimidinase-like 2 (DPYSL2), mRNA. /FEA=mRNA /GEN=DPYSL2 /PROD=dihydropyrimidinase-like 2 /DB_XREF=gi:4503376 /UG=Hs.173381 dihydropyrimidinase-like 2 /FL=gb:U17279.1 gb:D78013.1 gb:U97105.1 gb:NM_001386.1	

217949_s_at		NM_024006	gb:NM_024006.1 /DEF=Homo sapiens hypothetical protein IMAGE3455200 (IMAGE3455200), mRNA. /FEA=mRNA /GEN=IMAGE3455200 /PROD=hypothetical protein IMAGE3455200 /DB_XREF=gi:13124769 /UG=Hs.324844 hypothetical protein IMAGE3455200 /FL=gb:BC002911.1 gb:NM_024006.1	
217911_s_at		NM_004281	gb:NM_004281.1 /DEF=Homo sapiens BCL2-associated athanogene 3 (BAG3), mRNA. /FEA=mRNA /GEN=BAG3 /PROD=BCL2-associated athanogene 3 /DB_XREF=gi:6631072 /UG=Hs.15259 BCL2-associated athanogene 3 /FL=gb:AF095193.2 gb:NM_004281.1 gb:AF127139.1 gb:AF071218.2	

200069_at		NM_014706	Consensus includes gb:AI656011 /FEA=EST /DB_XREF=gi:4739990 /DB_XREF=est:tt42e08.x1 /CLONE=IMAGE:2243462 /UG=Hs.116875 KIAA0156 gene product /FL=gb:AB020880.1 gb:NM_014706.1 gb:D63879.1	
200924_s_at		NM_002394	gb:NM_002394.1 /DEF=Homo . sapiens solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (SLC3A2), mRNA. /FEA=mRNA /GEN=SLC3A2 /PROD=antigen identified by monoclonal antibodies 4F2,TRA1.10, TROP4, and T43 /DB_XREF=gi:4505140 /UG=Hs.79748 solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 /FL=gb:BC001061.1 gb:J02769.1 gb:J03569.1 gb:NM_002394.1 gb:AB018010.1	

44783_s_at	HEY1	R61374	hairy/enhancer-of-split related with YRPW motif 1	
200994_at		AL137335	Consensus includes gb:BG291787 /FEA=EST /DB_XREF=gi:13050002 /DB_XREF=est:602386007F1 /CLONE=IMAGE:4515240 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1	
200986_at		NM_000062	gb:NM_000062.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), mRNA. /FEA=mRNA /GEN=SERPING1 /PROD=complement component 1 inhibitor precursor /DB_XREF=gi:4557378 /UG=Hs.151242 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1 /FL=gb:M13690.1 gb:M13656.1 gb:NM_000062.1	



217161_x_at		X17406	Consensus includes gb:X17406.1 /DEF=Human mRNA for cartilage specific proteoglycan. /FEA=mRNA /PROD=cartilage specific proteoglycan (600 AA) /DB_XREF=gi:30248 /UG=Hs.2159 aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122)	
57163_at	ELOVL1	H93026	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)- like 1	

			Consensus includes gb:AL354872 /DEF=Human DNA sequence from clone RP11-42O15 on chromosome 1. Contains ESTs, STSs, GSSs and a CpG island. Contains the CTH gene for two isoforms of cystathionase (cystathionine gamma- lyase) and a CHORD containing protein 1 (CHP1) pseudogene /FEA=mRNA_1 /DB_XREF=gi:9717070 /UG=Hs.19904 cystathionase (cystathionine gamma-lyase)	
217127_at		AL354872		
222303_at		AV700891	ESTs	

201880_at		NM_005744	Consensus includes gb:AL040708 /FEA=EST /DB_XREF=gi:5409654 /DB_XREF=est:DKFZp434A1015_s1 /CLONE=DKFZp434A1015 /UG=Hs.181461 ariadne (Drosophila) homolog, ubiquitin- conjugating enzyme E2-binding protein, 1 /FL=gb:AF072832.1 gb:NM_005744.2	
201735_s_at		NM_001829	gb:NM_001829.1 /DEF=Homo sapiens chloride channel 3 (CLCN3), mRNA. /FEA=mRNA /GEN=CLCN3 /PROD=chloride channel 3 /DB_XREF=gi:4502868 /UG=Hs.174139 chloride channel 3 /FL=gb:AF029346.1 gb:NM_001829.1 gb:AF172729.1	
201829_at	NET1	AW263232	neuroepithelial cell transforming gene 1	

218062_x_at		NM_012121	gb:NM_012121.2 /DEF=Homo sapiens Cdc42 effector protein 4; binder of Rho GTPases 4 (CEP4), mRNA. /FEA=mRNA /GEN=CEP4 /PROD=Cdc42 effector protein 4; binder of Rho GTPases4 /DB_XREF=gi:13786126 /UG=Hs.3903 Cdc42 effector protein 4; binder of Rho GTPases 4 /FL=gb:AB042237.1 gb:NM_012121.2 gb:AF099664.1	
222146_s_at		AK026674	Consensus includes gb:AK026674.1 /DEF=Homo sapiens cDNA: FLJ23021 fis, clone LNG01014, highly similar to HUMSEF21B Human SEF2-1B protein (SEF2-1B) mRNA. /FEA=mRNA /DB_XREF=gi:10439577 /UG=Hs.326198 transcription factor 4	

201997_s_at		NM_015001	gb:NM_015001.1 /DEF=Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA. /FEA=mRNA /GEN=KIAA0929 /PROD=KIAA0929 protein Msx2 interacting nuclear target(MINT) homolog /DB_XREF=gi:7657266 /UG=Hs.184245 KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog /FL=gb:NM_015001.1	
214440_at		NM_000662	Consensus includes gb:NM_000662.1 /DEF=Homo sapiens N-acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA. /FEA=CDS /GEN=NAT1 /PROD=N-acetyltransferase 1 /DB_XREF=gi:4505334 /UG=Hs.155956 N-acetyltransferase 1 (arylamine N-acetyltransferase) /FL=gb:NM_000662.1	

201910_at	FARP1	BF213279	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	
214721_x_at		AL162074	Consensus includes gb:AL162074.1 /DEF=Homo sapiens mRNA; cDNA DKFZp762L106 (from clone DKFZp762L106); partial cds. /FEA=mRNA /GEN=DKFZp762L106 /PROD=hypothetical protein /DB_XREF=gi:7328153 /UG=Hs.3903 Cdc42 effector protein 4; binder of Rho GTPases 4	
214606_at	TSPAN-2	BF129969	tetraspan 2	
201949_x_at	CAPZB	AL572341	capping protein (actin filament) muscle Z-line, beta	
215076_s_at	COL3A1	AU144167	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	
36829_at	PER1	AF022991	period homolog 1 (Drosophila)	NM_002616
215091_s_at	MTIF3	BE542815	mitochondrial translational initiation factor 3	

201653_at		NM_005776	gb:NM_005776.1 /DEF=Homo sapiens cornichon-like (CNIL), mRNA. /FEA=mRNA /GEN=CNIL /PROD=cornichon-like /DB_XREF=gi:5031638 /UG=Hs.201673 cornichon-like /FL=gb:AF104398.1 gb:AF070654.1 gb:AF031379.1 gb:NM_005776.1	
201717_at		NM_004927	gb:NM_004927.1 /DEF=Homo sapiens chromosome 11 open reading frame 4 (C11ORF4), mRNA. /FEA=mRNA /GEN=C11ORF4 /PROD=chromosome 11 open reading frame 4 /DB_XREF=gi:4826648 /UG=Hs.75859 chromosome 11 open reading frame 4 /FL=gb:U39400.1 gb:BC004378.1 gb:NM_004927.1	

201525_at		NM_001647	gb:NM_001647.1 /DEF=Homo sapiens apolipoprotein D (APOD), mRNA. /FEA=mRNA /GEN=APOD /PROD=apolipoprotein D precursor /DB_XREF=gi:4502162 /UG=Hs.75736 apolipoprotein D /FL=gb:J02611.1 gb:NM_001647.1	
201506_at		NM_000358	gb:NM_000358.1 /DEF=Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA. /FEA=mRNA /GEN=TGFB1 /PROD=transforming growth factor, beta-induced, 68kD /DB_XREF=gi:4507466 /UG=Hs.118787 transforming growth factor, beta-induced, 68kD /FL=gb:BC000097.1 gb:BC004972.1 gb:M77349.1 gb:NM_000358.1	



208773_s_at	AL136943	gb:AL136943.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586G1024 (from clone DKFZp586G1024); complete cds. /FEA=mRNA /GEN=DKFZp586G1024 /PROD=hypothetical protein /DB_XREF=gi:12053380 /UG=Hs.301226 KIAA1085 protein /FL=gb:AL136943.1
208770_s_at	BC005057	gb:BC005057.1 /DEF=Homo sapiens, eukaryotic translation initiation factor 4E binding protein 2, clone MGC:12944, mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic translation initiation factor 4E binding protein 2 /DB_XREF=gi:13477190 /UG=Hs.278712 eukaryotic translation initiation factor 4E binding protein 2 /FL=gb:BC005057.1 gb:NM_004096.1 gb:L36056.1

208763_s_at		AL110191	gb:AL110191.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566A093 (from clone DKFZp566A093); complete cds. /FEA=mRNA /GEN=DKFZp566A093 /PROD=hypothetical protein /DB_XREF=gi:5817105 /UG=Hs.75450 delta sleep inducing peptide, immunoreactor /FL=gb:AF228339.1 gb:AF153603.1 gb:AL110191.1 gb:AF183393.1	
218643_s_at		NM_014171	gb:NM_014171.1 /DEF=Homo sapiens postsynaptic protein CRIPT (CRIPT), mRNA. /FEA=mRNA /GEN=CRIP1 /PROD=HSPC139 protein /DB_XREF=gi:7661797 /UG=Hs.39733 postsynaptic protein CRIPT /FL=gb:AF161488.1 gb:NM_014171.1	

208980_s_at	M26880	gb:M26880.1 /DEF=Human ubiquitin mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:340067 /UG=Hs.183704 ubiquitin C /FL=gb:M17597.1 gb:M26880.1
208898_at	AF077614	gb:AF077614.1 /DEF=Homo sapiens vacuolar ATP synthase subunit D homolog (VATD) mRNA, complete cds. /FEA=mRNA /GEN=VATD /PROD=vacuolar ATP synthase subunit D homolog /DB_XREF=gi:11999089 /UG=Hs.272630 vacuolar proton pump delta polypeptide /FL=gb:AF104629.1 gb:AF077614.1 gb:BC001411.1 gb:AF145316.1 gb:AF100741.1 gb:NM_015994.1

208833_s_at		AF119662	gb:AF119662.1 /DEF=Homo sapiens E46 protein mRNA, complete cds. /FEA=mRNA /PROD=E46 protein /DB_XREF=gi:6563249 /UG=Hs.13493 like mouse brain protein E46 /FL=gb:AL050282.1 gb:AF119662.1 gb:NM_013236.1	
219526_at		NM_024644	gb:NM_024644.1 /DEF=Homo sapiens hypothetical protein FLJ21802 (FLJ21802), mRNA. /FEA=mRNA /GEN=FLJ21802 /PROD=hypothetical protein FLJ21802 /DB_XREF=gi:13375884 /UG=Hs.48938 hypothetical protein FLJ21802 /FL=gb:NM_024644.1	

207692_s_at		NM_001135	gb:NM_001135.1 /DEF=Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 1, mRNA. /FEA=mRNA /GEN=AGC1 /PROD=aggrecan 1, isoform 1 precursor /DB_XREF=gi:4501990 /UG=Hs.2159 aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) /FL=gb:M55172.1 gb:NM_001135.1	
207614_s_at		NM_003592	gb:NM_003592.1 /DEF=Homo sapiens cullin 1 (CUL1), mRNA. /FEA=mRNA /GEN=CUL1 /PROD=cullin 1 /DB_XREF=gi:4503160 /UG=Hs.14541 cullin 1 /FL=gb:U58087.1 gb:NM_003592.1	

212333_at		AL049943	Consensus includes gb:AL049943.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522). /FEA=mRNA /GEN=DKFZp564F0522 /PROD=hypothetical protein /DB_XREF=gi:4884187 /UG=Hs.23060 DKFZP564F0522 protein	
212063_at		BE903880	ESTs, Weakly similar to TRHY_HUMAN Trichohyalin [H.sapiens]	
211998_at		NM_005324	Consensus includes gb:AW138159 /FEA=EST /DB_XREF=gi:6142559 /DB_XREF=est:UI-H-BI1-acy-d-03-0- UI.s1 /CLONE=IMAGE:2716060 /UG=Hs.180877 H3 histone, family 3B (H3.3B) /FL=gb:NM_005324.1	

208712_at		M73554	gb:M73554.1 /DEF=Human bcl-1 mRNA, complete CDS. /FEA=mRNA /GEN=bcl-1 /PROD=bcl-1 /DB_XREF=gi:179364 /UG=Hs.82932 cyclin D1 (PRAD1: parathyroid adenomatosis 1) /FL=gb:BC000076.1 gb:M73554.1	
208290_s_at		NM_001969	gb:NM_001969.1 /DEF=Homo sapiens eukaryotic translation initiation factor 5 (EIF5), mRNA. /FEA=mRNA /GEN=EIF5 /PROD=eukaryotic translation initiation factor 5 /DB_XREF=gi:4503542 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:U49436.1 gb:NM_001969.1	
212247_at	C7orf14	AW008531	chromosome 7 open reading frame 14	
212266_s_at	SFRS5	AW084582	splicing factor, arginine/serine-rich 5	

208498_s_at	NM_004038	gb:NM_004038.1 /DEF=Homo sapiens amylase, alpha 1A; salivary (AMY1A), mRNA. /FEA=CDS /GEN=AMY1A /PROD=amylase, alpha 1A; salivary /DB_XREF=gi:4757749 /UG=Hs.274376 amylase, alpha 1A; salivary /FL=gb:NM_004038.1
210216_x_at	AF084513	gb:AF084513.1 /DEF=Homo sapiens DNA repair exonuclease (REC1) mRNA, alternatively spliced product, complete cds. /FEA=mRNA /GEN=REC1 /PROD=DNA repair exonuclease /DB_XREF=gi:3600078 /UG=Hs.7179 RAD1 (S. pombe) homolog /FL=gb:AF084513.1 gb:AF090170.1



209298_s_at		AF114488	gb:AF114488.1 /DEF=Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds. /FEA=mRNA /GEN=ITSN /PROD=intersectin short isoform /DB_XREF=gi:4808824 /UG=Hs.66392 intersectin 1 (SH3 domain protein) /FL=gb:AF064243.1 gb:AF114488.1	
218997_at		NM_022490	gb:NM_022490.1 /DEF=Homo sapiens hypothetical protein FLJ13390 similar to PAF53 (FLJ13390), mRNA. /FEA=mRNA /GEN=FLJ13390 /PROD=hypothetical protein FLJ13390 similar to PAF53 /DB_XREF=gi:11968046 /UG=Hs.24884 hypothetical protein FLJ13390 similar to PAF53 /FL=gb:NM_022490.1 gb:BC001337.1	

219002_at		NM_024622	gb:NM_024622.1 /DEF=Homo sapiens hypothetical protein FLJ21901 (FLJ21901), mRNA. /FEA=mRNA /GEN=FLJ21901 /PROD=hypothetical protein FLJ21901 /DB_XREF=gi:13375843 /UG=Hs.32646 hypothetical protein FLJ21901 /FL=gb:NM_024622.1	
210275_s_at		AF062347	gb:AF062347.1 /DEF=Homo sapiens zinc finger protein 216 splice variant 2 (ZNF216) mRNA, complete cds. /FEA=mRNA /GEN=ZNF216 /PROD=zinc finger protein 216 splice variant 2 /DB_XREF=gi:3643810 /UG=Hs.3776 zinc finger protein 216 /FL=gb:AF062347.1	

209803_s_at		AF001294	gb:AF001294.1 /DEF=Homo sapiens IPL (IPL) mRNA, complete cds. /FEA=mRNA /GEN=IPL /PROD=IPL /DB_XREF=gi:2150049 /UG=Hs.154036 tumor suppressing subtransferable candidate 3 /FL=gb:BC005034.1 gb:AF001294.1 gb:AF019953.1 gb:AF035444.1 gb:NM_003311.1	
209409_at		D86962	gb:D86962.1 /DEF=Human mRNA for KIAA0207 gene, complete cds. /FEA=mRNA /GEN=KIAA0207 /DB_XREF=gi:1503997 /UG=Hs.81875 growth factor receptor-bound protein 10 /FL=gb:D86962.1 gb:AF000017.1	
209596_at		AF245505	gb:AF245505.1 /DEF=Homo sapiens adlcan mRNA, complete cds. /FEA=mRNA /PROD=adlcan /DB_XREF=gi:9280404 /UG=Hs.72157 DKFZP564I1922 protein /FL=gb:AF245505.1	

209561_at		L38969	gb:L38969.1 /DEF=Homo sapiens thrombospondin 3 (THBS3) mRNA, complete cds. /FEA=mRNA /GEN=THBS3 /PROD=thrombospondin 3 /DB_XREF=gi:886298 /UG=Hs.169875 thrombospondin 3 /FL=gb:NM_007112.1 gb:L38969.1	
209972_s_at		AF116615	gb:AF116615.1 /DEF=Homo sapiens PRO0992 mRNA, complete cds. /FEA=mRNA /PROD=PRO0992 /DB_XREF=gi:7959732 /UG=Hs.258730 heme-regulated initiation factor 2-alpha kinase /FL=gb:AF116615.1	
211161_s_at		AF130082	gb:AF130082.1 /DEF=Homo sapiens clone FLC1492 PRO3121 mRNA, complete cds. /FEA=mRNA /PROD=PRO3121 /DB_XREF=gi:11493468 /UG=Hs.119571 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) /FL=gb:AF130082.1	

209084_s_at		L14922	Consensus includes gb:BE504689 /FEA=EST /DB_XREF=gi:9707097 /DB_XREF=est:hz30h07.x1 /CLONE=IMAGE:3209533 /UG=Hs.166563 replication factor C (activator 1) 1 (145kD) /FL=gb:AF040250.1 gb:L14922.1	
209076_s_at		BC000974	gb:BC000974.2 /DEF=Homo sapiens, Similar to hypothetical protein 628, clone MGC:5116, mRNA, complete cds. /FEA=mRNA /PROD=Similar to hypothetical protein 628 /DB_XREF=gi:12803025 /UG=Hs.181349 hypothetical protein 628 /FL=gb:BC000974.2	

209014_at		AF217963	gb:AF217963.1 /DEF=Homo sapiens NRAGE mRNA, complete cds. /FEA=mRNA /PROD=NRAGE /DB_XREF=gi:9963809 /UG=Hs.177556 melanoma antigen, family D, 1 /FL=gb:AF132205.1 gb:AF124440.1 gb:NM_006986.1 gb:AF217963.1	
212240_s_at		M61906	Consensus includes gb:A1679268 /FEA=EST /DB_XREF=gi:4889450 /DB_XREF=est:tu62e04.x1 /CLONE=IMAGE:2255646 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
209025_s_at		AF037448	gb:AF037448.1 /DEF=Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds. /FEA=mRNA /GEN=GRY-RBP /PROD=Gry-rbp /DB_XREF=gi:3037012 /UG=Hs.155489 NS1-associated protein 1 /FL=gb:AF037448.1	

219038_at		NM_024657	gb:NM_024657.1 /DEF=Homo sapiens hypothetical protein FLJ11565 (FLJ11565), mRNA. /FEA=mRNA /GEN=FLJ11565 /PROD=hypothetical protein FLJ11565 /DB_XREF=gi:13375906 /UG=Hs.61763 hypothetical protein FLJ11565 /FL=gb:NM_024657.1	
209183_s_at		AL136653	gb:AL136653.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564P1263 (from clone DKFZp564P1263); complete cds. /FEA=mRNA /GEN=DKFZp564P1263 /PROD=hypothetical protein /DB_XREF=gi:6807650 /UG=Hs.93675 decidual protein induced by progesterone /FL=gb:AB022718.1 gb:NM_007021.1 gb:AL136653.1	

209185_s_at		AF073310	gb:AF073310.1 /DEF=Homo sapiens insulin receptor substrate-2 (IRS2) mRNA, complete cds. /FEA=mRNA /GEN=IRS2 /PROD=insulin receptor substrate-2 /DB_XREF=gi:4511968 /UG=Hs.143648 insulin receptor substrate 2 /FL=gb:NM_003749.1 gb:AF073310.1	
211058_x_at		BC006379	gb:BC006379.1 /DEF=Homo sapiens, tubulin alpha 1, clone MGC:12832, mRNA, complete cds. /FEA=mRNA /PROD=tubulin alpha 1 /DB_XREF=gi:13623540 /FL=gb:BC006379.1	
209118_s_at		AF141347	gb:AF141347.1 /DEF=Homo sapiens hum-a-tub2 alpha-tubulin mRNA, complete cds. /FEA=mRNA /PROD=alpha-tubulin /DB_XREF=gi:4929133 /UG=Hs.272897 Tubulin, alpha, brain-specific /FL=gb:AF141347.1 gb:NM_006009.1	



209106_at		U19179	Consensus includes gb:BF576458 /FEA=EST /DB_XREF=gi:11650170 /DB_XREF=est:602133875F1 /CLONE=IMAGE:4288891 /UG=Hs.74002 nuclear receptor coactivator 1 /FL=gb:U19179.1	
209169_at		AF016004	Consensus includes gb:N63576 /FEA=EST /DB_XREF=gi:1211405 /DB_XREF=est:yy63f07.s1 /CLONE=IMAGE:278245 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	
209168_at		AF016004	Consensus includes gb:AW148844 /FEA=EST /DB_XREF=gi:6196740 /DB_XREF=est:xf05c06.x1 /CLONE=IMAGE:2617162 /UG=Hs.5422 glycoprotein M6B /FL=gb:AF016004.1	

211063_s_at		BC006403	gb:BC006403.1 /DEF=Homo sapiens, NCK adaptor protein 1, clone MGC:12668, mRNA, complete cds. /FEA=mRNA /PROD=NCK adaptor protein 1 /DB_XREF=gi:13623576 /FL=gb:BC006403.1	
213004_at		AF007150	Consensus includes gb:AI074333 /FEA=EST /DB_XREF=gi:3400977 /DB_XREF=est:oz84a09.x1 /CLONE=IMAGE:1682008 /UG=Hs.8025 Homo sapiens clone 23767 and 23782 mRNA sequences	

203973_s_at		NM_005195	gb:NM_005195.1 /DEF=Homo sapiens CCAATenhancer binding protein (CEBP), delta (CEBPD), mRNA. /FEA=mRNA /GEN=CEBPD /PROD=CCAATenhancer binding protein (CEBP), delta /DB_XREF=gi:4885130 /UG=Hs.76722 CCAATenhancer binding protein (CEBP), delta /FL=gb:M83667.1 gb:NM_005195.1	
213068_at	DPT	AI146848	dermatopontin	
212918_at	RECQL	BF219234	RecQ protein-like (DNA helicase Q1-like)	
204615_x_at		NM_004508	gb:NM_004508.1 /DEF=Homo sapiens isopentenyl-diphosphate delta isomerase (IDI1), mRNA. /FEA=mRNA /GEN=IDI1 /PROD=isopentenyl-diphosphate delta isomerase /DB_XREF=gi:4758583 /UG=Hs.76038 isopentenyl-diphosphate delta isomerase /FL=gb:NM_004508.1	

204784_s_at		NM_022443	gb:NM_022443.1 /DEF=Homo sapiens myeloid leukemia factor 1 (MLF1), mRNA. /FEA=mRNA /GEN=MLF1 /PROD=myeloid leukemia factor 1 /DB_XREF=gi:11967974 /UG=Hs.85195 myeloid leukemia factor 1 /FL=gb:NM_022443.1	
204478_s_at		NM_002871	gb:NM_002871.1 /DEF=Homo sapiens RAB interacting factor (RABIF), mRNA. /FEA=mRNA /GEN=RABIF /PROD=RAB interacting factor /DB_XREF=gi:4506378 /UG=Hs.90875 RAB interacting factor /FL=gb:U74324.1 gb:NM_002871.1	
213001_at		AF007150	Consensus includes gb:AF007150.1 /DEF=Homo sapiens clone 23767 and 23782 mRNA sequences. /FEA=mRNA /DB_XREF=gi:2852628 /UG=Hs.8025 Homo sapiens clone 23767 and 23782 mRNA sequences	

204594_s_at		NM_013298	gb:NM_013298.1 /DEF=Homo sapiens hypothetical protein (HSU79252), mRNA. /FEA=mRNA /GEN=HSU79252 /PROD=hypothetical protein /DB_XREF=gi:9558736 /UG=Hs.240062 hypothetical protein /FL=gb:U79252.1 gb:NM_013298.1	
203659_s_at		NM_005798	gb:NM_005798.1 /DEF=Homo sapiens ret finger protein 2 (RFP2), mRNA. /FEA=mRNA /GEN=RFP2 /PROD=ret finger protein 2 /DB_XREF=gi:5031860 /UG=Hs.151428 ret finger protein 2 /FL=gb:AF220127.1 gb:AF220128.1 gb:NM_005798.1 gb:AF241850.1	

218315_s_at		NM_016408	gb:NM_016408.1 /DEF=Homo sapiens CGI-05 protein (LOC51654), mRNA. /FEA=mRNA /GEN=LOC51654 /PROD=hypothetical protein HSPC167 /DB_XREF=gi:7705484 /UG=Hs.306044 CGI-05 protein /FL=gb:AF161516.1 gb:NM_016408.1	
213198_at		AL117643	Consensus includes gb:AL117643.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245). /FEA=mRNA /DB_XREF=gi:5912233 /UG=Hs.5288 Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245)	

214823_at		AF033199	Consensus includes gb:AF033199.1 /DEF=Homo sapiens C2H2 zinc finger protein pseudogene, mRNA sequence. /FEA=mRNA /DB_XREF=gi:3252864 /UG=Hs.8198 zinc finger protein 204	
203656_at		NM_014845	gb:NM_014845.1 /DEF=Homo sapiens KIAA0274 gene product (KIAA0274), mRNA. /FEA=mRNA /GEN=KIAA0274 /PROD=KIAA0274 gene product /DB_XREF=gi:7662033 /UG=Hs.10037 KIAA0274 gene product /FL=gb:D87464.1 gb:NM_014845.1	

203910_at		NM_004815	gb:NM_004815.1 /DEF=Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA. /FEA=mRNA /GEN=PARG1 /PROD=PTPL1-associated RhoGAP 1 /DB_XREF=gi:4758881 /UG=Hs.70983 PTPL1-associated RhoGAP 1 /FL=gb:U90920.1 gb:NM_004815.1	
213139_at	SNAI2	AI572079	snail 2	
213113_s_at	EEG1	AI630178	likely ortholog of mouse embryonic epithelial gene 1	
220755_s_at		NM_016947	gb:NM_016947.1 /DEF=Homo sapiens G8 protein (G8), mRNA. /FEA=mRNA /GEN=G8 /PROD=G8 protein /DB_XREF=gi:8393383 /UG=Hs.109798 G8 protein /FL=gb:NM_016947.1	



220917_s_at		NM_025132	gb:NM_025132.1 /DEF=Homo sapiens KIAA1638 protein (KIAA1638), mRNA. /FEA=mRNA /GEN=KIAA1638 /PROD=hypothetical protein FLJ23127 /DB_XREF=gi:13386465 /UG=Hs.288821 KIAA1638 protein /FL=gb:NM_025132.1	
220936_s_at		NM_018267	gb:NM_018267.1 /DEF=Homo sapiens hypothetical protein FLJ10903 (FLJ10903), mRNA. /FEA=mRNA /GEN=FLJ10903 /PROD=hypothetical protein FLJ10903 /DB_XREF=gi:8922757 /UG=Hs.36727 hypothetical protein FLJ10903 /FL=gb:NM_018267.1	

203753_at		NM_003199	gb:NM_003199.1 /DEF=Homo sapiens transcription factor 4 (TCF4), mRNA. /FEA=mRNA /GEN=TCF4 /PROD=transcription factor 4, isoform b /DB_XREF=gi:4507398 /UG=Hs.326198 transcription factor 4 /FL=gb:M74719.1 gb:NM_003199.1	
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205679_x_at		NM_013227	gb:NM_013227.1 /DEF=Homo sapiens aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA. /FEA=mRNA /GEN=AGC1 /PROD=aggrecan 1, isoform 2 precursor /DB_XREF=gi:6995993 /UG=Hs.2159 aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) /FL=gb:NM_013227.1	
212485_at		AB011125	Consensus includes gb:AU146596 /FEA=EST /DB_XREF=gi:11008117 /DB_XREF=est:AU146596 /CLONE=HEMBB1000938 /UG=Hs.105749 KIAA0553 protein	

205499_at		NM_014467	gb:NM_014467.1 /DEF=Homo sapiens sushi-repeat protein (SRPUL), mRNA. /FEA=mRNA /GEN=SRPUL /PROD=sushi-repeat protein /DB_XREF=gi:7657618 /UG=Hs.126782 sushi-repeat protein /FL=gb:AF060567.1 gb:NM_014467.1	
212488_at	COL5A1	AI983428	collagen, type V, alpha 1	
205559_s_at		NM_006200	gb:NM_006200.1 /DEF=Homo sapiens proprotein convertase subtilisinkexin type 5 (PCSK5), mRNA. /FEA=mRNA /GEN=PCSK5 /PROD=proprotein convertase subtilisinkexin type 5 /DB_XREF=gi:11321618 /UG=Hs.94376 proprotein convertase subtilisinkexin type 5 /FL=gb:NM_006200.1 gb:U56387.2	

205510_s_at		NM_017976	gb:NM_017976.1 /DEF=Homo sapiens hypothetical protein FLJ10038 (FLJ10038), mRNA. /FEA=mRNA /GEN=FLJ10038 /PROD=hypothetical protein FLJ10038 /DB_XREF=gi:8922197 /UG=Hs.181202 hypothetical protein FLJ10038 /FL=gb:NM_017976.1	
218507_at		NM_013332	gb:NM_013332.1 /DEF=Homo sapiens hypoxia-inducible protein 2 (HIG2), mRNA. /FEA=mRNA /GEN=HIG2 /PROD=hypoxia-inducible protein 2 /DB_XREF=gi:7019408 /UG=Hs.61762 hypoxia-inducible protein 2 /FL=gb:BC001863.1 gb:AF144755.1 gb:NM_013332.1	

206307_s_at		NM_004472	gb:NM_004472.1 /DEF=Homo sapiens forkhead box D1 (FOXD1), mRNA. /FEA=mRNA /GEN=FOXD1 /PROD=forkhead box D1 /DB_XREF=gi:4758391 /UG=Hs.96028 forkhead box D1 /FL=gb:U59832.1 gb:NM_004472.1	
218465_at		NM_018126	gb:NM_018126.1 /DEF=Homo sapiens hypothetical protein FLJ10525 (FLJ10525), mRNA. /FEA=mRNA /GEN=FLJ10525 /PROD=hypothetical protein FLJ10525 /DB_XREF=gi:8922490 /UG=Hs.31082 hypothetical protein FLJ10525 /FL=gb:BC000948.1 gb:NM_018126.1	
212414_s_at		D50918	Consensus includes gb:D50918.1 /DEF=Human mRNA for KIAA0128 gene, partial cds. /FEA=mRNA /GEN=KIAA0128 /DB_XREF=gi:1469178 /UG=Hs.90998 KIAA0128 protein; septin 2	

220046_s_at		NM_020307	gb:NM_020307.1 /DEF=Homo sapiens cyclin L ania-6a (LOC57018), mRNA. /FEA=mRNA /GEN=LOC57018 /PROD=cyclin L ania-6a /DB_XREF=gi:9945319 /UG=Hs.4859 cyclin L ania-6a /FL=gb:AF180920.1 gb:NM_020307.1	
220137_at		NM_019086	gb:NM_019086.1 /DEF=Homo sapiens hypothetical protein FLJ20674 (FLJ20674), mRNA. /FEA=mRNA /GEN=FLJ20674 /PROD=hypothetical protein FLJ20674 /DB_XREF=gi:9506690 /UG=Hs.152519 hypothetical protein FLJ20674 /FL=gb:NM_019086.1	

212723_at		AK021780	Consensus includes gb:AK021780.1 /DEF=Homo sapiens cDNA FLJ11718 fis, clone HEMBA1005252, highly similar to Homo sapiens mRNA for KIAA0585 protein. /FEA=mRNA /DB_XREF=gi:10433034 /UG=Hs.72660 phosphatidylserine receptor	
205110_s_at		NM_004114	gb:NM_004114.1 /DEF=Homo sapiens fibroblast growth factor 13 (FGF13), mRNA. /FEA=mRNA /GEN=FGF13 /PROD=fibroblast growth factor 13 /DB_XREF=gi:4758365 /UG=Hs.6540 fibroblast growth factor 13 /FL=gb:U66198.1 gb:AF100143.1 gb:NM_004114.1	
212787_at	ZAP3	AI952986	ZAP3 protein	



204797_s_at	NM_004434	gb:NM_004434.1 /DEF=Homo sapiens echinoderm microtubule-associated protein-like (EMAPL), mRNA. /FEA=mRNA /GEN=EMAPL /PROD=echinoderm microtubule-associated protein-like /DB_XREF=gi:4758267 /UG=Hs.12451 echinoderm microtubule-associated protein-like /FL=gb:U97018.1 gb:NM_004434.1
205079_s_at	NM_003829	gb:NM_003829.1 /DEF=Homo sapiens multiple PDZ domain protein (MPDZ), mRNA. /FEA=mRNA /GEN=MPDZ /PROD=multiple PDZ domain protein /DB_XREF=gi:4505230 /UG=Hs.169378 multiple PDZ domain protein /FL=gb:AF093419.1 gb:NM_003829.1

205413_at		NM_001584	gb:NM_001584.1 /DEF=Homo sapiens chromosome 11 open reading frame 8 (C11ORF8), mRNA. /FEA=mRNA /GEN=C11ORF8 /PROD=chromosome 11 open reading frame 8 /DB_XREF=gi:4502484 /UG=Hs.46638 chromosome 11 open reading frame 8 /FL=gb:U57911.1 gb:NM_001584.1	
205351_at		NM_000821	gb:NM_000821.1 /DEF=Homo sapiens gamma-glutamyl carboxylase (GGCX), mRNA. /FEA=mRNA /GEN=GGCX /PROD=gamma-glutamyl carboxylase /DB_XREF=gi:4503984 /UG=Hs.77719 gamma-glutamyl carboxylase /FL=gb:L17128.1 gb:M81592.1 gb:NM_000821.1	
212463_at	CD59	BE379006	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	
212489_at	COL5A1	AI983428	collagen, type V, alpha 1	

212717_at		AJ002220	Consensus includes gb:AB002354.2 /DEF=Homo sapiens mRNA for KIAA0356 protein, partial cds. /FEA=mRNA /GEN=KIAA0356 /PROD=KIAA0356 protein /DB_XREF=gi:6634022 /UG=Hs.32312 KIAA0356 gene product	
205348_s_at		NM_004411	gb:NM_004411.1 /DEF=Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA. /FEA=mRNA /GEN=DNCI1 /PROD=dynein, cytoplasmic, intermediate polypeptide 1 /DB_XREF=gi:4758177 /UG=Hs.65248 dynein, cytoplasmic, intermediate polypeptide 1 /FL=gb:AF063228.1 gb:NM_004411.1	

**Table 7b: depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for (a) severe OA only in OA cartilage as compared to cartilage isolated from normal individuals using the Affymetrix™ U133A Array analysis as disclosed herein.**

Gene name	Common name	Genbank	Description	GefSeq
202465_at		NM_002593	gb:NM_002593.2 /DEF=Homo sapiens procollagen C-endopeptidase enhancer (PCOLCE), mRNA. /FEA=mRNA /GEN=PCOLCE /PROD=procollagen C-endopeptidase enhancer /DB_XREF=gi:7262388 /UG=Hs.202097 procollagen C-endopeptidase enhancer /FL=gb:BC000574.1 gb:AB008549.1 gb:L33799.1 gb:NM_002593.2	
202613_at		NM_001905	gb:NM_001905.1 /DEF=Homo sapiens CTP synthase (CTPS), mRNA. /FEA=mRNA /GEN=CTPS /PROD=CTP synthase /DB_XREF=gi:4503132 /UG=Hs.251871 CTP synthase /FL=gb:NM_001905.1	
205851_at		BC001808	gb:BC001808.1 /DEF=Homo sapiens, nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha), clone MGC:1889, mRNA, complete cds. /FEA=mRNA /PROD=nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha) /DB_XREF=gi:12804744 /UG=Hs.152717 nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha) /FL=gb:BC001808.1 gb:BC001850.1 gb:U90449.1 gb:AF051941.1 gb:NM_005793.1	
214005_at	FHL2	BE326952	four and a half LIM domains 2	

203190_at		NM_002496	gb:NM_002496.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase) (NDUFS8), mRNA. /FEA=mRNA /GEN=NDUFS8 /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 8(23kD) (NADH-coenzyme Q reductase) /DB_XREF=gi:4505370 /UG=Hs.90443 NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase) /FL=gb:U65579.1 gb:NM_002496.1	
209836_x_at		AF060511	gb:AF060511.1 /DEF=Homo sapiens clone 016b10 My016 protein mRNA, complete cds. /FEA=mRNA /PROD=My016 protein /DB_XREF=gi:12001971 /UG=Hs.181634 Homo sapiens cDNA: FLJ23602 fis, clone LNG15735 /FL=gb:AF060511.1	
34031_i_at	CCM1	U90268	cerebral cavernous malformations 1	NM_004912
206364_at		NM_014875	gb:NM_014875.1 /DEF=Homo sapiens KIAA0042 gene product (KIAA0042), mRNA. /FEA=mRNA /GEN=KIAA0042 /PROD=KIAA0042 gene product /DB_XREF=gi:7661877 /UG=Hs.3104 KIAA0042 gene product /FL=gb:D26361.1 gb:NM_014875.1	
204290_s_at		NM_005589	gb:NM_005589.1 /DEF=Homo sapiens methylmalonate-semialdehyde dehydrogenase (MMSDH), mRNA. /FEA=mRNA /GEN=MMSDH /PROD=methylmalonate-semialdehyde dehydrogenase /DB_XREF=gi:11095440 /UG=Hs.293970 methylmalonate-semialdehyde dehydrogenase /FL=gb:NM_005589.1 gb:BC004909.1 gb:M93405.1 gb:AF148505.1 gb:AF159889.1	

206085_s_at		NM_001902	gb:NM_001902.1 /DEF=Homo sapiens cystathionase (cystathionine gamma-lyase) (CTH), mRNA. /FEA=mRNA /GEN=CTH /PROD=cystathionase (cystathionine gamma-lyase) /DB_XREF=gi:4503124 /UG=Hs.19904 cystathionase (cystathionine gamma-lyase) /FL=gb:NM_001902.1	
201369_s_at		NM_006887	gb:NM_006887.1 /DEF=Homo sapiens butyrate response factor 2 (EGF-response factor 2) (BRF2), mRNA. /FEA=mRNA /GEN=BRF2 /PROD=butyrate response factor 2 (EGF-response factor2) /DB_XREF=gi:5901899 /UG=Hs.78909 butyrate response factor 2 (EGF-response factor 2) /FL=gb:BC005010.1 gb:NM_006887.1	
209439_s_at		D38616	gb:D38616.1 /DEF=Human mRNA for phosphorylase kinase alpha subunit, complete cds. /FEA=mRNA /PROD=phosphorylase kinase alpha subunit /DB_XREF=gi:1304117 /UG=Hs.54941 phosphorylase kinase, alpha 2 (liver) /FL=gb:D38616.1 gb:NM_000292.1	
207501_s_at		NM_004113	gb:NM_004113.2 /DEF=Homo sapiens fibroblast growth factor 12B (FGF12B), mRNA. /FEA=mRNA /GEN=FGF12B /PROD=fibroblast growth factor 12B /DB_XREF=gi:5729823 /UG=Hs.326401 fibroblast growth factor 12B /FL=gb:U76381.2 gb:NM_004113.2	
209770_at		U90552	gb:U90552.1 /DEF=Human butyrophilin (BTF5) mRNA, complete cds. /FEA=mRNA /GEN=BTF5 /PROD=butyrophilin /DB_XREF=gi:2062705 /UG=Hs.284283 butyrophilin, subfamily 3, member A1 /FL=gb:U90552.1	
209209_s_at	MIG2	AW469573	mitogen inducible 2	

			gb:NM_017566.1 /DEF=Homo sapiens hypothetical protein DKFZp434G0522 (DKFZp434G0522), mRNA. /FEA=mRNA /GEN=DKFZp434G0522 /PROD=hypothetical protein DKFZp434G0522 /DB_XREF=gi:8922135 /UG=Hs.67991 hypothetical protein DKFZp434G0522 /FL=gb:NM_017566.1	
221219_s_at		NM_017566		
217620_s_at	PIK3CB	AA805318	phosphoinositide-3-kinase, catalytic, beta polypeptide	
			gb:NM_014763.1 /DEF=Homo sapiens mitochondrial ribosomal protein L19 (MRPL19), mRNA. /FEA=mRNA /GEN=MRPL19 /PROD=mitochondrial ribosomal protein L19 /DB_XREF=gi:7661911 /UG=Hs.75574 mitochondrial ribosomal protein L19 /FL=gb:D14660.1 gb:NM_014763.1	
203465_at		NM_014763		
			gb:NM_014060.1 /DEF=Homo sapiens MCT-1 protein (MCT-1), mRNA. /FEA=mRNA /GEN=MCT-1 /PROD=MCT-1 protein /DB_XREF=gi:7662501 /UG=Hs.102696 MCT-1 protein /FL=gb:BC001013.1 gb:AB034206.1 gb:NM_014060.1	
218163_at		NM_014060		
			gb:U25147.1 /DEF=Human citrate transporter protein mRNA, nuclear gene encoding mitochondrial protein, complete cds. /FEA=mRNA /PROD=citrate transporter protein /DB_XREF=gi:950003 /UG=Hs.111024 solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 /FL=gb:U25147.1	
210010_s_at		U25147		
			gb:NM_003188.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase 7 (MAP3K7), mRNA. /FEA=mRNA /GEN=MAP3K7 /PROD=mitogen-activated protein kinase kinase kinase7 /DB_XREF=gi:4507360 /UG=Hs.7510 mitogen-activated protein kinase kinase kinase 7 /FL=gb:AB009356.1	
206854_s_at		NM_003188		

			gb:NM_003188.1	
212523_s_at		D63480	Consensus includes gb:D63480.1 /DEF=Human mRNA for KIAA0146 gene, partial cds. /FEA=mRNA /GEN=KIAA0146 /DB_XREF=gi:1469873 /UG=Hs.278634 KIAA0146 protein	
222023_at		AK022014	Consensus includes gb:AK022014.1 /DEF=Homo sapiens cDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA. /FEA=mRNA /DB_XREF=gi:10433327 /UG=Hs.306619 Homo sapiens cDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA	
202594_at		NM_015344	gb:NM_015344.1 /DEF=Homo sapiens MY047 protein (MY047), mRNA. /FEA=mRNA /GEN=MY047 /PROD=MY047 protein /DB_XREF=gi:7662509 /UG=Hs.11000 leptin receptor overlapping transcript-like 1 /FL=gb:BC000642.1 gb:AF063605.1 gb:AF161461.1 gb:NM_015344.1	
212764_at		U19969	Consensus includes gb:AI806174 /FEA=EST /DB_XREF=gi:5392740 /DB_XREF=est:wf06h03.x1 /CLONE=IMAGE:2349845 /UG=Hs.232068 transcription factor 8 (represses interleukin 2 expression)	
218518_at		NM_016603	gb:NM_016603.1 /DEF=Homo sapiens GAP-like protein (LOC51306), mRNA. /FEA=mRNA /GEN=LOC51306 /PROD=GAP-like protein /DB_XREF=gi:7706136 /UG=Hs.82035 potential nuclear	



			protein C5ORF5; GAP-like protein /FL=gb:AF251038.1 gb:AF157316.1 gb:NM_016603.1	
209575_at		BC001903	gb:BC001903.1 /DEF=Homo sapiens, Similar to interleukin 10 receptor, beta, clone MGC:2210, mRNA, complete cds. /FEA=mRNA /PROD=Similar to interleukin 10 receptor, beta /DB_XREF=gi:12804902 /UG=Hs.173936 interleukin 10 receptor, beta /FL=gb:BC001903.1 gb:NM_000628.1	
213766_x_at	MGC3298	N36926	hypothetical protein MGC3298	
207936_x_at		NM_006604	gb:NM_006604.1 /DEF=Homo sapiens ret finger protein-like 3 (RFPL3), mRNA. /FEA=mRNA /GEN=RFPL3 /PROD=ret finger protein-like 3 /DB_XREF=gi:5730012 /UG=Hs.167751 ret finger protein-like 3 /FL=gb:NM_006604.1	
208737_at		BC003564	gb:BC003564.1 /DEF=Homo sapiens, ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J, clone MGC:1970, mRNA, complete cds. /FEA=mRNA /PROD=ATPase, H+ transporting, lysosomal (vacuolarproton pump), member J /DB_XREF=gi:13097719 /UG=Hs.90336 ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J /FL=gb:BC003564.1 gb:AF038954.1 gb:NM_004888.1	
208792_s_at		M25915	gb:M25915.1 /DEF=Human complement cytolysis inhibitor (CLI) mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:180619 /UG=Hs.75106 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) /FL=gb:J02908.1 gb:M25915.1	

			gb:M64722.1 gb:NM_001831.1	
208643_s_at		J04977	gb:J04977.1 /DEF=Human Ku autoimmune antigen gene, complete cds. /FEA=mRNA /GEN=G22P1 /DB_XREF=gi:186791 /UG=Hs.84981 X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kD) /FL=gb:NM_021141.2 gb:J04977.1 gb:M30938.1	
208682_s_at		AF126181	gb:AF126181.1 /DEF=Homo sapiens breast cancer-associated gene 1 protein (BCG1) mRNA, complete cds. /FEA=mRNA /GEN=BCG1 /PROD=breast cancer-associated gene 1 protein /DB_XREF=gi:4732088 /UG=Hs.4943 hepatocellular carcinoma associated protein; breast cancer associated gene 1 /FL=gb:NM_006787.1 gb:BC000304.1 gb:U92544.1 gb:AF126181.1 gb:AF128527.1 gb:AF128528.1	
210554_s_at		BC002486	gb:BC002486.1 /DEF=Homo sapiens, C-terminal binding protein 2, clone MGC:1563, mRNA, complete cds. /FEA=mRNA /PROD=C-terminal binding protein 2 /DB_XREF=gi:12803334 /UG=Hs.171391 C-terminal binding protein 2 /FL=gb:BC002486.1	
209574_s_at	C18orf1	AI349506	chromosome 18 open reading frame 1	
209666_s_at		AF080157	gb:AF080157.1 /DEF=Homo sapiens Ikb kinase-a (IKK-alpha) mRNA, complete cds. /FEA=mRNA /GEN=IKK-alpha /PROD=Ikb kinase-a /DB_XREF=gi:4185272 /UG=Hs.198998 conserved helix-loop-helix ubiquitous	

			kinase /FL=gb:U22512.1 gb:AF012890.1 gb:AF009225.1 gb:AF080157.1 gb:NM_001278.1	
211068_x_at		BC006456	gb:BC006456.1 /DEF=Homo sapiens, clone MGC:1426, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:1426) /DB_XREF=gi:13623660 /FL=gb:BC006456.1	
211240_x_at		AB002382	gb:AB002382.1 /DEF=Human mRNA for KIAA0384 gene, complete cds. /FEA=mRNA /GEN=KIAA0384 /DB_XREF=gi:2224708 /UG=Hs.166011 catenin (cadherin-associated protein), delta 1 /FL=gb:AB002382.1	
210645_s_at		D83077	gb:D83077.1 /DEF=Homo sapiens mRNA for TPRD, complete cds. /FEA=mRNA /PROD=TPRD /DB_XREF=gi:1304131 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:D83077.1	
209056_s_at	CDC5L	AW268817	CDC5 cell division cycle 5-like (S. pombe)	
209148_at		BC001167	gb:BC001167.1 /DEF=Homo sapiens, retinoid X receptor, beta, clone MGC:1831, mRNA, complete cds. /FEA=mRNA /PROD=retinoid X receptor, beta /DB_XREF=gi:12654658 /UG=Hs.79372 retinoid X receptor, beta /FL=gb:NM_021976.1 gb:BC001167.1 gb:M84820.1	
209175_at		AK001135	Consensus includes gb:AK001135.1 /DEF=Homo sapiens cDNA FLJ10273 fis, clone HEMBB1001137, highly similar to Homo sapiens mRNA for putative phospholipase. /FEA=mRNA /DB_XREF=gi:7022202 /UG=Hs.300208 Sec23-interacting protein p125 /FL=gb:BC002540.1 gb:AB019435.1 gb:NM_007190.1	

209551_at		BC004875	gb:BC004875.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2310034L04 gene /DB_XREF=gi:13436109 /UG=Hs.66309 Homo sapiens, Similar to RIKEN cDNA 2310034L04 gene, clone MGC:11061, mRNA, complete cds /FL=gb:BC004875.1	
209046_s_at		AB030710	gb:AB030710.1 /DEF=Homo sapiens FLC3A mRNA for MAP1 light chain 3 related protein, complete cds. /FEA=mRNA /GEN=FLC3A /PROD=MAP1 light chain 3 related protein /DB_XREF=gi:12641848 /UG=Hs.6518 ganglioside expression factor 2 /FL=gb:AB030710.1 gb:AF087848.1 gb:AF077046.1 gb:NM_007285.1	
209267_s_at		AB040120	gb:AB040120.1 /DEF=Homo sapiens mRNA for BCG induced integral membrane protein BIGMo-103, complete cds. /FEA=mRNA /GEN=BIGMo-103 /PROD=BCG induced integral membrane protein BIGMo-103 /DB_XREF=gi:12657580 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:AB040120.1	
209355_s_at		AB000889	gb:AB000889.1 /DEF=Homo sapiens mRNA for phosphatidic acid phosphatase 2b, complete cds. /FEA=mRNA /PROD=phosphatidic acid phosphatase 2b /DB_XREF=gi:2467299 /UG=Hs.331371 phosphatidic acid phosphatase type 2B /FL=gb:U79294.1 gb:AB000889.1 gb:AF017786.1	
202867_s_at		NM_017626	gb:NM_017626.1 /DEF=Homo sapiens hypothetical protein FLJ20027 (FLJ20027), mRNA. /FEA=mRNA /GEN=FLJ20027 /PROD=hypothetical protein FLJ20027 /DB_XREF=gi:8923029	

			/UG=Hs.7960 DnaJ (Hsp40) homolog, subfamily B, member 12 /FL=gb:NM_017626.1	
202985_s_at		NM_004873	gb:NM_004873.1 /DEF=Homo sapiens BCL2-associated athanogene 5 (BAG5), mRNA. /FEA=mRNA /GEN=BAG5 /PROD=BCL2-associated athanogene 5 /DB_XREF=gi:6631076 /UG=Hs.5443 BCL2-associated athanogene 5 /FL=gb:AF095195.2 gb:NM_004873.1	
202753_at		NM_014814	gb:NM_014814.1 /DEF=Homo sapiens KIAA0107 gene product (KIAA0107), mRNA. /FEA=mRNA /GEN=KIAA0107 /PROD=KIAA0107 gene product /DB_XREF=gi:7661913 /UG=Hs.23488 KIAA0107 gene product /FL=gb:BC000630.1 gb:BC000904.2 gb:D14663.1 gb:AF215935.1 gb:NM_014814.1	
203359_s_at	MYCBP	AL525412	c-myc binding protein	
203491_s_at	KIAA0092	AI123527	KIAA0092 gene product	
203522_at		NM_005125	gb:NM_005125.1 /DEF=Homo sapiens copper chaperone for superoxide dismutase (CCS), mRNA. /FEA=mRNA /GEN=CCS /PROD=copper chaperone for superoxide dismutase /DB_XREF=gi:4826664 /UG=Hs.5002 copper chaperone for superoxide dismutase /FL=gb:AF002210.1 gb:NM_005125.1	
203168_at		NM_004381	gb:NM_004381.1 /DEF=Homo sapiens cAMP responsive element binding protein-like 1 (CREBL1), mRNA. /FEA=mRNA /GEN=CREBL1 /PROD=cAMP responsive element binding protein-like 1 /DB_XREF=gi:4758057 /UG=Hs.42853 cAMP responsive element binding protein-like 1 /FL=gb:U31903.1 gb:NM_004381.1	
203197_s_at	CPT2	AW157077	carnitine palmitoyltransferase II	

203351_s_at		AF047598	gb:AF047598.1 /DEF=Homo sapiens origin recognition complex subunit 4 (ORC4L) mRNA, complete cds. /FEA=mRNA /GEN=ORC4L /PROD=origin recognition complex subunit 4 /DB_XREF=gi:2906225 /UG=Hs.55055 origin recognition complex, subunit 4 (yeast homolog)-like /FL=gb:BC005388.1 gb:AF022108.1 gb:AF047598.1 gb:NM_002552.1 gb:AF132596.1	
201948_at		NM_013285	gb:NM_013285.1 /DEF=Homo sapiens nucleolar GTPase (HUMAUANTIG), mRNA. /FEA=mRNA /GEN=HUMAUANTIG /PROD=nucleolar GTPase /DB_XREF=gi:7019418 /UG=Hs.75528 nucleolar GTPase /FL=gb:BC000107.1 gb:L05425.1 gb:NM_013285.1	
201989_s_at		NM_001310	Consensus includes gb:AL529409 /FEA=EST /DB_XREF=gi:12792902 /DB_XREF=est:AL529409 /CLONE=CS0DD006YM17 (3 prime) /UG=Hs.13313 cAMP responsive element binding protein-like 2 /FL=gb:AF039081.1 gb:NM_001310.1	
202182_at		NM_021078	gb:NM_021078.1 /DEF=Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA. /FEA=mRNA /GEN=GCN5L2 /PROD=GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 /DB_XREF=gi:10835100 /UG=Hs.101067 GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 /FL=gb:NM_021078.1	
201842_s_at	EFEMP1	AI826799	EGF-containing fibulin-like extracellular matrix protein 1	
201912_s_at		NM_002094	gb:NM_002094.1 /DEF=Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA. /FEA=mRNA /GEN=GSPT1 /PROD=G1 to S phase transition 1	

			/DB_XREF=gi:4504166 /UG=Hs.2707 G1 to S phase transition 1 /FL=gb:NM_002094.1	
202662_s_at		NM_002223	gb:NM_002223.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA. /FEA=mRNA /GEN=ITPR2 /PROD=inositol 1,4,5-triphosphate receptor, type 2 /DB_XREF=gi:4504792 /UG=Hs.238272 inositol 1,4,5-triphosphate receptor, type 2 /FL=gb:D26350.1 gb:NM_002223.1	
202197_at		NM_021090	gb:NM_021090.1 /DEF=Homo sapiens myotubularin related protein 3 (MTMR3), mRNA. /FEA=mRNA /GEN=MTMR3 /PROD=myotubularin related protein 3 /DB_XREF=gi:10835108 /UG=Hs.63302 myotubularin related protein 3 /FL=gb:NM_021090.1 gb:AB002369.1 gb:AF233438.1	
202341_s_at	TRIM2	AA149745	tripartite motif-containing 2	
202361_at		NM_004922	gb:NM_004922.1 /DEF=Homo sapiens SEC24 (S. cerevisiae) related gene family, member C (SEC24C), mRNA. /FEA=mRNA /GEN=SEC24C /PROD=SEC24 (S. cerevisiae) related gene family, member C /DB_XREF=gi:4758633 /UG=Hs.81964 SEC24 (S. cerevisiae) related gene family, member C /FL=gb:NM_004922.1 gb:D38555.1	
204616_at		NM_006002	gb:NM_006002.1 /DEF=Homo sapiens ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3), mRNA. /FEA=mRNA /GEN=UCHL3 /PROD=ubiquitin carboxyl-terminal esterase L3(ubiquitin thiolesterase) /DB_XREF=gi:5174740 /UG=Hs.77917 ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) /FL=gb:M30496.1	

			gb:NM_006002.1	
204897_at		NM_000958	Consensus includes gb:AA897516 /FEA=EST /DB_XREF=gi:3034136 /DB_XREF=est:aj62c04.s1 /CLONE=IMAGE:1394886 /UG=Hs.199248 prostaglandin E receptor 4 (subtype EP4) /FL=gb:D28472.1 gb:L25124.1 gb:NM_000958.1 gb:L28175.1	
205412_at		NM_000019	gb:NM_000019.1 /DEF=Homo sapiens acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) (ACAT1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=ACAT1 /PROD=acetyl-Coenzyme A acetyltransferase 1 precursor /DB_XREF=gi:4557236 /UG=Hs.37 acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) /FL=gb:NM_000019.1	
206227_at		NM_003613	gb:NM_003613.1 /DEF=Homo sapiens cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA. /FEA=mRNA /GEN=CILP /PROD=cartilage intermediate layer protein /DB_XREF=gi:4502844 /UG=Hs.151407 cartilage intermediate layer protein, nucleotide pyrophosphohydrolase /FL=gb:AF035408.1 gb:NM_003613.1	
205908_s_at		NM_005014	gb:NM_005014.1 /DEF=Homo sapiens osteomodulin (OMD), mRNA. /FEA=mRNA /GEN=OMD /PROD=osteomodulin /DB_XREF=gi:4826875 /UG=Hs.94070 osteomodulin /FL=gb:AB000114.1 gb:NM_005014.1	



206007_at		NM_005807	gb:NM_005807.1 /DEF=Homo sapiens proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) (PRG4), mRNA. /FEA=mRNA /GEN=PRG4 /PROD=megakaryocyte stimulating factor /DB_XREF=gi:5031924 /UG=Hs.218791 proteoglycan 4, (megakaryocyte stimulating factor, articular superficial zone protein) /FL=gb:U70136.1 gb:NM_005807.1	
203730_s_at	ZFP95	BF196931	zinc finger protein 95 homolog (mouse)	
204012_s_at	KIAA0547	AL529189	KIAA0547 gene product	
203668_at		NM_006715	gb:NM_006715.1 /DEF=Homo sapiens mannosidase, alpha, class 2C, member 1 (MAN2C1), mRNA. /FEA=mRNA /GEN=MAN2C1 /PROD=mannosidase, alpha 6A8 /DB_XREF=gi:6631092 /UG=Hs.26232 mannosidase, alpha, class 2C, member 1 /FL=gb:U37248.1 gb:AF044414.2 gb:NM_006715.1	
204568_at		NM_014924	gb:NM_014924.1 /DEF=Homo sapiens KIAA0831 protein (KIAA0831), mRNA. /FEA=mRNA /GEN=KIAA0831 /PROD=KIAA0831 protein /DB_XREF=gi:7662325 /UG=Hs.103000 KIAA0831 protein /FL=gb:AB020638.1 gb:NM_014924.1	
204569_at		NM_014920	gb:NM_014920.1 /DEF=Homo sapiens MAK-related kinase (KIAA0936), mRNA. /FEA=mRNA /GEN=KIAA0936 /PROD=KIAA0936 protein /DB_XREF=gi:7662387 /UG=Hs.108850 MAK-related kinase /FL=gb:AF152469.1 gb:AB023153.1 gb:AF225919.1 gb:NM_014920.1 gb:NM_016513.1	
204604_at		NM_012395	gb:NM_012395.1 /DEF=Homo sapiens PFTAIR protein kinase 1 (PFTK1), mRNA. /FEA=mRNA /GEN=PFTK1 /PROD=PFTAIR protein kinase 1 /DB_XREF=gi:6912583	

			/UG=Hs.57856 PFTAIRES protein kinase 1 /FL=gb:AB020641.1 gb:NM_012395.1	
204145_at		NM_004477	gb:NM_004477.1 /DEF=Homo sapiens FSHD region gene 1 (FRG1), mRNA. /FEA=mRNA /GEN=FRG1 /PROD=FSHD region gene 1 /DB_XREF=gi:4758403 /UG=Hs.203772 FSHD region gene 1 /FL=gb:L76159.1 gb:NM_004477.1	
204279_at		NM_002800	gb:NM_002800.1 /DEF=Homo sapiens proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9), mRNA. /FEA=mRNA /GEN=PSMB9 /PROD=proteasome (prosome, macropain) subunit, betatype, 9 (large multifunctional protease 2) /DB_XREF=gi:4506204 /UG=Hs.9280 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) /FL=gb:U01025.1 gb:NM_002800.1	
218167_at		NM_016627	gb:NM_016627.1 /DEF=Homo sapiens hypothetical protein (LOC51321), mRNA. /FEA=mRNA /GEN=LOC51321 /PROD=hypothetical protein /DB_XREF=gi:7706167 /UG=Hs.268122 hypothetical protein /FL=gb:AF208856.1 gb:NM_016627.1	
218198_at		NM_018180	gb:NM_018180.1 /DEF=Homo sapiens hypothetical protein FLJ10889 (FLJ10889), mRNA. /FEA=mRNA /GEN=FLJ10889 /PROD=hypothetical protein FLJ10694 /DB_XREF=gi:9506626 /UG=Hs.171835 hypothetical protein FLJ10889 /FL=gb:BC002473.1 gb:NM_018180.1	

218027_at		NM_014175	gb:NM_014175.1 /DEF=Homo sapiens HSPC145 protein (HSPC145), mRNA. /FEA=mRNA /GEN=HSPC145 /PROD=HSPC145 protein /DB_XREF=gi:7661805 /UG=Hs.18349 HSPC145 protein /FL=gb:AL136665.1 gb:BC000891.1 gb:AF161494.1 gb:NM_014175.1	
217983_s_at		NM_003730	gb:NM_003730.2 /DEF=Homo sapiens ribonuclease 6 precursor (RNASE6PL), mRNA. /FEA=mRNA /GEN=RNASE6PL /PROD=ribonuclease 6 precursor /DB_XREF=gi:5231227 /UG=Hs.8297 ribonuclease 6 precursor /FL=gb:BC001660.1 gb:BC001819.1 gb:U85625.2 gb:NM_003730.2	
218341_at		NM_024664	gb:NM_024664.1 /DEF=Homo sapiens hypothetical protein FLJ11838 (FLJ11838), mRNA. /FEA=mRNA /GEN=FLJ11838 /PROD=hypothetical protein FLJ11838 /DB_XREF=gi:13375918 /UG=Hs.72531 hypothetical protein FLJ11838 /FL=gb:NM_024664.1	
217732_s_at		AF092128	gb:AF092128.1 /DEF=Homo sapiens putative transmembrane protein E3-16 mRNA, complete cds. /FEA=mRNA /PROD=putative transmembrane protein E3-16 /DB_XREF=gi:5138905 /UG=Hs.239625 integral membrane protein 2B /FL=gb:NM_021999.1 gb:AF136973.1 gb:BC000554.1 gb:AF092128.1 gb:AF152462.1 gb:AF246221.1	
216614_at		AL049988	Consensus includes gb:AL049988.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564F212 (from clone DKFZp564F212). /FEA=mRNA /DB_XREF=gi:4884239 /UG=Hs.306304 Homo sapiens mRNA; cDNA DKFZp564F212 (from clone DKFZp564F212)	

216396_s_at		AF131850	Consensus includes gb:AF131850.1 /DEF=Homo sapiens clone 24988 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4406694 /UG=Hs.286027 etoposide-induced mRNA	
217368_at		X69909	H.sapiens pseudogene for mitochondrial ATP synthase c subunit (P2 form).	
217907_at		NM_014161	gb:NM_014161.1 /DEF=Homo sapiens HSPC071 protein (HSPC071), mRNA. /FEA=mRNA /GEN=HSPC071 /PROD=HSPC071 protein /DB_XREF=gi:7661777 /UG=Hs.23038 HSPC071 protein /FL=gb:AL136633.1 gb:BC001623.1 gb:AF161556.1 gb:NM_014161.1	
217756_x_at		NM_005770	gb:NM_005770.1 /DEF=Homo sapiens small EDRK-rich factor 2 (SERF2), mRNA. /FEA=mRNA /GEN=SERF2 /PROD=small EDRK-rich factor 2 /DB_XREF=gi:5032084 /UG=Hs.323806 small EDRK-rich factor 2 /FL=gb:AF320073.1 gb:AF073298.1 gb:NM_005770.1	
217754_at		NM_019082	gb:NM_019082.1 /DEF=Homo sapiens putative nucleolar RNA helicase (NOH61), mRNA. /FEA=mRNA /GEN=NOH61 /PROD=putative nucleolar RNA helicase /DB_XREF=gi:9506930 /UG=Hs.10098 putative nucleolar RNA helicase /FL=gb:AF247666.1 gb:AL136700.1 gb:BC001235.1 gb:NM_019082.1	
217811_at		NM_016275	gb:NM_016275.1 /DEF=Homo sapiens selenoprotein T (LOC51714), mRNA. /FEA=mRNA /GEN=LOC51714 /PROD=selenoprotein T /DB_XREF=gi:7706470 /UG=Hs.8148 selenoprotein T /FL=gb:AF131856.1 gb:AF195141.1 gb:NM_016275.1	

216321_s_at		X03348	Consensus includes gb:X03348.1 /DEF=Human mRNA for beta-glucocorticoid receptor (clone OB10). /FEA=mRNA /PROD=beta- glucocorticoid receptor /DB_XREF=gi:31681 /UG=Hs.75772 nuclear receptor subfamily 3, group C, member 1	
221842_s_at	ZNF131	BE972394	zinc finger protein 131 (clone pHZ-10)	
221012_s_at		NM_030912	gb:NM_030912.1 /DEF=Homo sapiens tripartite motif protein TRIM8 (TRIM8), mRNA. /FEA=mRNA /GEN=TRIM8 /PROD=tripartite motif protein TRIM8 /DB_XREF=gi:13569865 /FL=gb:NM_030912.1	
221711_s_at		BC006244	gb:BC006244.1 /DEF=Homo sapiens, HSPC142 protein, clone MGC:11295, mRNA, complete cds. /FEA=mRNA /PROD=HSPC142 protein /DB_XREF=gi:13623286 /FL=gb:BC006244.1	
221564_at	HRMT1L1	AL570294	HMT1 hnRNP methyltransferase- like 1 (S. cerevisiae)	
46665_at	SEMA4C	AI949392	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	
64488_at		AW003091	Homo sapiens FKSG27 (FKSG27) mRNA, complete cds	
47530_at	HSPC219	AA748492	hypothetical protein HSPC219	
222370_x_at		N57781	ESTs, Moderately similar to neuronal thread protein [Homo sapiens] [H.sapiens]	
220467_at		NM_025032	gb:NM_025032.1 /DEF=Homo sapiens hypothetical protein FLJ21272 (FLJ21272), mRNA. /FEA=mRNA /GEN=FLJ21272 /PROD=hypothetical protein FLJ21272 /DB_XREF=gi:13376557 /UG=Hs.287653 hypothetical protein FLJ21272 /FL=gb:NM_025032.1	
219117_s_at		NM_016594	gb:NM_016594.1 /DEF=Homo sapiens FK506 binding protein precursor (LOC51303), mRNA. /FEA=mRNA /GEN=LOC51303 /PROD=FK506 binding protein	

			precursor /DB_XREF=gi:7706130 /UG=Hs.24048 FK506 binding protein precursor /FL=gb:AF238079.1 gb:NM_016594.1	
218487_at		BC000977	gb:BC000977.1 /DEF=Homo sapiens, aminolevulinate, delta- dehydratase, clone MGC:5057, mRNA, complete cds. /FEA=mRNA /PROD=aminolevulinate, delta- dehydratase /DB_XREF=gi:12654312 /UG=Hs.1227 aminolevulinate, delta-, dehydratase /FL=gb:BC000977.1 gb:M13928.1 gb:NM_000031.1	
218615_s_at		NM_018266	gb:NM_018266.1 /DEF=Homo sapiens hypothetical protein FLJ10902 (FLJ10902), mRNA. /FEA=mRNA /GEN=FLJ10902 /PROD=hypothetical protein FLJ10902 /DB_XREF=gi:8922755 /UG=Hs.247112 hypothetical protein FLJ10902 /FL=gb:NM_018266.1	
220419_s_at		NM_013396	gb:NM_013396.1 /DEF=Homo sapiens ubiquitin specific protease 25 (USP25), mRNA. /FEA=mRNA /GEN=USP25 /PROD=ubiquitin specific protease 25 /DB_XREF=gi:7019564 /UG=Hs.186961 ubiquitin specific protease 25 /FL=gb:AF134213.1 gb:NM_013396.1	
219200_at		NM_024091	gb:NM_024091.1 /DEF=Homo sapiens hypothetical protein MGC5297 (MGC5297), mRNA. /FEA=mRNA /GEN=MGC5297 /PROD=hypothetical protein MGC5297 /DB_XREF=gi:13129089 /UG=Hs.23856 hypothetical protein MGC5297 /FL=gb:BC001295.1 gb:NM_024091.1	

219303_at		NM_024546	gb:NM_024546.1 /DEF=Homo sapiens hypothetical protein FLJ13449 (FLJ13449), mRNA. /FEA=mRNA /GEN=FLJ13449 /PROD=hypothetical protein FLJ13449 /DB_XREF=gi:13375708 /UG=Hs.10711 hypothetical protein FLJ13449 /FL=gb:AL136651.1 gb:NM_024546.1	
212805_at		AB002365	Consensus includes gb:AB002365.1 /DEF=Human mRNA for KIAA0367 gene, partial cds. /FEA=mRNA /GEN=kIAA0367 /DB_XREF=gi:2224674 /UG=Hs.23311 KIAA0367 protein	
212603_at		NM_005830	Consensus includes gb:NM_005830.1 /DEF=Homo sapiens imogen 38 (IMOGN38), mRNA. /FEA=CDS /GEN=IMOGN38 /PROD=imogen 38 /DB_XREF=gi:5031786 /UG=Hs.154655 imogen 38 /FL=gb:NM_005830.1	
212846_at		D80001	Consensus includes gb:AA811192 /FEA=EST /DB_XREF=gi:2880803 /DB_XREF=est:ob72b08.s1 /CLONE=IMAGE:1336887 /UG=Hs.152629 KIAA0179 protein	
212538_at	zizimin1	AL576253	zizimin1	
212441_at		D86985	Consensus includes gb:D86985.2 /DEF=Homo sapiens mRNA for KIAA0232 protein, partial cds. /FEA=mRNA /GEN=KIAA0232 /PROD=KIAA0232 protein /DB_XREF=gi:6634002 /UG=Hs.79276 KIAA0232 gene product	
212542_s_at	PHIP	BF224151	pleckstrin homology domain interacting protein	
213010_at	PRKCDBP	AI088622	protein kinase C, delta binding protein	
213060_s_at		U58515	Consensus includes gb:U58515.1 /DEF=Human chitinase (HUMTCHIT) mRNA, exon 1b form, partial cds. /FEA=mRNA /GEN=HUMTCHIT /PROD=chitinase	

			/DB_XREF=gi:1439567 /UG=Hs.154138 chitinase 3-like 2	
212942_s_at		AB033025	Consensus includes gb:AB033025.1 /DEF=Homo sapiens mRNA for KIAA1199 protein, partial cds. /FEA=mRNA /GEN=KIAA1199 /PROD=KIAA1199 protein /DB_XREF=gi:6330400 /UG=Hs.50081 KIAA1199 protein	
212878_s_at	KNS2	AA284075	kinesin 2 60/70kDa	
212992_at	LOC113146	AI935123	hypothetical protein BC011859	
212977_at	RDC1	AI817041	G protein-coupled receptor	
212437_at		AL109804	Consensus includes gb:AL109804 /DEF=Human DNA sequence from clone RP5-1009E24 on chromosome 20 Contains a novel gene encoding two isoforms similar to mouse sialoadhesin (a macrophage sialic acid binding receptor), a novel gene similar to KIAA0417, the CENPB gene (centromere protein ... /FEA=mRNA_8 /DB_XREF=gi:11121192 /UG=Hs.85004 centromere protein B (80kD)	
211596_s_at		AB050468	gb:AB050468.1 /DEF=Homo sapiens mRNA for membrane glycoprotein LIG-1, complete cds. /FEA=mRNA /GEN=lig-1 /PROD=membrane glycoprotein LIG-1 /DB_XREF=gi:13537354 /FL=gb:AB050468.1	
211433_x_at		AL583909	gb:AL583909.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761J197 (from clone DKFZp761J197); complete cds. /FEA=mRNA /GEN=DKFZp761J197 /PROD=hypothetical protein /DB_XREF=gi:13093772 /UG=Hs.301696 hypothetical protein FLJ11560 /FL=gb:AL583909.1	



211760_s_at		BC005974	gb:BC005974.1 /DEF=Homo sapiens, vesicle-associated membrane protein 4, clone MGC:14658, mRNA, complete cds. /FEA=mRNA /PROD=vesicle-associated membrane protein 4 /DB_XREF=gi:13543647 /FL=gb:BC005974.1	
212243_at	GRINL1A	AI632774	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	
212061_at		AB002330	Consensus includes gb:AB002330.1 /DEF=Human mRNA for KIAA0332 gene, partial cds. /FEA=mRNA /GEN=KIAA0332 /DB_XREF=gi:2224604 /UG=Hs.7976 KIAA0332 protein	
212190_at	SERPINE2	AL541302	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	
215239_x_at	ZNF273	AU132789	zinc finger protein 273	
214783_s_at	ANXA11	BG177920	annexin A11	
214967_at		AU146983	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]	
216054_x_at	MYL4; GT1; ALC1; AMLC; PRO1957	X58851	Human MLC1emb gene for embryonic myosin alkaline light chain, promoter and exon 1.	NM_002476
216035_x_at	TCF7L2	AV721430	transcription factor 7-like 2 (T-cell specific, HMG-box)	
216095_x_at		AF057354	Consensus includes gb:AF057354.1 /DEF=Homo sapiens myotubularin-related protein 1a mRNA, partial cds. /FEA=mRNA /PROD=myotubularin-related protein 1a /DB_XREF=gi:5138901 /UG=Hs.23200 myotubularin related protein 1	
215336_at		AK002166	Consensus includes gb:AK002166.1 /DEF=Homo sapiens cDNA FLJ11304 fis, clone PLACE1009997, weakly similar to Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA. /FEA=mRNA /DB_XREF=gi:7023877 /UG=Hs.232076 A kinase (PRKA) anchor protein 11	

215333_x_at		X08020	Consensus includes gb:X08020.1 /DEF=Human mRNA for glutathione S- transferase subunit 4 (EC 2.5.1.18). /FEA=mRNA /DB_XREF=gi:31923 /UG=Hs.301961 glutathione S- transferase M4	
215898_at		AK021879	Consensus includes gb:AK021879.1 /DEF=Homo sapiens cDNA FLJ11817 fis, clone HEMBA1006421. /FEA=mRNA /DB_XREF=gi:10433165 /UG=Hs.293919 Homo sapiens cDNA FLJ11817 fis, clone HEMBA1006421	
214298_x_at	6-Sep	AL568374	septin 6	
213283_s_at	SALL2	BG285616	sal-like 2 (Drosophila)	
213154_s_at		AB014599	Consensus includes gb:AI934125 /FEA=EST /DB_XREF=gi:5672995 /DB_XREF=est:wn97c08.x1 /CLONE=IMAGE:2453774 /UG=Hs.17411 KIAA0699 protein	
213115_at		AL031177	Consensus includes gb:AL031177 /DEF=Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repea... /FEA=mRNA_3 /DB_XREF=gi:4071056 /UG=Hs.8763 Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protei	
213186_at	KIAA0675	BG502305	KIAA0675 gene product	
214080_x_at	PRKCSH	AI815793	protein kinase C substrate 80K-H	
213846_at	COX7C	AA382702	cytochrome c oxidase subunit VIIc	
213489_at	MAPRE2	BE671156	microtubule-associated protein,	

			RP/EB family, member 2	
213535_s_at	UBE2I	AA910614	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	
213103_at	STARD13	AA128023	START domain containing 13	
201040_at		NM_002070	gb:NM_002070.1 /DEF=Homo sapiens guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 (GNAI2), mRNA. /FEA=mRNA /GEN=GNAI2 /PROD=guanine nucleotide binding protein (G protein),alpha inhibiting activity polypeptide 2 /DB_XREF=gi:4504040 /UG=Hs.77269 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 /FL=gb:J03004.1 gb:NM_002070.1	
201088_at		NM_002266	gb:NM_002266.1 /DEF=Homo sapiens karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2), mRNA. /FEA=mRNA /GEN=KPNA2 /PROD=karyopherin alpha 2 /DB_XREF=gi:4504896 /UG=Hs.159557 karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /FL=gb:NM_002266.1 gb:U09559.1 gb:U28386.1	
201250_s_at		NM_006516	gb:NM_006516.1 /DEF=Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 1 (SLC2A1), mRNA. /FEA=mRNA /GEN=SLC2A1 /PROD=solute carrier family 2 (facilitated glucosetransporter), member 1 /DB_XREF=gi:5730050 /UG=Hs.169902 solute carrier family 2 (facilitated glucose transporter), member 1 /FL=gb:K03195.1 gb:NM_006516.1	
201577_at		NM_000269	gb:NM_000269.1 /DEF=Homo sapiens non-metastatic cells 1, protein (NME1), mRNA. /FEA=mRNA /GEN=NME1 /PROD=non-metastatic cells 1 protein /DB_XREF=gi:4557796 /UG=Hs.118638 non-metastatic	

			cells 1, protein (NM23A) expressed in /FL=gb:BC000293.1 gb:NM_000269.1	
201682_at		NM_004279	gb:NM_004279.1 /DEF=Homo sapiens peptidase (mitochondrial processing) beta (PMPCB), mRNA. /FEA=mRNA /GEN=PMPCB /PROD=peptidase (mitochondrial processing) beta /DB_XREF=gi:4758733 /UG=Hs.184211 peptidase (mitochondrial processing) beta /FL=gb:AF054182.1 gb:NM_004279.1	
201098_at		NM_004766	gb:NM_004766.1 /DEF=Homo sapiens coatomer protein complex, subunit beta 2 (beta prime) (COPB2), mRNA. /FEA=mRNA /GEN=COPB2 /PROD=coatomer protein complex, subunit beta 2 (betaprime) /DB_XREF=gi:4758031 /UG=Hs.75724 coatomer protein complex, subunit beta 2 (beta prime) /FL=gb:BC000326.1 gb:NM_004766.1	
200013_at		NM_000986	gb:NM_000986.1 /DEF=Homo sapiens ribosomal protein L24 (RPL24), mRNA. /FEA=mRNA /GEN=RPL24 /PROD=ribosomal protein L24 /DB_XREF=gi:4506618 /UG=Hs.184582 ribosomal protein L24 /FL=gb:BC000690.1 gb:M94314.1 gb:NM_000986.1	
200999_s_at		NM_006825	gb:NM_006825.1 /DEF=Homo sapiens transmembrane protein (63kD), endoplasmic reticulumGolgi intermediate compartment (P63), mRNA. /FEA=mRNA /GEN=P63 /PROD=transmembrane protein (63kD), endoplasmicreticulumGolgi intermediate compartment /DB_XREF=gi:5803112 /UG=Hs.74368 transmembrane protein (63kD), endoplasmic reticulumGolgi intermediate	

			compartment /FL=gb:NM_006825.1	
200008_s_at		D13988	gb:D13988.1 /DEF=Human rab GDI mRNA, complete cds. /FEA=mRNA /PROD=human rab GDI /DB_XREF=gi:285974 /UG=Hs.56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2	
201480_s_at		NM_003169	gb:NM_003169.1 /DEF=Homo sapiens suppressor of Ty (S.cerevisiae) 5 homolog (SUPT5H), mRNA. /FEA=mRNA /GEN=SUPT5H /PROD=suppressor of Ty (S.cerevisiae) 5 homolog /DB_XREF=gi:4507312 /UG=Hs.70186 suppressor of Ty (S.cerevisiae) 5 homolog /FL=gb:U56402.1 gb:AB000516.1 gb:NM_003169.1	
200892_s_at		BC000451	gb:BC000451.1 /DEF=Homo sapiens, splicing factor, arginineserine-rich (transformer 2 Drosophila homolog) 10, clone MGC:8454, mRNA, complete cds. /FEA=mRNA /PROD=splicing factor, arginineserine-rich(transformer 2 Drosophila homolog) 10 /DB_XREF=gi:12653362 /UG=Hs.30035 splicing factor, arginineserine-rich (transformer 2 Drosophila homolog) 10 /FL=gb:BC000160.1 gb:BC000451.1 gb:U61267.1 gb:U68063.1 gb:NM_004593.1	
200778_s_at	NEDD5	AI191427	neural precursor cell expressed, developmentally down-regulated 5	

200896_x_at		NM_004494	gb:NM_004494.1 /DEF=Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA. /FEA=mRNA /GEN=HDGF /PROD=hepatoma-derived growth factor (high-mobilitygroup protein 1-like) /DB_XREF=gi:4758515 /UG=Hs.89525 hepatoma-derived growth factor (high-mobility group protein 1-like) /FL=gb:NM_004494.1 gb:D16431.1	
212152_x_at	SMARCF1	AI679080	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1	
205393_s_at		NM_001274	gb:NM_001274.1 /DEF=Homo sapiens CHK1 (checkpoint, S.pombe) homolog (CHEK1), mRNA. /FEA=mRNA /GEN=CHK1 /PROD=CHK1 (checkpoint, S.pombe) homolog /DB_XREF=gi:4502802 /UG=Hs.20295 CHK1 (checkpoint, S.pombe) homolog /FL=gb:AF016582.1 gb:NM_001274.1	
218911_at		NM_006530	gb:NM_006530.1 /DEF=Homo sapiens glioma-amplified sequence-41 (GAS41), mRNA. /FEA=mRNA /GEN=GAS41 /PROD=glioma-amplified sequence-41 /DB_XREF=gi:5729837 /UG=Hs.4029 glioma-amplified sequence-41 /FL=gb:BC000994.2 gb:U61384.1 gb:NM_006530.1	
221605_s_at		AF136970	gb:AF136970.1 /DEF=Homo sapiens sarcosine oxidase mRNA, complete cds. /FEA=mRNA /PROD=sarcosine oxidase /DB_XREF=gi:12239317 /UG=Hs.271167 L-pipecolic acid oxidase /FL=gb:AF136970.1	
207016_s_at		AB015228	gb:AB015228.1 /DEF=Homo sapiens mRNA for RALDH2-T, complete cds. /FEA=mRNA /GEN=RALDH2 /PROD=RALDH2-T /DB_XREF=gi:3970845 /UG=Hs.95197 aldehyde dehydrogenase 1 family,	

			member A2 /FL=gb:NM_003888.1 gb:AB015226.1 gb:AB015227.1 gb:AB015228.1	
215424_s_at	SNW1	AV689564	SKI-interacting protein	
201635_s_at	FXR1	AI990766	fragile X mental retardation, autosomal homolog 1	
222082_at	FBI1	AI568395	HIV-1 inducer of short transcripts binding protein; lymphoma related factor	
211160_x_at		M95178	gb:M95178.1 /DEF=Human non- muscle alpha-actinin mRNA, complete cds. /FEA=mRNA /GEN=ACTN1 /PROD=alpha- actinin /DB_XREF=gi:178051 /UG=Hs.119000 actinin, alpha 1 /FL=gb:M95178.1	
207158_at		NM_001644	gb:NM_001644.2 /DEF=Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 (APOBEC1), transcript variant 1, mRNA. /FEA=mRNA /GEN=APOBEC1 /PROD=apolipoprotein B mRNA editing enzyme, catalyticpolypeptide 1, isoform 1 /DB_XREF=gi:5921993 /UG=Hs.560 apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 /FL=gb:L25877.1 gb:U72891.1 gb:NM_001644.2 gb:NM_005889.1 gb:L26234.1	
204230_s_at		NM_020309	gb:NM_020309.1 /DEF=Homo sapiens brain-specific Na- dependent inorganic phosphate cotransporter (BNPI), mRNA. /FEA=mRNA /GEN=BNPI /PROD=brain-specific Na- dependent inorganic phosphatecotransporter /DB_XREF=gi:9945321 /UG=Hs.6535 brain-specific Na- dependent inorganic phosphate cotransporter /FL=gb:AB032436.1 gb:NM_020309.1	
207995_s_at		NM_014257	gb:NM_014257.1 /DEF=Homo sapiens CD209 antigen-like (CD209L), mRNA. /FEA=mRNA /GEN=CD209L /PROD=CD209 antigen-like /DB_XREF=gi:7657173	

			/UG=Hs.23759 CD209 antigen-like /FL=gb:AB015629.1 gb:NM_014257.1	
205207_at		NM_000600	gb:NM_000600.1 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /FEA=mRNA /GEN=IL6 /PROD=interleukin 6 (interferon, beta 2) /DB_XREF=gi:10834983 /UG=Hs.93913 interleukin 6 (interferon, beta 2) /FL=gb:NM_000600.1 gb:M14584.1 gb:M18403.1 gb:M29150.1 gb:M54894.1	
206614_at		NM_000557	gb:NM_000557.2 /DEF=Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA. /FEA=mRNA /GEN=GDF5 /PROD=growth differentiation factor 5 preproprotein /DB_XREF=gi:5123452 /UG=Hs.1573 growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) /FL=gb:NM_000557.2 gb:U13660.1	
215378_at		AU148255	ESTs	
217831_s_at		NM_016143	gb:NM_016143.1 /DEF=Homo sapiens p47 (LOC51674), mRNA. /FEA=mRNA /GEN=LOC51674 /PROD=p47 /DB_XREF=gi:7706394 /UG=Hs.12865 p47 /FL=gb:BC002801.1 gb:AF078856.1 gb:NM_016143.1	
204477_at		U74324	gb:U74324.1 /DEF=Human guanine nucleotide exchange factor mss4 mRNA, complete cds. /FEA=mRNA /PROD=guanine nucleotide exchange factor mss4 /DB_XREF=gi:1658190 /UG=Hs.90875 RAB interacting factor /FL=gb:U74324.1 gb:NM_002871.1	



219412_at		NM_022337	gb:NM_022337.1 /DEF=Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA. /FEA=mRNA /GEN=RAB38 /PROD=RAB38, member RAS oncogene family /DB_XREF=gi:11641236 /UG=Hs.108923 RAB38, member RAS oncogene family /FL=gb:AF235022.1 gb:NM_022337.1	
219222_at		NM_022128	gb:NM_022128.1 /DEF=Homo sapiens ribokinase (RBSK), mRNA. /FEA=mRNA /GEN=RBSK /PROD=ribokinase /DB_XREF=gi:11545854 /UG=Hs.11916 ribokinase /FL=gb:NM_022128.1	
208961_s_at		AB017493	gb:AB017493.1 /DEF=Homo sapiens mRNA for DNA-binding zinc finger(GBF), complete cds. /FEA=mRNA /PROD=DNA-binding zinc finger(GBF) /DB_XREF=gi:3582142 /UG=Hs.285313 core promoter element binding protein /FL=gb:BC000311.1 gb:BC004301.1 gb:AF001461.1 gb:AB017493.1 gb:NM_001300.2	
219743_at		NM_012259	gb:NM_012259.1 /DEF=Homo sapiens hairyenhancer-of-split related with YRPW motif 2 (HEY2), mRNA. /FEA=mRNA /GEN=HEY2 /PROD=hairyenhancer-of-split related with YRPW motif2 /DB_XREF=gi:6912413 /UG=Hs.144287 hairyenhancer-of-split related with YRPW motif 2 /FL=gb:AF311884.1 gb:AF173901.1 gb:NM_012259.1 gb:AF232238.1 gb:AF237949.1 gb:AB044755.1	
219054_at		NM_024563	gb:NM_024563.1 /DEF=Homo sapiens. hypothetical protein FLJ14054 (FLJ14054), mRNA. /FEA=mRNA /GEN=FLJ14054 /PROD=hypothetical protein FLJ14054 /DB_XREF=gi:13375730 /UG=Hs.13528 hypothetical protein FLJ14054 /FL=gb:NM_024563.1	

205716_at		NM_018843	gb:NM_018843.1 /DEF=Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA. /FEA=mRNA /GEN=LOC55972 /PROD=mitochondrial carrier family protein /DB_XREF=gi:10047121 /UG=Hs.172294 mitochondrial carrier family protein /FL=gb:NM_018843.1 gb:AF125531.1	
213647_at		D42046	Consensus includes gb:D42046.1 /DEF=Human mRNA for KIAA0083 gene, partial cds. /FEA=mRNA /GEN=KIAA0083 /DB_XREF=gi:1531547 /UG=Hs.194665 DNA2 (DNA replication helicase, yeast, homolog)-like	
218892_at		NM_024542	gb:NM_024542.1 /DEF=Homo sapiens hypothetical protein FLJ11790 (FLJ11790), mRNA. /FEA=mRNA /GEN=FLJ11790 /PROD=hypothetical protein FLJ11790 /DB_XREF=gi:13375702 /UG=Hs.9658 hypothetical protein FLJ11790 /FL=gb:NM_024542.1	
205848_at		NM_005256	gb:NM_005256.1 /DEF=Homo sapiens growth arrest-specific 2 (GAS2), mRNA. /FEA=mRNA /GEN=GAS2 /PROD=growth arrest-specific 2 /DB_XREF=gi:4885252 /UG=Hs.129818 growth arrest-specific 2 /FL=gb:U95032.1 gb:NM_005256.1	
215867_x_at		AL050025	Consensus includes gb:AL050025.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D066 (from clone DKFZp564D066); partial cds. /FEA=mRNA /GEN=DKFZp564D066 /PROD=hypothetical protein /DB_XREF=gi:4884095 /UG=Hs.5344 adaptor-related protein complex 1, gamma 1 subunit	
64474_g_at	FLJ22127	AA203219	hypothetical protein FLJ22127	

57588_at	SLC24A3	R62432	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	
207464_at		NM_014121	gb:NM_014121.1 /DEF=Homo sapiens PRO0233 protein (PRO0233), mRNA. /FEA=mRNA /GEN=PRO0233 /PROD=PRO0233 protein /DB_XREF=gi:7662535 /UG=Hs.278933 PRO0233 protein /FL=gb:AF090905.1 gb:NM_014121.1	
216286_at		AV760769	AV760769 MDS Homo sapiens cDNA clone MDSBSE09 5', mRNA sequence.	
207714_s_at		NM_004353	gb:NM_004353.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1 (SERPINH1), mRNA. /FEA=mRNA /GEN=SERPINH1 /PROD=serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1 /DB_XREF=gi:4757923 /UG=Hs.241579 serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1 /FL=gb:NM_004353.1	
38241_at	BTN3A2	U90548	butyrophilin, subfamily 3, member A2	NM_006994
219892_at		NM_023003	gb:NM_023003.1 /DEF=Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), mRNA. /FEA=mRNA /GEN=TM6SF1 /PROD=transmembrane 6 superfamily member 1 /DB_XREF=gi:13194198 /UG=Hs.133865 transmembrane 6 superfamily member 1 /FL=gb:AF255922.1 gb:NM_023003.1	
206907_at		NM_003811	gb:NM_003811.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9), mRNA. /FEA=mRNA /GEN=TNFSF9 /PROD=tumor necrosis factor (ligand) superfamily, member 9 /DB_XREF=gi:4507608 /UG=Hs.1524 tumor necrosis factor (ligand) superfamily,	

			member 9 /FL=gb:NM_003811.1 gb:U03398.1	
218378_s_at		NM_024653	gb:NM_024653.1 /DEF=Homo sapiens hypothetical protein FLJ13902 (FLJ13902), mRNA. /FEA=mRNA /GEN=FLJ13902 /PROD=hypothetical protein FLJ13902 /DB_XREF=gi:13375900 /UG=Hs.58127 hypothetical protein FLJ13902 /FL=gb:NM_024653.1	
213257_at		AJ290445	Consensus includes gb:AJ290445.1 /DEF=Homo sapiens mRNA for KIAA0524SARM protein. /FEA=mRNA /GEN=KIAA0524SARM /PROD=KIAA0524SARM protein /DB_XREF=gi:7711001 /UG=Hs.128759 KIAA0524 protein	
205704_s_at		NM_012463	gb:NM_012463.1 /DEF=Homo sapiens TJ6 protein (TJ6), mRNA. /FEA=mRNA /GEN=TJ6 /PROD=TJ6 protein /DB_XREF=gi:6912717 /UG=Hs.12627 TJ6 protein /FL=gb:AF112972.1 gb:NM_012463.1	
219215_s_at		NM_017767	gb:NM_017767.1 /DEF=Homo sapiens hypothetical protein FLJ20327 (FLJ20327), mRNA. /FEA=mRNA /GEN=FLJ20327 /PROD=hypothetical protein FLJ20327 /DB_XREF=gi:8923304 /UG=Hs.72289 hypothetical protein FLJ20327 /FL=gb:BC001688.1 gb:NM_017767.1	
217977_at		NM_016332	gb:NM_016332.1 /DEF=Homo sapiens selenoprotein X, 1 (SEPX1), mRNA. /FEA=mRNA /GEN=SEPX1 /PROD=selenoprotein X, 1 /DB_XREF=gi:7706510 /UG=Hs.279623 selenoprotein X, 1 /FL=gb:AF187272.1	

			gb:BC003127.1 gb:AF166124.1 gb:NM_016332.1	
215828_at		AL359599	Consensus includes gb:AL359599.1 /DEF=Homo sapiens mRNA; cDNA DKFZp547C126 (from clone DKFZp547C126). /FEA=mRNA /DB_XREF=gi:8655666 /UG=Hs.283850 Homo sapiens mRNA; cDNA DKFZp547C126 (from clone DKFZp547C126)	
215302_at		AU150691	ESTs, Weakly similar to postmeiotic segregation increased 2-like 8 [Homo sapiens] [H.sapiens]	
222322_at		AI791860	ESTs	
214318_s_at		W58342	Homo sapiens cDNA FLJ34103 fis, clone FCBBF3007859, moderately similar to Human putative protein B2 mRNA	
218206_x_at		NM_016558	gb:NM_016558.1 /DEF=Homo sapiens SCAN domain- containing 1 (SCAND1), mRNA. /FEA=mRNA /GEN=SCAND1 /PROD=SCAN domain- containing 1 /DB_XREF=gi:7706088 /UG=Hs.274411 SCAN domain- containing 1 /FL=gb:BC000785.1 gb:AF204271.1 gb:NM_016558.1	
211665_s_at		L20686	gb:L20686.1 /DEF=Homo sapiens guanine nucleotide releasing factor (SOS2) mRNA, complete cds. /FEA=mRNA /GEN=SOS2 /PROD=guanine nucleotide releasing factor /DB_XREF=gi:1220367 /FL=gb:L20686.1	
218587_s_at		NM_020231	gb:NM_020231.1 /DEF=Homo sapiens x 010 protein (MDS010), mRNA. /FEA=mRNA /GEN=MDS010 /PROD=x 010 protein /DB_XREF=gi:9910427 /UG=Hs.159397 x 010 protein /FL=gb:AF168711.1 gb:NM_020231.1	
212621_at	KIAA0286	AW205215	KIAA0286 protein	

216715_at		AL080315	Consensus includes gb:AL080315 /DEF=Human DNA sequence from clone RP1-6P5 on chromosome 6 Contains a pseudogene similar to EEF1D (eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)), a pseudogene similar to ribosomal protein L21, ESTs, STSs and GSSs /FEA=CDS_1 /DB_XREF=gi:7838240 /UG=Hs.306507 Human DNA sequence from clone RP1-6P5 on chromosome 6 Contains a pseudogene similar to EEF1D (eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)), a pseudogene similar to ribosomal protein L21, ESTs, STSs and GSSs	
218717_s_at		NM_018192	gb:NM_018192.1 /DEF=Homo sapiens hypothetical protein FLJ10718 (FLJ10718), mRNA. /FEA=mRNA /GEN=FLJ10718 /PROD=hypothetical protein FLJ10718 /DB_XREF=gi:8922618 /UG=Hs.42824 hypothetical protein FLJ10718 /FL=gb:NM_018192.1	
212759_s_at	TCF7L2	AI703074	transcription factor 7-like 2 (T-cell specific, HMG-box)	
206415_at	TLL1	AI769310	tolloid-like 1	
212816_s_at	CBS	BE613178	cystathionine-beta-synthase	
200935_at		NM_004343	gb:NM_004343.2 /DEF=Homo sapiens calreticulin (CALR), mRNA. /FEA=mRNA /GEN=CALR /PROD=calreticulin precursor /DB_XREF=gi:5921996 /UG=Hs.16488 calreticulin /FL=gb:BC002500.1 gb:M84739.1 gb:M32294.1 gb:NM_004343.2	
220112_at		NM_024669	gb:NM_024669.1 /DEF=Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA. /FEA=mRNA /GEN=FLJ11795 /PROD=hypothetical protein FLJ11795 /DB_XREF=gi:13375927	

			/UG=Hs.84560 hypothetical protein FLJ11795 /FL=gb:NM_024669.1	
205968_at		NM_002252	gb:NM_002252.1 /DEF=Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 (KCNS3), mRNA. /FEA=mRNA /GEN=KCNS3 /PROD=potassium voltage-gated channel,delayed-rectifier, subfamily S, member 3 /DB_XREF=gi:4504862 /UG=Hs.47584 potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3 /FL=gb:BC004148.1 gb:BC004987.1 gb:AF043472.1 gb:NM_002252.1	
216532_x_at	dJ406P24.1	AL138831	dJ406P24.1 (Thioredoxin-like pseudogene); Human DNA sequence from clone RP3-406P24 on chromosome 6 Contains a thioredoxin-like pseudogene, 2 CpG islands, ESTs, STSs and GSSs, complete sequence.	
215436_at		AK023959	Consensus includes gb:AK023959.1 /DEF=Homo sapiens cDNA FLJ13897 fis, clone THYRO1001706. /FEA=mRNA /DB_XREF=gi:10436079 /UG=Hs.301488 Homo sapiens cDNA FLJ13897 fis, clone THYRO1001706	
220027_s_at		NM_017805	gb:NM_017805.1 /DEF=Homo sapiens hypothetical protein FLJ20401 (FLJ20401), mRNA. /FEA=mRNA /GEN=FLJ20401 /PROD=hypothetical protein FLJ20401 /DB_XREF=gi:8923375 /UG=Hs.233955 hypothetical protein FLJ20401 /FL=gb:NM_017805.1	
212362_at		AK000300	Consensus includes gb:AA805753 /FEA=EST /DB_XREF=gi:2874503 /DB_XREF=est:ns43e04.s1 /CLONE=IMAGE:1186398 /UG=Hs.1526 ATPase, Ca++	

			transporting, cardiac muscle, slow twitch 2	
220082_at		NM_017726	gb:NM_017726.1 /DEF=Homo sapiens hypothetical protein FLJ20251 (FLJ20251), mRNA. /FEA=mRNA /GEN=FLJ20251 /PROD=hypothetical protein FLJ20251 /DB_XREF=gi:8923225 /UG=Hs.192927 hypothetical protein FLJ20251 /FL=gb:NM_017726.1	
209595_at		BC001771	gb:BC001771.1 /DEF=Homo sapiens, general transcription factor IIF, polypeptide 2 (30kD subunit), clone MGC:1502, mRNA, complete cds. /FEA=mRNA /PROD=general transcription factor IIF, polypeptide 2(30kD subunit) /DB_XREF=gi:12804688 /UG=Hs.58593 general transcription factor IIF, polypeptide 2 (30kD subunit) /FL=gb:BC001771.1 gb:NM_004128.1	
207379_at		NM_005711	gb:NM_005711.1 /DEF=Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA. /FEA=mRNA /GEN=EDIL3 /PROD=EGF-like repeats and discoidin I-like domains 3 /DB_XREF=gi:5031660 /UG=Hs.129764 EGF-like repeats and discoidin I-like domains 3 /FL=gb:U70312.1 gb:NM_005711.1	
217586_x_at		N35922	ESTs, Weakly similar to hypothetical protein FLJ11267 [Homo sapiens] [H.sapiens]	
204054_at		NM_000314	gb:NM_000314.1 /DEF=Homo sapiens phosphatase and tensin homolog (mutated in multiple advanced cancers 1) (PTEN), mRNA. /FEA=mRNA /GEN=PTEN /PROD=phosphatase and tensin homolog (mutated in multiple advanced cancers 1) /DB_XREF=gi:4506248 /UG=Hs.10712 phosphatase	



			and tensin homolog (mutated in multiple advanced cancers 1) /FL=gb:U92436.1 gb:U93051.1 gb:U96180.1 gb:NM_000314.1	
218662_s_at		NM_022346	gb:NM_022346.1 /DEF=Homo sapiens chromosome condensation protein G (HCAP-G), mRNA. /FEA=mRNA /GEN=HCAP-G /PROD=chromosome condensation protein G /DB_XREF=gi:11641252 /UG=Hs.193602 chromosome condensation protein G /FL=gb:AF235023.1 gb:NM_022346.1 gb:AF331796.1 gb:BC000827.1 gb:AB013299.1	
205117_at	FGF1; AFGF; ECGF; FGFA; ECGF; ECGFB; HBGF1; ECGF-beta; FGF-alpha	X59065	Protein sequence is in conflict with the conceptual translation; H.sapiens FGF gene, exon 3.	NM_000800; NM_033136; NM_033137
218503_at		NM_017794	gb:NM_017794.1 /DEF=Homo sapiens hypothetical protein FLJ20375 (FLJ20375), mRNA. /FEA=mRNA /GEN=FLJ20375 /PROD=hypothetical protein FLJ20375 /DB_XREF=gi:8923357 /UG=Hs.274251 hypothetical protein FLJ20375 /FL=gb:BC001246.1 gb:NM_017794.1	
213052_at	PRKAR2A	BF246917	protein kinase, cAMP-dependent, regulatory, type II, alpha	
209470_s_at		D49958	gb:D49958.1 /DEF=Homo sapiens mRNA for membrane glycoprotein M6, complete cds. /FEA=mRNA /PROD=membrane glycoprotein M6 /DB_XREF=gi:1663516 /UG=Hs.75819 glycoprotein M6A /FL=gb:D49958.1	

			Consensus includes gb:BC002374.1 /DEF=Homo sapiens, karyopherin alpha 1 (importin alpha 5), clone MGC:8554, mRNA, complete cds. /FEA=mRNA /PROD=karyopherin alpha 1 (importin alpha 5) /DB_XREF=gi:12803140 /UG=Hs.169149 karyopherin alpha 1 (importin alpha 5) /FL=gb:BC002374.1 gb:BC003009.1 gb:NM_002264.1	
202057_at		NM_002264		
201259_s_at	SYPL	AI768845	synaptophysin-like protein	
209494_s_at	ZNF278	AI807017	zinc finger protein 278	
			Consensus includes gb:AK000002.1 /DEF=Homo sapiens mRNA for FLJ00002 protein, partial cds. /FEA=mRNA /GEN=FLJ00002 /PROD=FLJ00002 protein /DB_XREF=gi:7209304 /UG=Hs.55879 hypothetical protein MGC2487	
213485_s_at		AK000002		
			Consensus includes gb:AW168948 /FEA=EST /DB_XREF=gi:6400473 /DB_XREF=est:xj15f07.x1 /CLONE=IMAGE:2657317 /UG=Hs.286148 stromal antigen 1 /FL=gb:NM_005862.1	
202293_at		NM_005862		
			Consensus includes gb:AK023260.1 /DEF=Homo sapiens cDNA FLJ13198 fis, clone NT2RP3004454, highly similar to Homo sapiens mRNA for KIAA0448 protein. /FEA=mRNA /DB_XREF=gi:10435114 /UG=Hs.169939 heparan sulfate 2-O-sulfotransferase /FL=gb:NM_012262.2 gb:AB007917.1 gb:AB024568.1	
203283_s_at		NM_012262		
			gb:BC004892.1 /DEF=Homo sapiens, reticulocalbin 2, EF-hand calcium binding domain, clone MGC:1650, mRNA, complete cds. /FEA=mRNA /PROD=reticulocalbin 2, EF-hand calcium bindingdomain /DB_XREF=gi:13436151 /UG=Hs.79088 reticulocalbin 2, EF-hand calcium binding	
201485_s_at		BC004892		

			domain /FL=gb:BC004892.1 gb:NM_002902.1	
210876_at		M62896	gb:M62896.1 /DEF=Human lipocortin (LIP) 2 pseudogene mRNA, complete cds-like region. /FEA=mRNA /DB_XREF=gi:187146 /UG=Hs.234757 Human lipocortin (LIP) 2 pseudogene mRNA, complete cds-like region /FL=gb:M62896.1	
222245_s_at		AF218012	Consensus includes gb:AF218012.1 /DEF=Homo sapiens clone PP3795 unknown mRNA. /FEA=mRNA /PROD=unknown /DB_XREF=gi:10441953 /UG=Hs.72222 hypothetical protein FLJ13459	
204751_x_at		NM_004949	gb:NM_004949.1 /DEF=Homo sapiens desmocollin 2 (DSC2), transcript variant Dsc2b, mRNA. /FEA=mRNA /GEN=DSC2 /PROD=desmocollin 2, isoform Dsc2b preproprotein /DB_XREF=gi:13435365 /UG=Hs.239727 desmocollin 2 /FL=gb:NM_004949.1	
214719_at		AK026720	Consensus includes gb:AK026720.1 /DEF=Homo sapiens cDNA: FLJ23067 fis, clone LNG04993. /FEA=mRNA /DB_XREF=gi:10439638 /UG=Hs.117167 Homo sapiens cDNA: FLJ23067 fis, clone LNG04993	
220321_s_at		NM_024584	gb:NM_024584.1 /DEF=Homo sapiens hypothetical protein FLJ13646 (FLJ13646), mRNA. /FEA=mRNA /GEN=FLJ13646 /PROD=hypothetical protein FLJ13646 /DB_XREF=gi:13375767 /UG=Hs.21081 hypothetical protein FLJ13646 /FL=gb:NM_024584.1	
222280_at		BG491393	ESTs, Weakly similar to neuronal thread protein [Homo sapiens] [H.sapiens]	

209310_s_at	U25804	gb:U25804.1 /DEF=Human Ich-2 cysteine protease mRNA, complete cds. /FEA=mRNA /PROD=Ich-2 /DB_XREF=gi:886049 /UG=Hs.74122 caspase 4, apoptosis-related cysteine protease /FL=gb:U28976.1 gb:U28977.1 gb:U28978.1 gb:NM_001225.1 gb:U25804.1 gb:U28014.1	
219577_s_at	NM_019112	gb:NM_019112.1 /DEF=Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 7 (ABCA7), mRNA. /FEA=mRNA /GEN=ABCA7 /PROD=ATP-binding cassette, sub-family A (ABC1), member 7 /DB_XREF=gi:9506364 /UG=Hs.134514 ATP-binding cassette, sub-family A (ABC1), member 7 /FL=gb:AF328787.1 gb:AF250238.1 gb:NM_019112.1	
213143_at	AF007149	Consensus includes gb:BE856707 /FEA=EST /DB_XREF=gi:10370006 /DB_XREF=est:7f66f02.x1 /CLONE=IMAGE:3299643 /UG=Hs.12520 Homo sapiens clone 23568, 23621, 23795, 23873 and 23874 mRNA sequences	
201545_s_at	NM_004643	gb:NM_004643.1 /DEF=Homo sapiens poly(A)-binding protein, nuclear 1 (PABPN1), mRNA. /FEA=mRNA /GEN=PABPN1 /PROD=poly(A)-binding protein, nuclear 1 /DB_XREF=gi:4758875 /UG=Hs.117176 poly(A)-binding protein, nuclear 1 /FL=gb:NM_004643.1	
208937_s_at	D13889	gb:D13889.1 /DEF=Human mRNA for Id-1H, complete cds. /FEA=mRNA /GEN=Id-1H /PROD=Id-1H /DB_XREF=gi:464181 /UG=Hs.75424 inhibitor of DNA binding 1, dominant negative helix-loop-helix protein /FL=gb:BC000613.1 gb:NM_002165.1 gb:D13889.1	

212780_at		L13857	Consensus includes gb:AA700167 /FEA=EST /DB_XREF=gi:2703130 /DB_XREF=est:zj36h12.s1 /CLONE=IMAGE:452423 /UG=Hs.326392 son of sevenless (Drosophila) homolog 1 /FL=gb:L13857.1	
203531_at	CUL5	BF435809	cullin 5	
201421_s_at		NM_024102	gb:NM_024102.1 /DEF=Homo sapiens hypothetical protein MGC2722 (MGC2722), mRNA. /FEA=mRNA /GEN=MGC2722 /PROD=hypothetical protein MGC2722 /DB_XREF=gi:13129109 /UG=Hs.11039 hypothetical protein MGC2722 /FL=gb:BC001679.1 gb:NM_024102.1	
213959_s_at	KIAA1005	BF515597	KIAA1005 protein	
203538_at		NM_001745	gb:NM_001745.1 /DEF=Homo sapiens calcium modulating ligand (CAMLG), mRNA. /FEA=mRNA /GEN=CAMLG /PROD=calcium modulating ligand /DB_XREF=gi:4502558 /UG=Hs.13572 calcium modulating ligand /FL=gb:NM_001745.1 gb:U18242.1	
55616_at	MGC9753	AI703342	hypothetical gene MGC9753	
209571_at		U03644	gb:U03644.1 /DEF=Human recepin mRNA, complete cds. /FEA=mRNA /GEN=recepin /PROD=recepin /DB_XREF=gi:476104 /UG=Hs.89421 CBF1 interacting corepressor /FL=gb:AF098297.1 gb:NM_004882.1 gb:U03644.1	
218721_s_at		NM_017847	gb:NM_017847.1 /DEF=Homo sapiens hypothetical protein FLJ20505 (FLJ20505), mRNA. /FEA=mRNA /GEN=FLJ20505 /PROD=hypothetical protein FLJ20505 /DB_XREF=gi:8923461 /UG=Hs.69388 hypothetical protein FLJ20505 /FL=gb:BC003397.1 gb:NM_017847.1	

212196_at		AL049265	Consensus includes gb:AW242916 /FEA=EST /DB_XREF=gi:6576686 /DB_XREF=est:xn27f03.x1 /CLONE=IMAGE:2694941 /UG=Hs.71968 Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)	
218708_at		NM_013248	gb:NM_013248.1 /DEF=Homo sapiens NTF2-related export protein 1 (NXT1), mRNA. /FEA=mRNA /GEN=NXT1 /PROD=NTF2-related export protein 1 /DB_XREF=gi:7019470 /UG=Hs.24563 NTF2-related export protein 1 /FL=gb:BC000759.1 gb:BC002687.1 gb:BC003029.1 gb:BC003410.1 gb:AF156957.1 gb:NM_013248.1	
213531_s_at	RAB3GAP	AI040009	RAB3 GTPase-ACTIVATING PROTEIN	
203221_at	TLE1	AI951720	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	
200666_s_at		NM_006145	gb:NM_006145.1 /DEF=Homo sapiens heat shock 40kD protein 1 (HSPF1), mRNA. /FEA=mRNA /GEN=HSPF1 /PROD=heat shock 40kD protein 1 /DB_XREF=gi:5453689 /UG=Hs.82646 DnaJ (Hsp40) homolog, subfamily B, member 1 /FL=gb:BC002352.1 gb:NM_006145.1 gb:D49547.1	
209517_s_at		AB020982	gb:AB020982.1 /DEF=Homo sapiens ASH2L mRNA, complete cds, similar to Drosophila ash2 sequence. /FEA=mRNA /GEN=ASH2L /DB_XREF=gi:4417209 /UG=Hs.6856 ash2 (absent, small, or homeotic, Drosophila, homolog)-like /FL=gb:AF056718.1 gb:AB020982.1 gb:NM_004674.1	
213454_at		AL578583	Homo sapiens, clone MGC:32686 IMAGE:4051739, mRNA, complete cds	

208753_s_at		BC002387	gb:BC002387.1 /DEF=Homo sapiens, nucleosome assembly protein 1-like 1, clone MGC:8688, mRNA, complete cds. /FEA=mRNA /PROD=nucleosome assembly protein 1-like 1 /DB_XREF=gi:12803166 /UG=Hs.179662 nucleosome assembly protein 1-like 1 /FL=gb:BC002387.1 gb:AL162068.1	
212226_s_at	RPS20	AL576654	ribosomal protein S20	
211538_s_at		U56725	gb:U56725.1 /DEF=Human heat shock protein mRNA, complete cds. /FEA=mRNA /PROD=heat shock protein /DB_XREF=gi:4204879 /UG=Hs.75452 heat shock 70kD protein 2 /FL=gb:U56725.1	
200940_s_at		AB036737	gb:AB036737.1 /DEF=Homo sapiens mRNA for RERE, complete cds. /FEA=mRNA /PROD=RERE /DB_XREF=gi:8096339 /UG=Hs.194369 arginine-glutamic acid dipeptide (RE) repeats /FL=gb:AF118275.1 gb:NM_012102.1 gb:AB036737.1	
208644_at		M32721	gb:M32721.1 /DEF=Human poly(ADP-ribose) polymerase mRNA, complete cds. /FEA=mRNA /GEN=PPOL /DB_XREF=gi:190266 /UG=Hs.177766 ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase) /FL=gb:NM_001618.2 gb:M18112.1 gb:M32721.1 gb:J03473.1	
200870_at		NM_007178	gb:NM_007178.1 /DEF=Homo sapiens unr-interacting protein (UNRIP), mRNA. /FEA=mRNA /GEN=UNRIP /PROD=unr-interacting protein /DB_XREF=gi:6005931 /UG=Hs.3727 unr-interacting protein /FL=gb:BC000162.1 gb:AB024327.1 gb:NM_007178.1 gb:AL136691.1 gb:AF161496.1	

203445_s_at		NM_005730	gb:NM_005730.1 /DEF=Homo sapiens conserved gene amplified in osteosarcoma (OS4), mRNA. /FEA=mRNA /GEN=OS4 /PROD=conserved gene amplified in osteosarcoma /DB_XREF=gi:5031964 /UG=Hs.180669 conserved gene amplified in osteosarcoma /FL=gb:U81556.1 gb:NM_005730.1	
208598_s_at		NM_005703	gb:NM_005703.2 /DEF=Homo sapiens upstream regulatory element binding protein 1 (UREB1), mRNA. /FEA=CDS /GEN=UREB1 /PROD=upstream regulatory element binding protein 1 /DB_XREF=gi:6692990 /UG=Hs.3383 upstream regulatory element binding protein 1 /FL=gb:NM_005703.2	
205684_s_at		NM_017925	gb:NM_017925.1 /DEF=Homo sapiens hypothetical protein FLJ20686 (FLJ20686), mRNA. /FEA=mRNA /GEN=FLJ20686 /PROD=hypothetical protein FLJ20686 /DB_XREF=gi:8923616 /UG=Hs.271480 hypothetical protein FLJ20686 /FL=gb:NM_017925.1	
219035_s_at		NM_025126	gb:NM_025126.1 /DEF=Homo sapiens hypothetical protein FLJ21786 (FLJ21786), mRNA. /FEA=mRNA /GEN=FLJ21786 /PROD=hypothetical protein FLJ21786 /DB_XREF=gi:13376704 /UG=Hs.316809 hypothetical protein FLJ21786 /FL=gb:NM_025126.1	
51228_at		N36928	ESTs, Weakly similar to RNA binding motif protein 12; putative brain nuclearly-targeted protein [Homo sapiens] [H.sapiens]	
213491_x_at	RPN2	AL514285	ribophorin II	
219091_s_at		NM_024756	gb:NM_024756.1 /DEF=Homo sapiens hypothetical protein FLJ13465 (FLJ13465), mRNA. /FEA=mRNA /GEN=FLJ13465 /PROD=hypothetical protein FLJ13465 /DB_XREF=gi:13376090	



			/UG=Hs.127216 hypothetical protein FLJ13465 /FL=gb:NM_024756.1	
205741_s_at		NM_001392	gb:NM_001392.1 /DEF=Homo sapiens dystrobrevin, alpha (DTNA), mRNA. /FEA=mRNA /GEN=DTNA /PROD=dystrobrevin, alpha /DB_XREF=gi:4503410 /UG=Hs.54435 dystrobrevin, alpha /FL=gb:BC005300.1 gb:NM_001392.1	
200843_s_at		NM_004446	gb:NM_004446.1 /DEF=Homo sapiens glutamyl-prolyl-tRNA synthetase (EPRS), mRNA. /FEA=mRNA /GEN=EPRS /PROD=glutamyl-prolyl tRNA synthetase /DB_XREF=gi:4758293 /UG=Hs.55921 glutamyl-prolyl-tRNA synthetase /FL=gb:NM_004446.1	
218156_s_at		NM_018128	gb:NM_018128.1 /DEF=Homo sapiens hypothetical protein FLJ10534 (FLJ10534), mRNA. /FEA=mRNA /GEN=FLJ10534 /PROD=hypothetical protein FLJ10534 /DB_XREF=gi:8922495 /UG=Hs.204501 hypothetical protein FLJ10534 /FL=gb:NM_018128.1	
214844_s_at		AL050069	Consensus includes gb:AL050069.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566A0946 (from clone DKFZp566A0946); partial cds. /FEA=mRNA /GEN=DKFZp566A0946 /PROD=hypothetical protein /DB_XREF=gi:4884299 /UG=Hs.78006 DKFZP566A0946 protein	
218088_s_at		NM_022157	gb:NM_022157.1 /DEF=Homo sapiens Rag C protein (GTR2), mRNA. /FEA=mRNA /GEN=GTR2 /PROD=Rag C protein /DB_XREF=gi:11995471 /UG=Hs.110950 Rag C protein /FL=gb:AF272035.1 gb:NM_022157.1 gb:AF323609.1	

206510_at	AF332197	gb:AF332197.1 /DEF=Homo sapiens adult SIX2 (SIX2) mRNA, complete cds. /FEA=mRNA /GEN=SIX2 /PROD=SIX2 /DB_XREF=gi:13242164 /UG=Hs.101937 sine oculis homeobox (Drosophila) homolog 2 /FL=gb:AF332197.1 gb:AF136940.1 gb:NM_016932.1	
204421_s_at	M27968	gb:M27968.1 /DEF=Human basic fibroblast growth factor (FGF) mRNA, complete cds. /FEA=mRNA /GEN=FGF2 /DB_XREF=gi:182562 /UG=Hs.284244 fibroblast growth factor 2 (basic) /FL=gb:M27968.1 gb:NM_002006.1	
217794_at	NM_018457	gb:NM_018457.1 /DEF=Homo sapiens DKFZp564J157 protein (DKFZP564J157), mRNA. /FEA=mRNA /GEN=DKFZP564J157 /PROD=DKFZp564J157 protein /DB_XREF=gi:8922156 /UG=Hs.63042 DKFZp564J157 protein /FL=gb:AF217517.1 gb:NM_018457.1	
204257_at	NM_021727	gb:NM_021727.1 /DEF=Homo sapiens fatty acid desaturase 3 (FADS3), mRNA. /FEA=mRNA /GEN=FADS3 /PROD=fatty acid desaturase 3 /DB_XREF=gi:13375615 /UG=Hs.21765 fatty acid desaturase 3 /FL=gb:AF084560.1 gb:NM_021727.1 gb:BC004901.1 gb:AF134404.1	
214715_x_at	AK024789	Consensus includes gb:AK024789.1 /DEF=Homo sapiens cDNA: FLJ21136 fis, clone CAS07469. /FEA=mRNA /DB_XREF=gi:10437175 /UG=Hs.206882 Homo sapiens mRNA for FLJ00032 protein, partial cds	
218202_x_at	NM_022915	gb:NM_022915.1 /DEF=Homo sapiens hypothetical protein FLJ12701 (FLJ12701), mRNA. /FEA=mRNA /GEN=FLJ12701 /PROD=hypothetical protein FLJ12701 /DB_XREF=gi:12597660	

			/UG=Hs.203559 hypothetical protein FLJ12701 /FL=gb:NM_022915.1	
214672_at		AB023215	Consensus includes gb:AB023215.1 /DEF=Homo sapiens mRNA for KIAA0998 protein, partial cds. /FEA=mRNA /GEN=KIAA0998 /PROD=KIAA0998 protein /DB_XREF=gi:4589639 /UG=Hs.131525 KIAA0998 protein	
217758_s_at		NM_020123	gb:NM_020123.1 /DEF=Homo sapiens endomembrane protein emp70 precursor isolog (LOC56889), mRNA. /FEA=mRNA /GEN=LOC56889 /PROD=endomembrane protein emp70 precursor isolog /DB_XREF=gi:10047129 /UG=Hs.8203 endomembrane protein emp70 precursor isolog /FL=gb:NM_020123.1 gb:AF160213.1 gb:AF269150.1	
201792_at		NM_001129	gb:NM_001129.2 /DEF=Homo sapiens AE-binding protein 1 (AEBP1), mRNA. /FEA=mRNA /GEN=AEBP1 /PROD=adipocyte enhancer binding protein 1 precursor /DB_XREF=gi:4755145 /UG=Hs.118397 AE-binding protein 1 /FL=gb:D86479.1 gb:AF053944.1 gb:NM_001129.2	
217917_s_at		NM_014183	gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB_XREF=gi:7661821 /UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1 gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1 gb:AF165516.1	
201566_x_at		D13891	gb:D13891.1 /DEF=Human mRNA for Id-2H, complete cds. /FEA=mRNA /GEN=Id-2H /PROD=Id-2H /DB_XREF=gi:464183 /UG=Hs.180919 inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	

			/FL=gb:M97796.1 gb:NM_002166.1 gb:D13891.1	
121_at	PAX8	X69699	EST, Highly similar to PAX8_HUMAN Paired box protein Pax-8 [H.sapiens]	NM_003466; NM_013951; NM_013952; NM_013953; NM_013992
217900_at		NM_018060	gb:NM_018060.1 /DEF=Homo sapiens hypothetical protein FLJ10326 (FLJ10326), mRNA. /FEA=mRNA /GEN=FLJ10326 /PROD=hypothetical protein FLJ10326 /DB_XREF=gi:8922355 /UG=Hs.262823 hypothetical protein FLJ10326 /FL=gb:NM_018060.1	
206257_at		NM_015603	gb:NM_015603.1 /DEF=Homo sapiens DKFZP586M1019 protein (DKFZP586M1019), mRNA. /FEA=mRNA /GEN=DKFZP586M1019 /PROD=DKFZP586M1019 protein /DB_XREF=gi:7661689 /UG=Hs.227782 DKFZP586M1019 protein /FL=gb:BC002787.1 gb:AL050284.1 gb:NM_015603.1	
205907_s_at	OMD	AI765819	osteomodulin	
207979_s_at		NM_004931	gb:NM_004931.1 /DEF=Homo sapiens CD8 antigen, beta polypeptide 1 (p37) (CD8B1), mRNA. /FEA=mRNA /GEN=CD8B1 /PROD=CD8 antigen, beta polypeptide 1 (p37) /DB_XREF=gi:4826666 /UG=Hs.2299 CD8 antigen, beta polypeptide 1 (p37) /FL=gb:NM_004931.1	
218401_s_at		NM_012482	gb:NM_012482.1 /DEF=Homo sapiens zinc finger protein 281 (ZNF281), mRNA. /FEA=mRNA /GEN=ZNF281 /PROD=zinc finger protein 281 /DB_XREF=gi:6912751 /UG=Hs.59757 zinc finger protein 281 /FL=gb:AF125158.1 gb:NM_012482.1	

218383_at		NM_017815	gb:NM_017815.1 /DEF=Homo sapiens hypothetical protein FLJ20424 (FLJ20424), mRNA. /FEA=mRNA /GEN=FLJ20424 /PROD=hypothetical protein FLJ20424 /DB_XREF=gi:8923395 /UG=Hs.8886 hypothetical protein FLJ20424 /FL=gb:BC002554.1 gb:BC001916.1 gb:NM_017815.1	
203823_at		NM_021106	gb:NM_021106.1 /DEF=Homo sapiens regulator of G-protein signalling 3 (RGS3), mRNA. /FEA=mRNA /GEN=RGS3 /PROD=regulator of G-protein signalling 3 /DB_XREF=gi:10864074 /UG=Hs.82294 regulator of G-protein signalling 3 /FL=gb:NM_021106.1 gb:U27655.1	
218626_at		NM_019843	gb:NM_019843.2 /DEF=Homo sapiens eIF4E-transporter (4E-T), mRNA. /FEA=mRNA /GEN=4E-T /PROD=eIF4E-transporter /DB_XREF=gi:10947034 /UG=Hs.12720 eIF4E-transporter /FL=gb:NM_019843.2 gb:AF240775.1	
203695_s_at		NM_004403	gb:NM_004403.1 /DEF=Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA. /FEA=mRNA /GEN=DFNA5 /PROD=deafness, autosomal dominant 5 protein /DB_XREF=gi:4758153 /UG=Hs.13530 deafness, autosomal dominant 5 /FL=gb:AF073308.1 gb:NM_004403.1 gb:AF007790.2	
218306_s_at		NM_003922	gb:NM_003922.1 /DEF=Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA. /FEA=mRNA /GEN=HERC1 /PROD=guanine nucleotide exchange factor p532 /DB_XREF=gi:4557025 /UG=Hs.76127 hect (homologous to the E6-AP (UBE3A) carboxyl terminus)	

			domain and RCC1 (CHC1)-like domain (RLD) 1 /FL=gb:U50078.1 gb:NM_003922.1	
207076_s_at		NM_000050	gb:NM_000050.1 /DEF=Homo sapiens argininosuccinate synthetase (ASS), mRNA. /FEA=mRNA /GEN=ASS /PROD=argininosuccinate synthetase /DB_XREF=gi:4557336 /UG=Hs.160786 argininosuccinate synthetase /FL=gb:NM_000050.1	
214433_s_at		NM_003944	Consensus includes gb:NM_003944.1 /DEF=Homo sapiens selenium binding protein 1 (SELENBP1), mRNA. /FEA=CDS /GEN=SELENBP1 /PROD=selenium binding protein 1 /DB_XREF=gi:4506872 /UG=Hs.288973 selenium binding protein 1 /FL=gb:U29091.1 gb:NM_003944.1	
210276_s_at		AF281030	gb:AF281030.1 /DEF=Homo sapiens Tara mRNA, complete cds. /FEA=mRNA /PROD=Tara /DB_XREF=gi:12006357 /UG=Hs.40342 putative nuclear protein /FL=gb:AF281030.1 gb:BC003618.1	
203943_at		NM_004798	gb:NM_004798.1 /DEF=Homo sapiens kinesin family member 3B (KIF3B), mRNA. /FEA=mRNA /GEN=KIF3B /PROD=kinesin family member 3B /DB_XREF=gi:4758645 /UG=Hs.168212 kinesin family member 3B /FL=gb:AB002357.1 gb:NM_004798.1	
205904_at		NM_000247	gb:NM_000247.1 /DEF=Homo sapiens MHC class I polypeptide-related sequence A (MICA), mRNA. /FEA=mRNA /GEN=MICA /PROD=MHC class I chain-related gene A protein /DB_XREF=gi:4557750 /UG=Hs.90598 MHC class I	

			polypeptide-related sequence A /FL=gb:NM_000247.1 gb:L14848.1	
212336_at		AB002336	Consensus includes gb:AA912711 /FEA=EST /DB_XREF=gi:3052103 /DB_XREF=est:ol30f08.s1 /CLONE=IMAGE:1524999 /UG=Hs.26395 erythrocyte membrane protein band 4.1-like 1	
			gb:NM_012090.1 /DEF=Homo sapiens actin binding protein; macrophin (microfilament and actin filament cross-linker protein) (ACF7), mRNA. /FEA=mRNA /GEN=ACF7 /PROD=actin binding protein; macrophin (microfilament and actin filament cross-linker protein) /DB_XREF=gi:10048480 /UG=Hs.108258 actin binding protein; macrophin (microfilament and actin filament cross-linker protein) /FL=gb:NM_012090.1 gb:AF141968.1	
207358_x_at		NM_012090	gb:NM_017635.1 /DEF=Homo sapiens hypothetical protein FLJ20039 (FLJ20039), mRNA. /FEA=mRNA /GEN=FLJ20039 /PROD=hypothetical protein FLJ20039 /DB_XREF=gi:8923045 /UG=Hs.267448 hypothetical protein FLJ20039 /FL=gb:NM_017635.1	
218242_s_at		NM_017635	gb:NM_018235.1 /DEF=Homo sapiens hypothetical protein FLJ10830 (FLJ10830), mRNA. /FEA=mRNA /GEN=FLJ10830 /PROD=hypothetical protein FLJ10830 /DB_XREF=gi:8922698 /UG=Hs.273230 hypothetical protein FLJ10830 /FL=gb:BC001375.1 gb:BC003176.1 gb:NM_018235.1	
217752_s_at		NM_018235		

207508_at		NM_001689	gb:NM_001689.1 /DEF=Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA. /FEA=mRNA /GEN=ATP5G3 /PROD=ATP synthase, H <sup>+</sup> transporting, mitochondrial F0complex, subunit c (subunit 9) isoform 3 /DB_XREF=gi:4502300 /UG=Hs.429 ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 /FL=gb:U09813.1 gb:NM_001689.1	
220202_s_at		NM_018835	gb:NM_018835.1 /DEF=Homo sapiens membrane-associated nucleic acid binding protein (MNAB), mRNA. /FEA=mRNA /GEN=MNAB /PROD=membrane-associated nucleic acid bindingprotein /DB_XREF=gi:9256536 /UG=Hs.112227 membrane-associated nucleic acid binding protein /FL=gb:NM_018835.1	
215983_s_at		D83768	Consensus includes gb:D83768.1 /DEF=Human clone N9S Rep-8 mRNA, partial cds. /FEA=mRNA /GEN=Rep-8 /DB_XREF=gi:1913786 /UG=Hs.153678 reproduction 8	
209471_s_at		L00634	gb:L00634.1 /DEF=Human farnesyl-protein transferase alpha-subunit mRNA, complete cds. /FEA=mRNA /PROD=farnesyl-protein transferase alpha-subunit /DB_XREF=gi:292030 /UG=Hs.138381 farnesyltransferase, CAAX box, alpha /FL=gb:L00634.1 gb:L10413.1 gb:NM_002027.1	
212263_at		AF142419	Consensus includes gb:A114716 /FEA=EST /DB_XREF=gi:6360061 /DB_XREF=est:HA1315 /UG=Hs.15020 homolog of mouse quaking QKI (KH domain RNA binding protein) /FL=gb:AF142419.1 gb:AF142422.1	



202477_s_at		NM_006659	gb:NM_006659.1 /DEF=Homo sapiens gamma-tubulin complex protein 2 (GCP2), mRNA. /FEA=mRNA /GEN=GCP2 /PROD=gamma-tubulin complex protein 2 /DB_XREF=gi:5729839 /UG=Hs.13386 gamma-tubulin complex protein 2 /FL=gb:BC005011.1 gb:AF042379.1 gb:NM_006659.1	
221534_at		AF073483	gb:AF073483.1 /DEF=Homo sapiens p5326 mRNA, complete cds. /FEA=mRNA /PROD=p5326 /DB_XREF=gi:12002057 /UG=Hs.93678 Homo sapiens, clone IMAGE:3640823, mRNA, partial cds /FL=gb:AF073483.1	
202863_at		NM_003113	gb:NM_003113.1 /DEF=Homo sapiens nuclear antigen Sp100 (SP100), mRNA. /FEA=mRNA /GEN=SP100 /PROD=nuclear antigen Sp100 /DB_XREF=gi:4507164 /UG=Hs.77617 nuclear antigen Sp100 /FL=gb:M60618.1 gb:NM_003113.1	
220036_s_at		NM_018113	gb:NM_018113.1 /DEF=Homo sapiens hypothetical protein FLJ10494 (FLJ10494), mRNA. /FEA=mRNA /GEN=FLJ10494 /PROD=hypothetical protein FLJ10494 /DB_XREF=gi:8922462 /UG=Hs.272838 hypothetical protein FLJ10494 /FL=gb:NM_018113.1	
200080_s_at	H3F3A	BE869922	H3 histone, family 3A	
216250_s_at		X77598	Consensus includes gb:X77598.1 /DEF=H.sapiens LAM A3 mRNA for laminin alpha 3 chain. /FEA=mRNA /DB_XREF=gi:9716101 /UG=Hs.83450 laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)	
208950_s_at		BC002515	gb:BC002515.1 /DEF=Homo sapiens, antiquitin 1, clone MGC:1569, mRNA, complete cds. /FEA=mRNA /PROD=antiquitin 1 /DB_XREF=gi:12803386 /UG=Hs.74294 aldehyde	

			dehydrogenase 7 family, member A1 /FL=gb:BC002515.1 gb:NM_001182.1	
202369_s_at		NM_012288	gb:NM_012288.1 /DEF=Homo sapiens TRAM-like protein (KIAA0057), mRNA. /FEA=mRNA /GEN=KIAA0057 /PROD=TRAM-like protein /DB_XREF=gi:6912449 /UG=Hs.153954 TRAM-like protein /FL=gb:D31762.1 gb:NM_012288.1	
202697_at		NM_007006	gb:NM_007006.1 /DEF=Homo sapiens cleavage and polyadenylation specific factor 5, 25 kD subunit (CPSF5), mRNA. /FEA=mRNA /GEN=CPSF5 /PROD=cleavage and polyadenylation specific factor 5,25 kD subunit /DB_XREF=gi:5901925 /UG=Hs.9605 cleavage and polyadenylation specific factor 5, 25 kD subunit /FL=gb:BC001403.1 gb:NM_007006.1	
200858_s_at		NM_001012	gb:NM_001012.1 /DEF=Homo sapiens ribosomal protein S8 (RPS8), mRNA. /FEA=mRNA /GEN=RPS8 /PROD=ribosomal protein S8 /DB_XREF=gi:4506742 /UG=Hs.151604 ribosomal protein S8 /FL=gb:NM_001012.1	
221009_s_at		NM_016109	gb:NM_016109.1 /DEF=Homo sapiens PPAR(gamma) angiopoietin related protein (PGAR), mRNA. /FEA=mRNA /GEN=PGAR /PROD=PPAR(gamma) angiopoietin related protein /DB_XREF=gi:7705828 /UG=Hs.9613 PPAR(gamma) angiopoietin related protein /FL=gb:AF153606.1 gb:NM_016109.1	

220566_at		NM_014308	gb:NM_014308.1 /DEF=Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide p101 (P101-PI3K), mRNA. /FEA=mRNA /GEN=P101-PI3K /PROD=phosphoinositide-3-kinase, regulatory subunit, polypeptide p101 /DB_XREF=gi:7657432 /UG=Hs.278901 phosphoinositide-3-kinase, regulatory subunit, polypeptide p101 /FL=gb:AF128881.1 gb:NM_014308.1	
220720_x_at		NM_025029	gb:NM_025029.1 /DEF=Homo sapiens hypothetical protein FLJ14346 (FLJ14346), mRNA. /FEA=mRNA /GEN=FLJ14346 /PROD=hypothetical protein FLJ14346 /DB_XREF=gi:13376551 /UG=Hs.287640 hypothetical protein FLJ14346 /FL=gb:NM_025029.1	
220949_s_at		NM_024033	gb:NM_024033.1 /DEF=Homo sapiens hypothetical protein MGC5242 (MGC5242), mRNA. /FEA=mRNA /GEN=MGC5242 /PROD=hypothetical protein MGC5242 /DB_XREF=gi:13162284 /UG=Hs.77365 hypothetical protein MGC5242 /FL=gb:BC000168.2 gb:NM_024033.1	
212246_at	SDNSF	BE880828	neural stem cell derived neuronal survival protein	
220355_s_at		NM_018165	gb:NM_018165.1 /DEF=Homo sapiens hypothetical protein FLJ10645 (FLJ10645), mRNA. /FEA=mRNA /GEN=FLJ10645 /PROD=hypothetical protein FLJ10645 /DB_XREF=gi:8922564 /UG=Hs.44143 polybromo 1 /FL=gb:AF177387.1 gb:NM_018165.1	
221255_s_at		NM_031298	gb:NM_031298.1 /DEF=Homo sapiens hypothetical protein MGC2963 (MGC2963), mRNA. /FEA=mRNA /GEN=MGC2963 /PROD=hypothetical protein MGC2963 /DB_XREF=gi:13775219	

			/FL=gb:NM_031298.1	
200633_at		NM_018955	gb:NM_018955.1 /DEF=Homo sapiens ubiquitin B (UBB), mRNA. /FEA=mRNA /GEN=UBB /PROD=ubiquitin B /DB_XREF=gi:11024713 /UG=Hs.183842 ubiquitin B /FL=gb:NM_018955.1 gb:BC000379.1	
220352_x_at		NM_024305	gb:NM_024305.1 /DEF=Homo sapiens hypothetical protein MGC4278 (MGC4278), mRNA. /FEA=mRNA /GEN=MGC4278 /PROD=hypothetical protein MGC4278 /DB_XREF=gi:13236535 /UG=Hs.318780 hypothetical protein MGC4278 /FL=gb:BC002659.1 gb:NM_024305.1	
202561_at		AF070613	Consensus includes gb:AF070613.1 /DEF=Homo sapiens clone 24585 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3387995 /UG=Hs.131814 tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase /FL=gb:AF082556.1 gb:NM_003747.1	
202723_s_at	FOXO1A	AW117498	forkhead box O1A (rhabdomyosarcoma)	
208999_at		D86957	Consensus includes gb:D86957.1 /DEF=Human mRNA for KIAA0202 gene, partial cds. /FEA=mRNA /GEN=KIAA0202 /DB_XREF=gi:1503987 /UG=Hs.80712 KIAA0202 protein /FL=gb:BC001329.1	
215978_x_at		AK021514	Consensus includes gb:AK021514.1 /DEF=Homo sapiens cDNA FLJ11452 fis, clone HEMBA1001435. /FEA=mRNA /DB_XREF=gi:10432710 /UG=Hs.148598 Homo sapiens cDNA FLJ11452 fis, clone HEMBA1001435	

203023_at		NM_016391	gb:NM_016391.1 /DEF=Homo sapiens hypothetical protein (HSPC111), mRNA. /FEA=mRNA /GEN=HSPC111 /PROD=hypothetical protein /DB_XREF=gi:7705450 /UG=Hs.279918 hypothetical protein /FL=gb:AF151875.1 gb:AF161460.1 gb:AF151019.1 gb:NM_016391.1	
212509_s_at		BF968134	ESTs, Weakly similar to hypothetical protein FLJ22184 [Homo sapiens] [H.sapiens]	
202181_at		NM_014734	gb:NM_014734.1 /DEF=Homo sapiens KIAA0247 gene product (KIAA0247), mRNA. /FEA=mRNA /GEN=KIAA0247 /PROD=KIAA0247 gene product /DB_XREF=gi:7662019 /UG=Hs.82426 KIAA0247 gene product /FL=gb:D87434.1 gb:NM_014734.1	
203028_s_at		NM_000101	gb:NM_000101.1 /DEF=Homo sapiens cytochrome b-245, alpha polypeptide (CYBA), mRNA. /FEA=mRNA /GEN=CYBA /PROD=flavocytochrome b-558 alpha polypeptide /DB_XREF=gi:4557504 /UG=Hs.68877 cytochrome b-245, alpha polypeptide /FL=gb:M21186.1 gb:NM_000101.1	
209435_s_at		BC000265	gb:BC000265.1 /DEF=Homo sapiens, clone MGC:3182, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:3182) /DB_XREF=gi:12653008 /UG=Hs.315417 Homo sapiens, clone MGC:3182, mRNA, complete cds /FL=gb:BC000265.1	
200045_at		NM_001090	gb:NM_001090.1 /DEF=Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1), mRNA. /FEA=mRNA /GEN=ABCF1 /PROD=ATP-binding cassette, sub-family F, member 1 /DB_XREF=gi:10947134 /UG=Hs.9573 ATP-binding cassette, sub-family F (GCN20), member 1 /FL=gb:NM_001090.1	

			gb:AF027302.1	
205297_s_at		NM_000626	gb:NM_000626.1 /DEF=Homo sapiens CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 1, mRNA. /FEA=mRNA /GEN=CD79B /PROD=CD79B antigen, isoform 1 precursor /DB_XREF=gi:11038673 /UG=Hs.89575 CD79B antigen (immunoglobulin-associated beta) /FL=gb:NM_000626.1 gb:M80461.1 gb:M89957.1	
222036_s_at	MCM4	AI859865	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	
211048_s_at		BC006344	gb:BC006344.1 /DEF=Homo sapiens, protein disulfide isomerase related protein (calcium-binding protein, intestinal-related), clone MGC:13117, mRNA, complete cds. /FEA=mRNA /PROD=protein disulfide isomerase related protein(calcium-binding protein, intestinal-related) /DB_XREF=gi:13623480 /FL=gb:BC006344.1	
219696_at		NM_019049	gb:NM_019049.1 /DEF=Homo sapiens hypothetical protein (FLJ20054), mRNA. /FEA=mRNA /GEN=FLJ20054 /PROD=hypothetical protein /DB_XREF=gi:9506654 /UG=Hs.101590 hypothetical protein /FL=gb:NM_019049.1	
202070_s_at		NM_005530	gb:NM_005530.1 /DEF=Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), mRNA. /FEA=mRNA /GEN=IDH3A /PROD=isocitrate dehydrogenase 3 (NAD+) alpha /DB_XREF=gi:5031776 /UG=Hs.250616 isocitrate dehydrogenase 3 (NAD+) alpha /FL=gb:NM_005530.1 gb:U07681.1	

209452_s_at	AF035824	gb:AF035824.1 /DEF=Homo sapiens vesicle soluble NSF attachment protein receptor (VTI1) mRNA, complete cds. /FEA=mRNA /GEN=VTI1 /PROD=vesicle soluble NSF attachment protein receptor /DB_XREF=gi:2687399 /UG=Hs.169206 vesicle-associated soluble NSF attachment protein receptor (v-SNARE; homolog of S. cerevisiae VTI1) /FL=gb:BC003142.1 gb:AF035824.1 gb:AF060902.1 gb:NM_006370.1	
218350_s_at	NM_015895	gb:NM_015895.1 /DEF=Homo sapiens geminin (LOC51053), mRNA. /FEA=mRNA /GEN=LOC51053 /PROD=geminin /DB_XREF=gi:7705681 /UG=Hs.234896 geminin /FL=gb:AF067855.1 gb:NM_015895.1	
211070_x_at	BC006466	gb:BC006466.1 /DEF=Homo sapiens, clone MGC:2310, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:2310) /DB_XREF=gi:13623678 /FL=gb:BC006466.1	
213434_at	H95263	ESTs, Weakly similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precursor [Homo sapiens] [H.sapiens]	
200041_s_at	NM_004640	gb:NM_004640.1 /DEF=Homo sapiens HLA-B associated transcript-1 (D6S81E), mRNA. /FEA=mRNA /GEN=D6S81E /PROD=HLA-B associated transcript-1 /DB_XREF=gi:4758111 /UG=Hs.55296 HLA-B associated transcript-1 /FL=gb:BC004350.1 gb:NM_004640.1	

200971_s_at	NM_014445	gb:NM_014445.1 /DEF=Homo sapiens stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 (SERP1), mRNA. /FEA=mRNA /GEN=SERP1 /PROD=stress-associated endoplasmic reticulum protein1; ribosome associated membrane protein 4 /DB_XREF=gi:7657551 /UG=Hs.76698 stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 /FL=gb:AL136807.1 gb:AF136975.1 gb:AB022427.1 gb:NM_014445.1
202125_s_at	NM_015049	gb:NM_015049.1 /DEF=Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA. /FEA=mRNA /GEN=ALS2CR3 /PROD=amyotrophic lateral sclerosis 2 (juvenile)chromosome region, candidate 3 /DB_XREF=gi:13027379 /UG=Hs.154248 amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 /FL=gb:AB038951.1 gb:NM_015049.1
208799_at	BC004146	gb:BC004146.1 /DEF=Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 5, clone MGC:2175, mRNA, complete cds. /FEA=mRNA /PROD=proteasome (prosome, macropain) subunit, betatype, 5 /DB_XREF=gi:13278740 /UG=Hs.78596 proteasome (prosome, macropain) subunit, beta type, 5 /FL=gb:BC004146.1 gb:NM_002797.1 gb:D29011.1



202268_s_at		NM_003905	gb:NM_003905.1 /DEF=Homo sapiens amyloid beta precursor protein-binding protein 1, 59kD (APPBP1), mRNA. /FEA=mRNA /GEN=APPBP1 /PROD=Amyloid beta precursor protein-binding protein1 /DB_XREF=gi:4502168 /UG=Hs.61828 amyloid beta precursor protein-binding protein 1, 59kD /FL=gb:AL136798.1 gb:BC000480.1 gb:U50939.1 gb:NM_003905.1	
212450_at		D87445	Consensus includes gb:D87445.2 /DEF=Homo sapiens mRNA for KIAA0256 protein, partial cds. /FEA=mRNA /GEN=KIAA0256 /PROD=KIAA0256 protein /DB_XREF=gi:6634006 /UG=Hs.118978 KIAA0256 gene product	
208869_s_at		AF087847	gb:AF087847.1 /DEF=Homo sapiens GABA-A receptor-associated protein like 1 (GABARAPL1) mRNA, complete cds. /FEA=mRNA /GEN=GABARAPL1 /PROD=GABA-A receptor-associated protein like 1 /DB_XREF=gi:13375570 /UG=Hs.282654 Homo sapiens mRNA; cDNA DKFZp564N1272 (from clone DKFZp564N1272); complete cds /FL=gb:AL136676.1 gb:AF087847.1	
213238_at	ATP10D	AI478147	ATPase, Class V, type 10D	
216028_at		AL049980	Consensus includes gb:AL049980.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564C152 (from clone DKFZp564C152). /FEA=mRNA /GEN=DKFZp564C152 /PROD=hypothetical protein /DB_XREF=gi:4884230 /UG=Hs.184216 DKFZP564C152 protein	
202950_at		NM_001889	gb:NM_001889.1 /DEF=Homo sapiens crystallin, zeta (quinone reductase) (CRYZ), mRNA. /FEA=mRNA /GEN=CRYZ /PROD=crystallin, zeta (quinone reductase) /DB_XREF=gi:4503066	

			/UG=Hs.83114 crystallin, zeta (quinone reductase) /FL=gb:L13278.1 gb:S58039.1 gb:Nm_001889.1	
205618_at		NM_000950	gb:Nm_000950.1 /DEF=Homo sapiens proline-rich Gla (G-carboxyglutamic acid) polypeptide 1 (PRRG1), mRNA. /FEA=mRNA /GEN=PRRG1 /PROD=proline-rich Gla (G-carboxyglutamic acid)polypeptide 1 /DB_XREF=gi:4506134 /UG=Hs.40637 proline-rich Gla (G-carboxyglutamic acid) polypeptide 1 /FL=gb:AF009242.1 gb:Nm_000950.1	
200006_at		NM_007262	gb:Nm_007262.1 /DEF=Homo sapiens RNA-binding protein regulatory subunit (DJ-1), mRNA. /FEA=mRNA /GEN=DJ-1 /PROD=RNA-binding protein regulatory subunit /DB_XREF=gi:6005748 /UG=Hs.10958 RNA-binding protein regulatory subunit /FL=gb:AF021819.1 gb:Nm_007262.1 gb:D61380.1	
208847_s_at		M29872	gb:M29872.1 /DEF=Human alcohol dehydrogenase class III (ADH5) mRNA, complete cds. /FEA=mRNA /GEN=ADH5 /DB_XREF=gi:178131 /UG=Hs.78989 alcohol dehydrogenase 5 (class III), chi polypeptide /FL=gb:Nm_000671.2 gb:M29872.1 gb:M30471.1	
202961_s_at		NM_004889	gb:Nm_004889.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 (ATP5J2), mRNA. /FEA=mRNA /GEN=ATP5J2 /PROD=ATP synthase, H+ transporting, mitochondrial F0complex, subunit f, isoform 2 /DB_XREF=gi:4757811 /UG=Hs.155751 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2 /FL=gb:BC003678.1	

			gb:AF047436.1 gb:NM_004889.1	
213397_x_at	RNASE4	AI761728	ribonuclease, RNase A family, 4	
213241_at		AF035307	Consensus includes gb:AF035307.1 /DEF=Homo sapiens clone 23785 mRNA sequence. /FEA=mRNA /DB_XREF=gi:2661068 /UG=Hs.184697 Homo sapiens clone 23785 mRNA sequence	
210175_at		BC000853	gb:BC000853.1 /DEF=Homo sapiens, Similar to chromosome 2 open reading frame 3, clone MGC:4994, mRNA, complete cds. /FEA=mRNA /PROD=Similar to chromosome 2 open reading frame 3 /DB_XREF=gi:12654086 /UG=Hs.184175 chromosome 2 open reading frame 3 /FL=gb:BC000853.1	
215980_s_at		AF052128	Consensus includes gb:AF052128.1 /DEF=Homo sapiens clone 23677 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3360437 /UG=Hs.1521 immunoglobulin mu binding protein 2	
212153_at		AB007930	Consensus includes gb:AB007930.1 /DEF=Homo sapiens mRNA for KIAA0461 peroteine, partial cds. /FEA=mRNA /GEN=KIAA0461 /PROD=KIAA0461 peroteine /DB_XREF=gi:3413883 /UG=Hs.107088 KIAA0461 protein	
203564_at		NM_004629	gb:NM_004629.1 /DEF=Homo sapiens Fanconi anemia, complementation group G (FANCG), mRNA. /FEA=mRNA /GEN=FANCG /PROD=X-ray repair complementing defective repair inChinese hamster cells 9 /DB_XREF=gi:4759335 /UG=Hs.8047 Fanconi anemia, complementation group G /FL=gb:BC000032.1	

			gb:U70310.1 gb:NM_004629.1	
218178_s_at		NM_020412	gb:NM_020412.1 /DEF=Homo sapiens CHMP1.5 protein (CHMP1.5), mRNA. /FEA=mRNA /GEN=CHMP1.5 /PROD=CHMP1.5 protein /DB_XREF=gi:9966900 /UG=Hs.42733 CHMP1.5 protein /FL=gb:AF281064.1 gb:NM_020412.1	
204889_s_at		AF029729	gb:AF029729.1 /DEF=Homo sapiens neuralized mRNA, complete cds. /FEA=mRNA /PROD=neuralized /DB_XREF=gi:4103927 /UG=Hs.172700 neuralized (Drosophila)-like /FL=gb:U87864.1 gb:AF029729.1 gb:NM_004210.1	
215162_at		AB020691	Consensus includes gb:AB020691.1 /DEF=Homo sapiens mRNA for KIAA0884 protein, partial cds. /FEA=mRNA /GEN=KIAA0884 /PROD=KIAA0884 protein /DB_XREF=gi:4240256 /UG=Hs.198232 KIAA0884 protein	
203130_s_at		NM_004522	gb:NM_004522.1 /DEF=Homo sapiens kinesin family member 5C (KIF5C), mRNA. /FEA=mRNA /GEN=KIF5C /PROD=kinesin family member 5C /DB_XREF=gi:4758649 /UG=Hs.6641 kinesin family member 5C /FL=gb:AB011103.1 gb:NM_004522.1	
216775_at		AK025301	Consensus includes gb:AK025301.1 /DEF=Homo sapiens cDNA: FLJ21648 fis, clone COL08469. /FEA=mRNA /DB_XREF=gi:10437789 /UG=Hs.306797 Homo sapiens cDNA: FLJ21648 fis, clone COL08469	

205428_s_at		NM_001740	gb:NM_001740.2 /DEF=Homo sapiens calbindin 2, (29kD, calretinin) (CALB2), transcript variant CALB2, mRNA. /FEA=mRNA /GEN=CALB2 /PROD=calbindin 2, full length protein isoform /DB_XREF=gi:6031158 /UG=Hs.106857 calbindin 2, (29kD, calretinin) /FL=gb:NM_001740.2	
216692_at		AL137428	Consensus includes gb:AL137428.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761N1323 (from clone DKFZp761N1323). /FEA=mRNA /DB_XREF=gi:6807985 /UG=Hs.306459 Homo sapiens mRNA; cDNA DKFZp761N1323 (from clone DKFZp761N1323)	
216859_x_at		AL080112	Consensus includes gb:AL080112.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586H0722 (from clone DKFZp586H0722). /FEA=mRNA /DB_XREF=gi:5262539 /UG=Hs.332731 Homo sapiens mRNA; cDNA DKFZp586H0722 (from clone DKFZp586H0722)	
203988_s_at		NM_004480	gb:NM_004480.1 /DEF=Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA. /FEA=mRNA /GEN=FUT8 /PROD=fucosyltransferase 8 (alpha (1,6)fucosyltransferase) /DB_XREF=gi:4758407 /UG=Hs.118722 fucosyltransferase 8 (alpha (1,6) fucosyltransferase) /FL=gb:D89289.1 gb:NM_004480.1	
209577_at		BC000351	gb:BC000351.1 /DEF=Homo sapiens, phosphate cytidyltransferase 2, ethanolamine, clone MGC:8624, mRNA, complete cds. /FEA=mRNA /PROD=phosphate cytidyltransferase 2, ethanolamine /DB_XREF=gi:12653166 /UG=Hs.226377 phosphate cytidyltransferase 2, ethanolamine /FL=gb:BC000351.1	

			gb:D84307.1 gb:NM_002861.1	
210664_s_at		AF021834	gb:AF021834.1 /DEF=Homo sapiens tissue factor pathway inhibitor beta (TFPIbeta) mRNA, complete cds. /FEA=mRNA /GEN=TFPIbeta /PROD=tissue factor pathway inhibitor beta /DB_XREF=gi:4103170 /UG=Hs.170279 tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) /FL=gb:AF021834.1	
212076_at		NM_005933	Consensus includes gb:AI701430 /FEA=EST /DB_XREF=gi:4989330 /DB_XREF=est:we29h08.x1 /CLONE=IMAGE:2342559 /UG=Hs.199160 myeloidlymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog) /FL=gb:L04284.1 gb:NM_005933.1	
210104_at		AF074723	gb:AF074723.1 /DEF=Homo sapiens RNA polymerase transcriptional regulation mediator (MED6) mRNA, complete cds. /FEA=mRNA /GEN=MED6 /PROD=RNA polymerase transcriptional regulationmediator /DB_XREF=gi:3329505 /UG=Hs.167738 RNA polymerase II transcriptional regulation mediator (Med6, S. cerevisiae, homolog of) /FL=gb:BC004106.1 gb:AF074723.1	
205895_s_at		NM_004741	gb:NM_004741.1 /DEF=Homo sapiens nucleolar phosphoprotein p130 (P130), mRNA. /FEA=mRNA /GEN=P130 /PROD=nucleolar phosphoprotein p130 /DB_XREF=gi:4758859 /UG=Hs.75337 nucleolar phosphoprotein p130 /FL=gb:BC001883.1	

			gb:NM_004741.1	
204805_s_at		NM_006026	gb:NM_006026.1 /DEF=Homo sapiens H1 histone family, member X (H1FX), mRNA. /FEA=mRNA /GEN=H1FX /PROD=H1 histone family, member X /DB_XREF=gi:5174448 /UG=Hs.109804 H1 histone family, member X /FL=gb:BC000426.1 gb:D64142.1 gb:NM_006026.1	
218849_s_at		NM_006663	gb:NM_006663.1 /DEF=Homo sapiens RelA-associated inhibitor (RAI), mRNA. /FEA=mRNA /GEN=RAI /PROD=RelA-associated inhibitor /DB_XREF=gi:5730000 /UG=Hs.324051 RelA-associated inhibitor /FL=gb:AF078037.1 gb:NM_006663.1	
52731_at	FLJ20294	AI359466	hypothetical protein FLJ20294	
201831_s_at	VDP	BE875592	vesicle docking protein p115	
205811_at		NM_007215	gb:NM_007215.1 /DEF=Homo sapiens polymerase (DNA directed), gamma 2, accessory subunit (POLG2), mRNA. /FEA=mRNA /GEN=POLG2 /PROD=polymerase (DNA directed), gamma 2, accessory subunit /DB_XREF=gi:6005837 /UG=Hs.30541 polymerase (DNA directed), gamma 2, accessory subunit /FL=gb:BC000913.1 gb:U94703.1 gb:AF142992.1 gb:AF184344.1 gb:AF177201.1 gb:NM_007215.1	
216813_at		AL512728	Consensus includes gb:AL512728.1 /DEF=Homo sapiens mRNA; cDNA DKFZp547P082 (from clone DKFZp547P082). /FEA=mRNA /GEN=DKFZp547P082 /PROD=hypothetical protein /DB_XREF=gi:12224871 /UG=Hs.307068 Homo sapiens mRNA; cDNA DKFZp547P082 (from clone DKFZp547P082)	

208096_s_at		NM_030820	gb:NM_030820.1 /DEF=Homo sapiens hypothetical protein DKFZp564B052 (DKFZp564B052), mRNA. /FEA=mRNA /GEN=DKFZp564B052 /PROD=hypothetical protein DKFZp564B052 /DB_XREF=gi:13540617 /FL=gb:NM_030820.1	
218131_s_at		NM_017660	gb:NM_017660.1 /DEF=Homo sapiens hypothetical protein FLJ20085 (FLJ20085), mRNA. /FEA=mRNA /GEN=FLJ20085 /PROD=hypothetical protein FLJ20085 /DB_XREF=gi:8923093 /UG=Hs.118964 hypothetical protein FLJ20085 /FL=gb:NM_017660.1	
214213_x_at	LMNA	AA063189	lamin A/C	
215908_at		AF009267	Consensus includes gb:AF009267.1 /DEF=Homo sapiens clone FBA1 Cri-du-chat region mRNA. /FEA=mRNA /DB_XREF=gi:2331069 /UG=Hs.102238 Homo sapiens clone FBA1 Cri-du-chat region mRNA	
217482_at		AK021987	Consensus includes gb:AK021987.1 /DEF=Homo sapiens cDNA FLJ11925 fis, clone HEMBB1000354. /FEA=mRNA /DB_XREF=gi:10433296 /UG=Hs.191158 Homo sapiens cDNA FLJ11925 fis, clone HEMBB1000354	
218225_at		NM_016581	gb:NM_016581.1 /DEF=Homo sapiens ECSIT (LOC51295), mRNA. /FEA=mRNA /GEN=LOC51295 /PROD=ECSIT /DB_XREF=gi:7706114 /UG=Hs.22199 ECSIT /FL=gb:BC000193.1 gb:BC005119.1 gb:AF243044.1 gb:NM_016581.1	
202480_s_at		NM_004216	gb:NM_004216.1 /DEF=Homo sapiens death effector domain-containing (DEDD), mRNA. /FEA=mRNA /GEN=DEDD /PROD=death effector domain-containing /DB_XREF=gi:4758143	



			/UG=Hs.169681 death effector domain-containing /FL=gb:AF083236.1 gb:AF043733.1 gb:AF100341.1 gb:NM_004216.1	
210281_s_at		AL136621	gb:AL136621.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564B162 (from clone DKFZp564B162); complete cds. /FEA=mRNA /GEN=DKFZp564B162 /PROD=hypothetical protein /DB_XREF=gi:12052767 /UG=Hs.109526 zinc finger protein 198 /FL=gb:AL136621.1	
203749_s_at	RARA	AI806984	retinoic acid receptor, alpha	
220159_at		NM_024903	gb:NM_024903.1 /DEF=Homo sapiens hypothetical protein FLJ14297 (FLJ14297), mRNA. /FEA=mRNA /GEN=FLJ14297 /PROD=hypothetical protein FLJ14297 /DB_XREF=gi:13435146 /UG=Hs.245043 hypothetical protein FLJ14297 /FL=gb:NM_024903.1	
206829_x_at		NM_025189	gb:NM_025189.1 /DEF=Homo sapiens hypothetical protein FLJ13659 (FLJ13659), mRNA. /FEA=mRNA /GEN=FLJ13659 /PROD=hypothetical protein FLJ13659 /DB_XREF=gi:13430887 /UG=Hs.301651 hypothetical protein FLJ13659 /FL=gb:NM_025189.1	
214417_s_at	FETUB	N39010	fetuin B	
204466_s_at	SNCA	BG260394	synuclein, alpha (non A4 component of amyloid precursor)	
202878_s_at		NM_012072	gb:NM_012072.2 /DEF=Homo sapiens complement component C1q receptor (C1QR), mRNA. /FEA=mRNA /GEN=C1QR /PROD=complement component C1q receptor /DB_XREF=gi:11496985 /UG=Hs.97199 complement component C1q receptor /FL=gb:NM_012072.2 gb:U94333.1	

218938_at		NM_024326	gb:NM_024326.1 /DEF=Homo sapiens hypothetical protein MGC11279 (MGC11279), mRNA. /FEA=mRNA /GEN=MGC11279 /PROD=hypothetical protein MGC11279 /DB_XREF=gi:13236572 /UG=Hs.10915 hypothetical protein MGC11279 /FL=gb:BC002912.1 gb:NM_024326.1	
218405_at		NM_013375	gb:NM_013375.1 /DEF=Homo sapiens TATA-binding protein-binding protein (ABT1), mRNA. /FEA=mRNA /GEN=ABT1 /PROD=TATA-binding protein-binding protein /DB_XREF=gi:7019318 /UG=Hs.109428 TATA-binding protein-binding protein /FL=gb:AB027258.1 gb:NM_013375.1	
208903_at	RPS28	BF431363	ribosomal protein S28	
203206_at		NM_014661	gb:NM_014661.1 /DEF=Homo sapiens KIAA0140 gene product (KIAA0140), mRNA. /FEA=mRNA /GEN=KIAA0140 /PROD=KIAA0140 gene product /DB_XREF=gi:7661937 /UG=Hs.156016 KIAA0140 gene product /FL=gb:D50930.1 gb:NM_014661.1	
203802_x_at		NM_018044	gb:NM_018044.1 /DEF=Homo sapiens hypothetical protein FLJ10267 (FLJ10267), mRNA. /FEA=mRNA /GEN=FLJ10267 /PROD=hypothetical protein FLJ10267 /DB_XREF=gi:8922321 /UG=Hs.272820 hypothetical protein FLJ10267 /FL=gb:NM_018044.1	
206309_at		NM_007015	gb:NM_007015.1 /DEF=Homo sapiens chondromodulin I precursor (CHM-I), mRNA. /FEA=mRNA /GEN=CHM-I /PROD=chondromodulin I precursor /DB_XREF=gi:5901931 /UG=Hs.97932 chondromodulin I precursor /FL=gb:AB006000.1 gb:NM_007015.1	

212908_at		AB023179	Consensus includes gb:AK022530.1 /DEF=Homo sapiens cDNA FLJ12468 fis, clone NT2RM1000857, highly similar to Homo sapiens mRNA for KIAA0962 protein. /FEA=mRNA /DB_XREF=gi:10433971 /UG=Hs.9059 KIAA0962 protein	
210942_s_at		AB022918	gb:AB022918.1 /DEF=Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds. /FEA=mRNA /GEN=ST3Gal VI /PROD=alpha2,3-sialyltransferase ST3Gal VI /DB_XREF=gi:4827246 /UG=Hs.34578 alpha2,3-sialyltransferase /FL=gb:AB022918.1	
204642_at		NM_001400	gb:NM_001400.2 /DEF=Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA. /FEA=mRNA /GEN=EDG1 /PROD=endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 /DB_XREF=gi:13027635 /UG=Hs.154210 endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 /FL=gb:NM_001400.2 gb:M31210.1 gb:AF233365.1	
220663_at		NM_014271	gb:NM_014271.1 /DEF=Homo sapiens interleukin 1 receptor accessory protein-like 1 (IL1RAPL1), mRNA. /FEA=mRNA /GEN=IL1RAPL1 /PROD=interleukin 1 receptor accessory protein-like 1 /DB_XREF=gi:7657231 /UG=Hs.241385 interleukin 1 receptor accessory protein-like 1 /FL=gb:AF284435.1 gb:AF181284.1 gb:NM_014271.1	
215170_s_at		AB020719	Consensus includes gb:AB020719.1 /DEF=Homo sapiens mRNA for KIAA0912 protein, partial cds. /FEA=mRNA /GEN=KIAA0912 /PROD=KIAA0912 protein /DB_XREF=gi:4240312 /UG=Hs.207802 KIAA0912 protein	

211249_at		U35398	gb:U35398.1 /DEF=Human G protein-coupled receptor mRNA, complete cds. /FEA=mRNA /PROD=G protein-coupled receptor /DB_XREF=gi:1015418 /UG=Hs.166607 G protein-coupled receptor 68 /FL=gb:U35398.1 gb:NM_003485.1	
215167_at		BE567032	ESTs	
215576_at		AU146809	AU146809 HEMBB1 Homo sapiens cDNA clone HEMBB1001564 3', mRNA sequence.	
215285_s_at	PHTF1	AA927671	putative homeodomain transcription factor 1	
210356_x_at		BC002807	gb:BC002807.1 /DEF=Homo sapiens, membrane-spanning 4-domains, subfamily A, member 2, clone MGC:3969, mRNA, complete cds. /FEA=mRNA /PROD=membrane-spanning 4-domains, subfamily A, member2 /DB_XREF=gi:12803920 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) /FL=gb:NM_021950.1 gb:BC002807.1	
205166_at		NM_004055	gb:NM_004055.2 /DEF=Homo sapiens calpain 5 (CAPN5), mRNA. /FEA=mRNA /GEN=CAPN5 /PROD=calpain 5 /DB_XREF=gi:6552324 /UG=Hs.6133 calpain 5 /FL=gb:U94346.1 gb:NM_004055.2	
213130_at		AB032967	Consensus includes gb:AB032967.1 /DEF=Homo sapiens mRNA for KIAA1141 protein, partial cds. /FEA=mRNA /GEN=KIAA1141 /PROD=KIAA1141 protein /DB_XREF=gi:6329951 /UG=Hs.59255 DKFZP434N043 protein	
2028_s_at	E2F1	M96577	E2F transcription factor 1	NM_005225
218073_s_at		NM_018087	gb:NM_018087.1 /DEF=Homo sapiens hypothetical protein FLJ10407 (FLJ10407), mRNA. /FEA=mRNA /GEN=FLJ10407 /PROD=hypothetical protein	

			FLJ10407 /DB_XREF=gi:8922408 /UG=Hs.30738 hypothetical protein FLJ10407 /FL=gb:BC003082.1 gb:NM_018087.1	
213517_at	PCBP2	AW103422	poly(rC) binding protein 2	
205480_s_at		NM_006759	gb:NM_006759.2 /DEF=Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA. /FEA=mRNA /GEN=UGP2 /PROD=UDP- glucose pyrophosphorylase 2 /DB_XREF=gi:13027637 /UG=Hs.77837 UDP-glucose pyrophosphorylase 2 /FL=gb:NM_006759.2	
217871_s_at		NM_002415	gb:NM_002415.1 /DEF=Homo sapiens macrophage migration inhibitory factor (glycosylation- inhibiting factor) (MIF), mRNA. /FEA=mRNA /GEN=MIF /PROD=macrophage migration inhibitory factor(glycosylation- inhibiting factor) /DB_XREF=gi:4505184 /UG=Hs.73798 macrophage migration inhibitory factor (glycosylation-inhibiting factor) /FL=gb:BC000447.1 gb:M25639.1 gb:L10612.1 gb:NM_002415.1	
212566_at	MAP4	AL523310	microtubule-associated protein 4	
212581_x_at	GAPD	BE561479	glyceraldehyde-3-phosphate dehydrogenase	
205466_s_at		NM_005114	gb:NM_005114.1 /DEF=Homo sapiens heparan sulfate (glucosamine) 3-O- sulfotransferase 1 (HS3ST1), mRNA. /FEA=mRNA /GEN=HS3ST1 /PROD=heparan sulfate D-glucosaminyl3-O- sulfotransferase 1 precursor /DB_XREF=gi:4826763 /UG=Hs.40968 heparan sulfate (glucosamine) 3-O- sulfotransferase 1 /FL=gb:AF019386.1 gb:NM_005114.1	

219439_at		NM_020156	gb:NM_020156.1 /DEF=Homo sapiens core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase (C1GALT1), mRNA. /FEA=mRNA /GEN=C1GALT1 /PROD=core1UDP-galactose:N-acetylgalactosamine-alpha-R beta1,3-galactosyltransferase /DB_XREF=gi:9910143 /UG=Hs.46744 core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase /FL=gb:AF155582.1 gb:NM_020156.1	
200020_at		NM_007375	gb:NM_007375.1 /DEF=Homo sapiens TAR DNA binding protein (TARDBP), mRNA. /FEA=mRNA /GEN=TARDBP /PROD=TAR DNA binding protein /DB_XREF=gi:6678270 /UG=Hs.193989 TAR DNA binding protein /FL=gb:AL050265.1 gb:NM_007375.1 gb:U23731.1	
213423_x_at	N33	AI884858	Putative prostate cancer tumor suppressor	
208804_s_at		AL031681	Consensus includes gb:AL031681 /DEF=Human DNA sequence from clone 862K6 on chromosome 20q12-13.13. Contains the gene for a protein similar to Drosophila lethal (3) malignant brain tumor (l(3)mbt) protein, the SFRS6 gene for arginineserine-rich splicing factor 6 (SRP55), a 4E-BP2 (4... /FEA=mRNA_3 /DB_XREF=gi:10198606 /UG=Hs.6891 splicing factor, arginineserine-rich 6 /FL=gb:U30828.1	
209442_x_at		AL136710	gb:AL136710.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566P0524 (from clone DKFZp566P0524); complete cds. /FEA=mRNA /GEN=DKFZp566P0524 /PROD=hypothetical protein /DB_XREF=gi:12052939 /UG=Hs.75893 ankyrin 3, node of Ranvier (ankyrin G) /FL=gb:AL136710.1	

37793_r_at	RAD51L3	AF034956	RAD51-like 3 ( <i>S. cerevisiae</i> )	NM_002878; NM_133627; NM_133628; NM_133629; NM_133630
203083_at		NM_003247	gb:NM_003247.1 /DEF=Homo sapiens thrombospondin 2 (THBS2), mRNA. /FEA=mRNA /GEN=THBS2 /PROD=thrombospondin 2 /DB_XREF=gi:4507486 /UG=Hs.108623 thrombospondin 2 /FL=gb:L12350.1 gb:NM_003247.1	
215513_at		AF241534	Consensus includes gb:AF241534.1 /DEF=Homo sapiens hydatidiform mole associated and imprinted (HYMAI) mRNA, complete sequence. /FEA=mRNA /DB_XREF=gi:9502099 /UG=Hs.196015 hydatidiform mole associated and imprinted	
37996_s_at		L08835	Cluster Incl. L08835:Homo sapiens DMR-N9, partial cds; and myotonic dystrophy kinase (DM kinase) gene, complete cds /cds=(776,2665) /gb=L08835 /gi=181601 /ug=Hs.898 /len=3407	
201760_s_at		NM_018639	gb:NM_018639.1 /DEF=Homo sapiens CS box-containing WD protein (LOC55884), mRNA. /FEA=mRNA /GEN=LOC55884 /PROD=CS box-containing WD protein /DB_XREF=gi:8923880 /UG=Hs.136644 CS box-containing WD protein /FL=gb:AF229181.1 gb:AF163324.1 gb:NM_018639.1	
213360_s_at	WBSCR20C	AA514622	Williams Beuren syndrome chromosome region 20C	
213500_at	COPB2	AI307760	coatamer protein complex, subunit beta 2 (beta prime)	
202199_s_at	SRPK1	AW082913	SFRS protein kinase 1	
209628_at		AK023289	Consensus includes gb:AK023289.1 /DEF=Homo sapiens cDNA FLJ13227 fis, clone OVARC1000071, weakly similar to Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA. /FEA=mRNA /DB_XREF=gi:10435160 /UG=Hs.25010 hypothetical	

			protein P15-2 /FL=gb:AF246127.1 gb:NM_018698.1 gb:AF201942.1	
215418_at		AK022316	Consensus includes gb:AK022316.1 /DEF=Homo sapiens cDNA FLJ12254 fis, clone MAMMA1001465. /FEA=mRNA /DB_XREF=gi:10433685 /UG=Hs.44077 alpha-parvin	
222282_at		AV761453	AV761453 MDS Homo sapiens cDNA clone MDSBZA03 5', mRNA sequence.	
222077_s_at	RACGAP1	AU153848	Rac GTPase activating protein 1	
202056_at		NM_002264	Consensus includes gb:AW051311 /FEA=EST /DB_XREF=gi:5913581 /DB_XREF=est:wy89b01.x1 /CLONE=IMAGE:2555689 /UG=Hs.169149 karyopherin alpha 1 (importin alpha 5) /FL=gb:BC002374.1 gb:BC003009.1 gb:NM_002264.1	
222132_s_at		AJ278150	Consensus includes gb:AJ278150.1 /DEF=Homo sapiens mRNA for putative lipid kinase. /FEA=mRNA /PROD=putative lipid kinase /DB_XREF=gi:8250242 /UG=Hs.260238 hypothetical protein FLJ10842	
211940_x_at	H3F3A	BE869922	H3 histone, family 3A	
203987_at		NM_003506	gb:NM_003506.1 /DEF=Homo sapiens frizzled (Drosophila) homolog 6 (FZD6), mRNA. /FEA=mRNA /GEN=FZD6 /PROD=frizzled 6 /DB_XREF=gi:4503830 /UG=Hs.114218 frizzled (Drosophila) homolog 6 /FL=gb:AB012911.1 gb:NM_003506.1 gb:AF072873.1	
201719_s_at		NM_001431	gb:NM_001431.1 /DEF=Homo sapiens erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA. /FEA=mRNA /GEN=EPB41L2 /PROD=erythrocyte membrane	



			protein band 4.1-like 2 /DB_XREF=gi:4503578 /UG=Hs.7857 erythrocyte membrane protein band 4.1-like 2 /FL=gb:AF027299.1 gb:NM_001431.1	
221540_x_at		AF078847	gb:AF078847.1 /DEF=Homo sapiens basic transcription factor 2 mRNA, complete cds. /FEA=mRNA /PROD=basic transcription factor 2 /DB_XREF=gi:5531808 /UG=Hs.191356 general transcription factor IIH, polypeptide 2 (44kD subunit) /FL=gb:AF078847.1 gb:NM_001515.1	
220495_s_at		NM_024715	gb:NM_024715.1 /DEF=Homo sapiens hypothetical protein FLJ22625 (FLJ22625), mRNA. /FEA=mRNA /GEN=FLJ22625 /PROD=hypothetical protein FLJ22625 /DB_XREF=gi:13376016 /UG=Hs.106534 hypothetical protein FLJ22625 /FL=gb:NM_024715.1	
207551_s_at		NM_006800	gb:NM_006800.1 /DEF=Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA. /FEA=mRNA /GEN=MSL3L1 /PROD=male- specific lethal-3 (Drosophila)-like 1 /DB_XREF=gi:5803103 /UG=Hs.88764 male-specific lethal-3 (Drosophila)-like 1 /FL=gb:AF117065.1 gb:NM_006800.1	
214152_at	PIGB	AU144243	phosphatidylinositol glycan, class B	
201457_x_at		AF081496	gb:AF081496.1 /DEF=Homo sapiens kinetochore protein BUB3 (BUB3) mRNA, complete cds. /FEA=mRNA /GEN=BUB3 /PROD=kinetochore protein BUB3 /DB_XREF=gi:3639059 /UG=Hs.40323 BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog /FL=gb:BC005138.1 gb:AF047472.1 gb:AF053304.1 gb:AF081496.1 gb:NM_004725.1	

221204_s_at		NM_018058	gb:NM_018058.1 /DEF=Homo sapiens hypothetical protein FLJ10320 (FLJ10320), mRNA. /FEA=mRNA /GEN=FLJ10320 /PROD=hypothetical protein FLJ10320 /DB_XREF=gi:8922351 /UG=Hs.326444 chondrocyte expressed protein 68 kDa CEP-68 /FL=gb:NM_018058.1	
200856_x_at		NM_006311	Consensus includes gb:BF437948 /FEA=EST /DB_XREF=gi:11450465 /DB_XREF=est:7q63b10.x1 /CLONE=IMAGE:3702882 /UG=Hs.144904 nuclear receptor co-repressor 1 /FL=gb:AF044209.1 gb:NM_006311.1	
208619_at		L40326	gb:L40326.1 /DEF=Homo sapiens Hepatitis B virus X-associated protein 1 mRNA, complete cds. /FEA=mRNA /PROD=X-associated protein 1 /DB_XREF=gi:695361 /UG=Hs.108327 damage-specific DNA binding protein 1 (127kD) /FL=gb:U18299.1 gb:U32986.1 gb:NM_001923.2 gb:L40326.1	
201855_s_at		NM_015251	gb:NM_015251.1 /DEF=Homo sapiens KIAA0431 protein (KIAA0431), mRNA. /FEA=mRNA /GEN=KIAA0431 /PROD=KIAA0431 protein /DB_XREF=gi:7662115 /UG=Hs.16349 KIAA0431 protein /FL=gb:NM_015251.1	
218057_x_at		NM_006067	gb:NM_006067.1 /DEF=Homo sapiens neighbor of COX4 (NOC4), mRNA. /FEA=mRNA /GEN=NOC4 /PROD=neighbor of COX4 /DB_XREF=gi:5174614 /UG=Hs.173162 neighbor of COX4 /FL=gb:BC001472.1 gb:AF005888.1 gb:NM_006067.1	
204518_s_at		NM_000943	gb:NM_000943.1 /DEF=Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), mRNA. /FEA=mRNA /GEN=PPIC /PROD=peptidylprolyl isomerase C (cyclophilin C) /DB_XREF=gi:4505990 /UG=Hs.110364 peptidylprolyl isomerase C (cyclophilin C)	

			/FL=gb:BC002678.1 gb:NM_000943.1	
64900_at	FLJ22167	AA401703	hypothetical protein FLJ22167	
214696_at		AF070569	Consensus includes gb:AF070569.1 /DEF=Homo sapiens clone 24659 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3387938 /UG=Hs.29206 Homo sapiens clone 24659 mRNA sequence	
200993_at		AL137335	Consensus includes gb:AA939270 /FEA=EST /DB_XREF=gi:3099183 /DB_XREF=est:0q31b02.s1 /CLONE=IMAGE:1587915 /UG=Hs.5151 RAN binding protein 7 /FL=gb:AF098799.1 gb:NM_006391.1	
202429_s_at		AL353950	gb:AL353950.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761L0516 (from clone DKFZp761L0516); complete cds. /FEA=mRNA /GEN=DKFZp761L0516 /PROD=hypothetical protein /DB_XREF=gi:7669991 /UG=Hs.272458 protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) /FL=gb:J05480.1 gb:L14778.1 gb:NM_000944.1 gb:AL353950.1	
208968_s_at		BC002568	gb:BC002568.1 /DEF=Homo sapiens, hypothetical protein, clone MGC:2478, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein /DB_XREF=gi:12803484 /UG=Hs.4900 hypothetical protein /FL=gb:AF248964.1 gb:BC002568.1 gb:AF116609.1	

218226_s_at		NM_004547	gb:NM_004547.2 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) (NDUFB4), mRNA. /FEA=mRNA /GEN=NDUFB4 /PROD=NADH dehydrogenase (ubiquinone) 1 betasubcomplex, 4 (15kD, B15) /DB_XREF=gi:6041668 /UG=Hs.227750 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD, B15) /FL=gb:BC000855.1 gb:AF044957.1 gb:NM_004547.2	
218089_at		NM_015511	gb:NM_015511.1 /DEF=Homo sapiens DKFZP564N1363 protein (DKFZP564N1363), mRNA. /FEA=mRNA /GEN=DKFZP564N1363 /PROD=DKFZP564N1363 protein /DB_XREF=gi:7661627 /UG=Hs.11314 DKFZP564N1363 protein /FL=gb:BC001751.1 gb:AF132957.1 gb:AL117419.1 gb:AF113672.1 gb:NM_015511.1	
218873_at		NM_017710	gb:NM_017710.1 /DEF=Homo sapiens hypothetical protein FLJ20203 (FLJ20203), mRNA. /FEA=mRNA /GEN=FLJ20203 /PROD=hypothetical protein FLJ20203 /DB_XREF=gi:8923193 /UG=Hs.20594 hypothetical protein FLJ20203 /FL=gb:NM_017710.1	
204332_s_at		M64073	Consensus includes gb:M64073.1 /DEF=Human glycosylasparaginase mRNA, complete cds. /FEA=CDS /PROD=glycosylasparaginase /DB_XREF=gi:183329 /UG=Hs.207776 aspartylglucosaminidase /FL=gb:M64073.1 gb:NM_000027.1	
212627_s_at	KIAA0116	AL581473	KIAA0116 protein	
209150_s_at		U94831	gb:U94831.1 /DEF=Homo sapiens multispanning membrane protein mRNA, complete cds. /FEA=mRNA /PROD=multispanning membrane protein /DB_XREF=gi:2276459 /UG=Hs.91586 transmembrane	

			9 superfamily member 1 /FL=gb:U94831.1 gb:NM_006405.1	
209657_s_at		M65217	gb:M65217.1 /DEF=Human heat shock factor 2 (HSF2) mRNA, complete cds. /FEA=mRNA /GEN=heat shock factor 2 /PROD=HSF2 /DB_XREF=gi:184404 /UG=Hs.158195 heat shock transcription factor 2 /FL=gb:M65217.1 gb:NM_004506.2	
212440_at	RY1	BG252325	putative nucleic acid binding protein RY-1	
212373_at		NM_015322	Consensus includes gb:AW139179 /FEA=EST /DB_XREF=gi:6143497 /DB_XREF=est:UI-H-BI1-aet-f-06-0-UI.s1 /CLONE=IMAGE:2720411 /UG=Hs.6048 FEM-1 (C.elegans) homolog b /FL=gb:AF178632.1 gb:NM_015322.1 gb:AF204883.1	
212322_at		AF144638	Consensus includes gb:BE999972 /FEA=EST /DB_XREF=gi:10700248 /DB_XREF=est:7h15b02.x1 /CLONE=IMAGE:3316011 /UG=Hs.186613 sphingosine-1-phosphate lyase 1 /FL=gb:AF144638.1	
209388_at		BC000927	gb:BC000927.1 /DEF=Homo sapiens, Similar to poly (A) polymerase, clone MGC:5378, mRNA, complete cds. /FEA=mRNA /PROD=Similar to poly (A) polymerase /DB_XREF=gi:12654216 /UG=Hs.49007 poly(A) polymerase alpha /FL=gb:BC000927.1	
212594_at	PDCD4	N92498	programmed cell death 4 (neoplastic transformation inhibitor)	

209308_s_at	BC002461	gb:BC002461.1 /DEF=Homo sapiens, BCL2adenovirus E1B 19kD-interacting protein 2, clone MGC:1529, mRNA, complete cds. /FEA=mRNA /PROD=BCL2adenovirus E1B 19kD-interacting protein 2 /DB_XREF=gi:12803290 /UG=Hs.155596 BCL2adenovirus E1B 19kD-interacting protein 2 /FL=gb:BC002461.1	
209467_s_at	BC002755	gb:BC002755.1 /DEF=Homo sapiens, Similar to MAP kinase-interacting serinethreonine kinase 1, clone MGC:3690, mRNA, complete cds. /FEA=mRNA /PROD=Similar to MAP kinase-interactingserinethreonine kinase 1 /DB_XREF=gi:12803828 /UG=Hs.5591 MAP kinase-interacting serinethreonine kinase 1 /FL=gb:BC002755.1	
209406_at	AF095192	gb:AF095192.1 /DEF=Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds. /FEA=mRNA /PROD=BAG-family molecular chaperone regulator-2 /DB_XREF=gi:4322819 /UG=Hs.55220 BCL2-associated athanogene 2 /FL=gb:AF095192.1 gb:AL050287.1 gb:NM_004282.2	
209089_at	BC001267	gb:BC001267.1 /DEF=Homo sapiens, RAB5A, member RAS oncogene family, clone MGC:5048, mRNA, complete cds. /FEA=mRNA /PROD=RAB5A, member RAS oncogene family /DB_XREF=gi:12654846 /UG=Hs.73957 RAB5A, member RAS oncogene family /FL=gb:BC001267.1	
212144_at	AL021707	Consensus includes gb:AL021707 /DEF=Human DNA sequence from clone RP3-508I15 on chromosome 22q12-13 Contains the gene for GTPBP1 (GTP binding protein 1), two novel genes KIAA0063 and KIAA0668, a novel gene based on ESTs	

			and cDNA, a pseudogene similar to AOP1 (antioxidant protein 1)... /FEA=mRNA_3 /DB_XREF=gi:4582132 /UG=Hs.5898 KIAA0668 protein	
213786_at	NUDT1	AI935415	nudix (nucleoside diphosphate linked moiety X)-type motif 1	
205961_s_at		NM_004682	gb:NM_004682.1 /DEF=Homo sapiens PC4 and SFRS1 interacting protein 2 (PSIP2), mRNA. /FEA=mRNA /GEN=PSIP2 /PROD=PC4 and SFRS1 interacting protein 2 /DB_XREF=gi:4758869 /UG=Hs.306179 PC4 and SFRS1 interacting protein 2 /FL=gb:AF098483.1 gb:NM_004682.1	
207233_s_at		NM_000248	gb:NM_000248.1 /DEF=Homo sapiens microphthalmia-associated transcription factor (MITF), mRNA. /FEA=mRNA /GEN=MITF /PROD=microphthalmia-associated transcription factor /DB_XREF=gi:4557754 /UG=Hs.166017 microphthalmia-associated transcription factor /FL=gb:NM_000248.1	
214766_s_at		AL080144	Consensus includes gb:AL080144.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N093 (from clone DKFZp434N093); partial cds. /FEA=mRNA /GEN=DKFZp434N093 /PROD=hypothetical protein /DB_XREF=gi:5262592 /UG=Hs.33363 DKFZP434N093 protein	
213285_at		AV691491	ESTs, Weakly similar to MUC2_HUMAN Mucin 2 precursor (Intestinal mucin 2) [H.sapiens]	
201379_s_at		NM_003288	gb:NM_003288.1 /DEF=Homo sapiens tumor protein D52-like 2 (TPD52L2), mRNA. /FEA=mRNA /GEN=TPD52L2 /PROD=tumor protein D52-like 2 /DB_XREF=gi:4507642 /UG=Hs.154718 tumor protein D52-like 2 /FL=gb:AF004430.1	

			gb:NM_003288.1	
213623_at		NM_007054	Consensus includes gb:NM_007054.1 /DEF=Homo sapiens kinesin family member 3A (KIF3A), mRNA. /FEA=CDS /GEN=KIF3A /PROD=kinesin family member 3A /DB_XREF=gi:6857803 /UG=Hs.43670 kinesin family member 3A /FL=gb:AF041853.1 gb:NM_007054.1	
213655_at	YWHAЕ	AA502643	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	
208788_at		AL136939	gb:AL136939.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586B1824 (from clone DKFZp586B1824); complete cds. /FEA=mRNA /GEN=DKFZp586B1824 /PROD=hypothetical protein /DB_XREF=gi:12053372 /UG=Hs.250175 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2 /FL=gb:NM_021814.1 gb:AL136939.1 gb:AF111849.1 gb:AF231981.1	
219762_s_at		NM_015414	gb:NM_015414.1 /DEF=Homo sapiens ribosomal protein L36 (RPL36), mRNA. /FEA=mRNA /GEN=RPL36 /PROD=ribosomal protein L36 /DB_XREF=gi:7661637 /UG=Hs.300759 ribosomal protein L36 /FL=gb:AF077043.1 gb:NM_015414.1	
217990_at		NM_016576	gb:NM_016576.1 /DEF=Homo sapiens GMPR2 for guanosine monophosphate reductase isolog (LOC51292), mRNA. /FEA=mRNA /GEN=LOC51292 /PROD=GMPR2 for guanosine monophosphate reductaseisolog /DB_XREF=gi:7706108 /UG=Hs.234546 GMPR2 for guanosine monophosphate reductase isolog	



			/FL=gb:AB032903.1 gb:NM_016576.1 gb:AF135159.1	
210573_s_at		BC004424	gb:BC004424.1 /DEF=Homo sapiens, clone MGC:3538, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:3538) /DB_XREF=gi:13325209 /UG=Hs.250745 polymerase (RNA) III (DNA directed) (62kD) /FL=gb:BC004424.1	
217945_at		NM_025238	gb:NM_025238.1 /DEF=Homo sapiens BTB (POZ) domain containing 1 (BTBD1), mRNA. /FEA=mRNA /GEN=BTBD1 /PROD=BTB (POZ) domain containing 1 /DB_XREF=gi:13376847 /UG=Hs.21332 BTB (POZ) domain containing 1 /FL=gb:AL136853.1 gb:AF257241.1 gb:NM_025238.1 gb:AF355402.1	
200659_s_at		NM_002634	gb:NM_002634.2 /DEF=Homo sapiens prohibitin (PHB), mRNA. /FEA=mRNA /GEN=PHB /PROD=prohibitin /DB_XREF=gi:6031190 /UG=Hs.75323 prohibitin /FL=gb:NM_002634.2	
219232_s_at		NM_022073	gb:NM_022073.1 /DEF=Homo sapiens hypothetical protein FLJ21620 (FLJ21620), mRNA. /FEA=mRNA /GEN=FLJ21620 /PROD=hypothetical protein FLJ21620 /DB_XREF=gi:11545786 /UG=Hs.18878 hypothetical protein FLJ21620 /FL=gb:NM_022073.1	

203059_s_at	NM_004670	gb:NM_004670.1 /DEF=Homo sapiens 3-phosphoadenosine 5-phosphosulfate synthase 2 (PAPSS2), mRNA. /FEA=mRNA /GEN=PAPSS2 /PROD=3-prime-phosphoadenosine 5-prime-phosphosulfatesynthase 2 /DB_XREF=gi:4758879 /UG=Hs.274230 3-phosphoadenosine 5-phosphosulfate synthase 2 /FL=gb:AF150754.2 gb:AF313907.1 gb:AF091242.1 gb:NM_004670.1 gb:AF074331.1 gb:AF173365.1
202565_s_at	NM_003174	gb:NM_003174.2 /DEF=Homo sapiens supervillin (SVIL), transcript variant 1, mRNA. /FEA=mRNA /GEN=SVIL /PROD=supervillin, isoform 1 /DB_XREF=gi:11496980 /UG=Hs.154567 supervillin /FL=gb:NM_003174.2 gb:AF051850.1 gb:AF051851.1
221016_s_at	NM_031283	gb:NM_031283.1 /DEF=Homo sapiens HMG-box transcription factor TCF-3 (TCF-3), mRNA. /FEA=mRNA /GEN=TCF-3 /PROD=HMG-box transcription factor TCF-3 /DB_XREF=gi:13786122 /FL=gb:NM_031283.1
211990_at	M27487	Consensus includes gb:M27487.1 /DEF=Homo sapiens MHC class II DPw3-alpha-1 chain mRNA, complete cds. /FEA=CDS /GEN=HLA-DPA1 /PROD=MHC class II DP3-alpha /DB_XREF=gi:703088 /UG=Hs.914 Human mRNA for SB classII histocompatibility antigen alpha-chain /FL=gb:M27487.1
204622_x_at	NM_006186	gb:NM_006186.1 /DEF=Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), mRNA. /FEA=mRNA /GEN=NR4A2 /PROD=nuclear receptor subfamily 4, group A, member 2 /DB_XREF=gi:5453821 /UG=Hs.82120 nuclear receptor subfamily 4, group A, member 2 /FL=gb:NM_006186.1

204686_at		NM_005544	gb:NM_005544.1 /DEF=Homo sapiens insulin receptor substrate 1 (IRS1), mRNA. /FEA=mRNA /GEN=IRS1 /PROD=insulin receptor substrate 1 /DB_XREF=gi:5031804 /UG=Hs.96063 insulin receptor substrate 1 /FL=gb:NM_005544.1	
201166_s_at		NM_014676	gb:NM_014676.1 /DEF=Homo sapiens pumilio (Drosophila) homolog 1 (PUM1), mRNA. /FEA=mRNA /GEN=PUM1 /PROD=pumilio (Drosophila) homolog 1 /DB_XREF=gi:13491165 /UG=Hs.153834 pumilio (Drosophila) homolog 1 /FL=gb:AF315592.1 gb:NM_014676.1	
204070_at		NM_004585	gb:NM_004585.2 /DEF=Homo sapiens retinoic acid receptor responder (tazarotene induced) 3 (RARRES3), mRNA. /FEA=mRNA /GEN=RARRES3 /PROD=retinoic acid receptor responder (tazaroteneinduced) 3 /DB_XREF=gi:8051633 /UG=Hs.17466 retinoic acid receptor responder (tazarotene induced) 3 /FL=gb:AF060228.1 gb:AF092922.1 gb:NM_004585.2 gb:AB030815.1	
218570_at		NM_018095	gb:NM_018095.1 /DEF=Homo sapiens hypothetical protein FLJ10450 (FLJ10450), mRNA. /FEA=mRNA /GEN=FLJ10450 /PROD=hypothetical protein FLJ10450 /DB_XREF=gi:8922425 /UG=Hs.267604 hypothetical protein FLJ10450 /FL=gb:BC002736.1 gb:NM_018095.1	
218316_at		NM_012460	gb:NM_012460.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 9 (yeast) homolog (TIMM9), mRNA. /FEA=mRNA /GEN=TIMM9 /PROD=translocase of inner mitochondrial membrane 9(yeast) homolog /DB_XREF=gi:6912713	

			/UG=Hs.323914 translocase of inner mitochondrial membrane 9 (yeast) homolog /FL=gb:AF150100.1 gb:AF152353.1 gb:NM_012460.1	
218314_s_at		NM_018195	gb:NM_018195.1 /DEF=Homo sapiens hypothetical protein FLJ10726 (FLJ10726), mRNA. /FEA=mRNA /GEN=FLJ10726 /PROD=hypothetical protein FLJ10726 /DB_XREF=gi:8922622 /UG=Hs.268561 hypothetical protein FLJ10726 /FL=gb:NM_018195.1	
218311_at		NM_003618	gb:NM_003618.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA. /FEA=mRNA /GEN=MAP4K3 /PROD=mitogen-activated protein kinase kinase kinasekinase 3 /DB_XREF=gi:4506376 /UG=Hs.227400 mitogen-activated protein kinase kinase kinase kinase 3 /FL=gb:AF000145.1 gb:NM_003618.1	
204342_at		NM_013386	gb:NM_013386.1 /DEF=Homo sapiens hypothetical protein (DKFZp586G0123), mRNA. /FEA=mRNA /GEN=DKFZp586G0123 /PROD=hypothetical protein /DB_XREF=gi:9558726 /UG=Hs.24713 hypothetical protein /FL=gb:AL050209.1 gb:NM_013386.1	
218776_s_at		NM_024956	gb:NM_024956.1 /DEF=Homo sapiens hypothetical protein FLJ23375 (FLJ23375), mRNA. /FEA=mRNA /GEN=FLJ23375 /PROD=hypothetical protein FLJ23375 /DB_XREF=gi:13376442 /UG=Hs.285996 hypothetical protein FLJ23375 /FL=gb:NM_024956.1	

205206_at		NM_000216	gb:NM_000216.1 /DEF=Homo sapiens Kallmann syndrome 1 sequence (KAL1), mRNA. /FEA=mRNA /GEN=KAL1 /PROD=Kallmann syndrome 1 protein /DB_XREF=gi:4557682 /UG=Hs.89591 Kallmann syndrome 1 sequence /FL=gb:M97252.1 gb:NM_000216.1	
202176_at		NM_000122	gb:NM_000122.1 /DEF=Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3), mRNA. /FEA=mRNA /GEN=ERCC3 /PROD=excision repair cross-complementing rodent repair deficiency, complementation group 3 (xerodermapigmentosum group B complementing) /DB_XREF=gi:4557562 /UG=Hs.77929 excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing) /FL=gb:M31899.1 gb:NM_000122.1	
205251_at		NM_022817	gb:NM_022817.1 /DEF=Homo sapiens period (Drosophila) homolog 2 (PER2), transcript variant 1, mRNA. /FEA=mRNA /GEN=PER2 /PROD=period 2, isoform 2 /DB_XREF=gi:12707561 /UG=Hs.153405 period (Drosophila) homolog 2 /FL=gb:NM_022817.1	
202167_s_at		NM_022362	gb:NM_022362.1 /DEF=Homo sapiens MMS19 (MET18 S. cerevisiae)-like (MMS19L), mRNA. /FEA=mRNA /GEN=MMS19L /PROD=MMS19 (MET18 S. cerevisiae)-like /DB_XREF=gi:13375625 /UG=Hs.288891 MMS19 (MET18 S. cerevisiae)-like /FL=gb:NM_022362.1	

217122_s_at		AL031282	Consensus includes gb:AL031282 /DEF=Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP2122A, -B and -C, a novel gene, the alternatively spliced CDC2L2 ... /FEA=mRNA_6 /DB_XREF=gi:3860395 /UG=Hs.214646 KIAA0447 gene product	
221985_at	FLJ20059	AW006750	hypothetical protein FLJ20059	
202231_at		NM_006360	gb:NM_006360.1 /DEF=Homo sapiens dendritic cell protein (GA17), mRNA. /FEA=mRNA /GEN=GA17 /PROD=dendritic cell protein /DB_XREF=gi:5453653 /UG=Hs.69469 dendritic cell protein /FL=gb:AF277183.1 gb:AF064603.1 gb:NM_006360.1	
222027_at	NUCKS	AW515443	similar to rat nuclear ubiquitous casein kinase 2	
217478_s_at		X76775	Consensus includes gb:X76775 /DEF=H.sapiens HLA-DMA gene /FEA=mRNA_1 /DB_XREF=gi:512468 /UG=Hs.77522 major histocompatibility complex, class II, DM alpha	
202214_s_at		NM_003588	gb:NM_003588.1 /DEF=Homo sapiens cullin 4B (CUL4B), mRNA. /FEA=mRNA /GEN=CUL4B /PROD=cullin 4B /DB_XREF=gi:13270466 /UG=Hs.155976 cullin 4B /FL=gb:NM_003588.1 gb:AB014595.1	
201993_x_at		NM_005463	gb:NM_005463.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), mRNA. /FEA=mRNA /GEN=HNRPDL /PROD=heterogeneous nuclear ribonucleoprotein D-like /DB_XREF=gi:4885422 /UG=Hs.170311 heterogeneous nuclear ribonucleoprotein D-like /FL=gb:AB017019.1 gb:NM_005463.1	

			Consensus includes gb:S77154.1 /DEF=TINUR= NGFI-Bnur77 beta-type transcription factor homolog human, T lymphoid cell line, PEER, mRNA, 2469 nt. /FEA=mRNA /GEN=TINUR /DB_XREF=gi:913966 /UG=Hs.82120 nuclear receptor subfamily 4, group A, member 2	
216248_s_at		S77154		
63009_at	FLJ10539	AI188402	hypothetical protein FLJ10539	
			gb:Nm_000285.1 /DEF=Homo sapiens peptidase D (PEPD), mRNA. /FEA=mRNA /GEN=PEPD /PROD=Xaa-Pro dipeptidase /DB_XREF=gi:4557834 /UG=Hs.73947 peptidase D /FL=gb:BC004305.1 gb:J04605.1 gb:Nm_000285.1	
202108_at		NM_000285		
			gb:BC000651.1 /DEF=Homo sapiens, Similar to solute carrier family 1 (glutamate transporter), member 7, clone MGC:2078, mRNA, complete cds. /FEA=mRNA /PROD=Similar to solute carrier family 1 (glutamatetransporter), member 7 /DB_XREF=gi:12653730 /UG=Hs.307039 Homo sapiens, Similar to solute carrier family 1 (glutamate transporter), member 7, clone MGC:2078, mRNA, complete cds /FL=gb:BC000651.1	
210923_at		BC000651		
			Consensus includes gb:BF511091 /FEA=EST /DB_XREF=gi:11594389 /DB_XREF=est:UI-H-BI4-apn-c- 05-0-UI.s1 /CLONE=IMAGE:3087753 /UG=Hs.75231 solute carrier family 16 (monocarboxylic acid transporters), member 1 /FL=gb:Nm_003051.1 gb:L31801.1	
202234_s_at		NM_003051		
			gb:Nm_006109.1 /DEF=Homo sapiens skb1 (S. pombe) homolog (SKB1), mRNA. /FEA=mRNA /GEN=SKB1 /PROD=skb1 (S. pombe) homolog /DB_XREF=gi:5174682	
217786_at		NM_006109		

			/UG=Hs.12912 skb1 (S. pombe) homolog /FL=gb:AF015913.1 gb:NM_006109.1 gb:AF167572.1	
221637_s_at		BC001434	gb:BC001434.1 /DEF=Homo sapiens, clone MGC:2477, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:2477) /DB_XREF=gi:12655158 /UG=Hs.9061 hypothetical protein MGC2477 /FL=gb:BC001434.1	
200051_at		NM_005146	gb:NM_005146.1 /DEF=Homo sapiens squamous cell carcinoma antigen recognised by T cells (SART1), mRNA. /FEA=mRNA /GEN=SART1 /PROD=squamous cell carcinoma antigen recognised by Tcells /DB_XREF=gi:10863888 /UG=Hs.288319 squamous cell carcinoma antigen recognised by T cells /FL=gb:NM_005146.1 gb:BC001058.1 gb:AB006198.1	
201170_s_at		NM_003670	gb:NM_003670.1 /DEF=Homo sapiens basic helix-loop-helix domain containing, class B, 2 (BHLHB2), mRNA. /FEA=mRNA /GEN=BHLHB2 /PROD=differentiated embryo chondrocyte expressed gene1 /DB_XREF=gi:4503298 /UG=Hs.171825 basic helix-loop-helix domain containing, class B, 2 /FL=gb:AB004066.1 gb:NM_003670.1	
205061_s_at		NM_005033	gb:NM_005033.1 /DEF=Homo sapiens polymyositis scleroderma autoantigen 1 (75kD) (PMSCL1), mRNA. /FEA=mRNA /GEN=PMSCL1 /PROD=polymyositis scleroderma autoantigen 1 (75kD) /DB_XREF=gi:4826921 /UG=Hs.91728 polymyositis scleroderma autoantigen 1 (75kD) /FL=gb:M58460.1 gb:NM_005033.1	



217588_at		AW971983	Homo sapiens, Similar to putative ion channel protein CATSPER2, clone MGC:33346 IMAGE:4828636, mRNA, complete cds	
212641_at		AL023584	Consensus includes gb:AL023584 /DEF=Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorp... /FEA=mRNA /DB_XREF=gi:3790154 /UG=Hs.75063 human immunodeficiency virus type 1 enhancer-binding protein 2 /FL=gb:NM_006734.1	
209970_x_at		M87507	gb:M87507.1 /DEF=Homo sapien interleukin-1 beta convertase (IL1BCE) mRNA, complete cds. /FEA=mRNA /GEN=IL1BCE /PROD=interleukin 1-beta convertase /DB_XREF=gi:435598 /UG=Hs.2490 caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase) /FL=gb:M87507.1	
202273_at		NM_002609	gb:NM_002609.1 /DEF=Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB), mRNA. /FEA=mRNA /GEN=PDGFRB /PROD=platelet-derived growth factor receptor, betapolypeptide /DB_XREF=gi:4505682 /UG=Hs.76144 platelet-derived growth factor receptor, beta polypeptide /FL=gb:M21616.1 gb:J03278.1 gb:NM_002609.1	
219459_at		NM_018082	gb:NM_018082.1 /DEF=Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA. /FEA=mRNA /GEN=FLJ10388 /PROD=hypothetical protein FLJ10388 /DB_XREF=gi:8922398 /UG=Hs.197642 hypothetical protein FLJ10388	

			/FL=gb:NM_018082.1	
217671_at		BE466926	ESTs, Weakly similar to 2109260A B cell growth factor [Homo sapiens] [H.sapiens]	
217973_at		NM_016286	gb:NM_016286.1 /DEF=Homo sapiens carbonyl reductase (LOC51181), mRNA. /FEA=mRNA /GEN=LOC51181 /PROD=carbonyl reductase /DB_XREF=gi:7705924 /UG=Hs.9857 carbonyl reductase /FL=gb:BC001470.1 gb:AF113123.1 gb:NM_016286.1	
213076_at		D38169	Consensus includes gb:D38169.1 /DEF=Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3-kinase isoenzyme, partial cds. /FEA=mRNA /PROD=inositol 1,4,5-trisphosphate 3-kinase isoenzyme /DB_XREF=gi:2463541 /UG=Hs.21453 inositol 1,4,5- trisphosphate 3-kinase C	
203453_at		NM_001038	gb:NM_001038.1 /DEF=Homo sapiens sodium channel, nonvoltage-gated 1 alpha (SCNN1A), mRNA. /FEA=mRNA /GEN=SCNN1A /PROD=sodium channel, nonvoltage-gated 1 alpha /DB_XREF=gi:4506814 /UG=Hs.2794 sodium channel, nonvoltage-gated 1 alpha /FL=gb:NM_001038.1	
202734_at		NM_004240	gb:NM_004240.1 /DEF=Homo sapiens thyroid hormone receptor interactor 10 (TRIP10), mRNA. /FEA=mRNA /GEN=TRIP10 /PROD=thyroid hormone receptor interactor 10 /DB_XREF=gi:11342675 /UG=Hs.73999 thyroid hormone receptor interactor 10 /FL=gb:NM_004240.1	

209357_at		AF109161	gb:AF109161.1 /DEF=Homo sapiens p35srj (MRG1) mRNA, complete cds. /FEA=mRNA /GEN=MRG1 /PROD=p35srj /DB_XREF=gi:4193945 /UG=Hs.82071 Cbpb300-interacting transactivator, with GluAsp-rich carboxy-terminal domain, 2 /FL=gb:BC004377.1 gb:AF109161.1	
217599_s_at	HIC	BE910600	I-mfa domain-containing protein	
221314_at		NM_005260	gb:NM_005260.2 /DEF=Homo sapiens growth differentiation factor 9 (GDF9), mRNA. /FEA=CDS /GEN=GDF9 /PROD=growth differentiation factor 9 precursor /DB_XREF=gi:6715598 /UG=Hs.248113 growth differentiation factor 9 /FL=gb:NM_005260.2	
211097_s_at		BC003111	gb:BC003111.1 /DEF=Homo sapiens, Similar to pre-B-cell leukemia transcription factor 2, clone MGC:2174, mRNA, complete cds. /FEA=mRNA /PROD=Similar to pre-B-cell leukemia transcriptionfactor 2 /DB_XREF=gi:13111886 /UG=Hs.93728 pre-B-cell leukemia transcription factor 2 /FL=gb:BC003111.1	
213634_s_at		AL031588	Consensus includes gb:AL031588 /DEF=Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3 part of a gene for a novel KIAA0279 LIKE EGF-like domain containing protein (similar to mouse Celsr1, rat MEGF2), a novel gene for a protein similar to C. elegans B0... /FEA=mRNA_1 /DB_XREF=gi:4007108 /UG=Hs.250671 hypothetical protein FLJ10140	
206536_s_at		U32974	gb:U32974.1 /DEF=Human IAP-like protein ILP mRNA, complete cds. /FEA=mRNA /PROD=IAP-like protein ILP /DB_XREF=gi:1016687 /UG=Hs.172777 baculoviral IAP repeat-containing 4	

			/FL=gb:U32974.1 gb:U45880.1 gb:Nm_001167.1	
205396_at	DKFZP586N0721	BF971416	DKFZP586N0721 protein	
218899_s_at		NM_024812	gb:Nm_024812.1 /DEF=Homo sapiens hypothetical protein FLJ12015 (FLJ12015), mRNA. /FEA=mRNA /GEN=FLJ12015 /PROD=hypothetical protein FLJ12015 /DB_XREF=gi:13376199 /UG=Hs.169395 hypothetical protein FLJ12015 /FL=gb:Nm_024812.1	
203793_x_at		NM_007144	gb:Nm_007144.1 /DEF=Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA. /FEA=mRNA /GEN=ZNF144 /PROD=zinc finger protein 144 (Mel-18) /DB_XREF=gi:6005963 /UG=Hs.184669 zinc finger protein 144 (Mel-18) /FL=gb:BC004858.1 gb:D13969.1 gb:Nm_007144.1	
221031_s_at		NM_030817	gb:Nm_030817.1 /DEF=Homo sapiens hypothetical protein DKFZp434F0318 (DKFZP434F0318), mRNA. /FEA=mRNA /GEN=DKFZP434F0318 /PROD=hypothetical protein DKFZp434F0318 /DB_XREF=gi:13540611 /FL=gb:Nm_030817.1	
202638_s_at		NM_000201	gb:Nm_000201.1 /DEF=Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1), mRNA. /FEA=mRNA /GEN=ICAM1 /PROD=intercellular adhesion molecule 1 precursor /DB_XREF=gi:4557877 /UG=Hs.168383 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor /FL=gb:M24283.1 gb:J03132.1 gb:Nm_000201.1	

220161_s_at		NM_019114	gb:NM_019114.1 /DEF=Homo sapiens EHM2 gene (EHM2), mRNA. /FEA=mRNA /GEN=EHM2 /PROD=EHM2 gene /DB_XREF=gi:9506568 /UG=Hs.267997 EHM2 gene /FL=gb:NM_019114.1	
211654_x_at		M17565	gb:M17565.1 /DEF=Human MHC class II DQ-beta associated with DRw6, DQw1 protein, complete cds. /FEA=mRNA /GEN=HLA-DQB1 /DB_XREF=gi:188188 /FL=gb:M17565.1	
202809_s_at		NM_023015	gb:NM_023015.1 /DEF=Homo sapiens hypothetical protein FLJ21919 (FLJ21919), mRNA. /FEA=mRNA /GEN=FLJ21919 /PROD=hypothetical protein FLJ21919 /DB_XREF=gi:12711679 /UG=Hs.105894 hypothetical protein FLJ21919 /FL=gb:NM_023015.1	
218392_x_at		NM_022754	gb:NM_022754.1 /DEF=Homo sapiens hypothetical protein FLJ12876 (FLJ12876), mRNA. /FEA=mRNA /GEN=FLJ12876 /PROD=hypothetical protein FLJ12876 /DB_XREF=gi:12232420 /UG=Hs.16131 hypothetical protein FLJ12876 /FL=gb:NM_022754.1	
205883_at		NM_006006	gb:NM_006006.1 /DEF=Homo sapiens zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145), mRNA. /FEA=mRNA /GEN=ZNF145 /PROD=zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) /DB_XREF=gi:5174752 /UG=Hs.37096 zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) /FL=gb:NM_006006.1	
220041_at		NM_025163	gb:NM_025163.1 /DEF=Homo sapiens hypothetical protein FLJ12768 (FLJ12768), mRNA. /FEA=mRNA /GEN=FLJ12768 /PROD=hypothetical protein FLJ12768 /DB_XREF=gi:13376764	

			/UG=Hs.289077 hypothetical protein FLJ12768 /FL=gb:NM_025163.1	
208578_at		NM_006514	gb:NM_006514.1 /DEF=Homo sapiens sodium channel, voltage-gated, type X, alpha polypeptide (SCN10A), mRNA. /FEA=CDS /GEN=SCN10A /PROD=sodium channel, voltage-gated, type X, alphapolypeptide /DB_XREF=gi:5730032 /UG=Hs.250443 sodium channel, voltage-gated, type X, alpha polypeptide /FL=gb:AF117907.1 gb:NM_006514.1	
209005_at		AF157323	gb:AF157323.1 /DEF=Homo sapiens p45SKP2-like protein mRNA, complete cds. /FEA=mRNA /PROD=p45SKP2-like protein /DB_XREF=gi:7688696 /UG=Hs.5548 f-box and leucine-rich repeat protein 5 /FL=gb:AF199420.1 gb:AF142481.1 gb:AF157323.1	
209049_s_at		BC001004	gb:BC001004.1 /DEF=Homo sapiens, clone MGC:5439, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:5439) /DB_XREF=gi:12654362 /UG=Hs.75871 protein kinase C binding protein 1 /FL=gb:BC001004.1	
220239_at		NM_018846	gb:NM_018846.1 /DEF=Homo sapiens SBBI26 protein (SBBI26), mRNA. /FEA=mRNA /GEN=SBBI26 /PROD=SBBI26 protein /DB_XREF=gi:9055325 /UG=Hs.26481 SBBI26 protein /FL=gb:AF111113.1 gb:NM_018846.1	
200802_at		NM_006513	gb:NM_006513.1 /DEF=Homo sapiens seryl-tRNA synthetase (SARS), mRNA. /FEA=mRNA /GEN=SARS /PROD=seryl-tRNA synthetase /DB_XREF=gi:5730028 /UG=Hs.4888 seryl-tRNA synthetase /FL=gb:BC000716.1	

			gb:NM_006513.1 gb:D49914.1	
209165_at		AF083208	gb:AF083208.1 /DEF=Homo sapiens Che-1 mRNA, complete cds. /FEA=mRNA /PROD=Che-1 /DB_XREF=gi:5813798 /UG=Hs.16178 apoptosis antagonizing transcription factor /FL=gb:BC000591.1 gb:AF083208.1 gb:NM_012138.1	
200804_at		NM_003217	gb:NM_003217.1 /DEF=Homo sapiens testis enhanced gene transcript (TEGT), mRNA. /FEA=mRNA /GEN=TEGT /PROD=testis enhanced gene transcript /DB_XREF=gi:4507432 /UG=Hs.74637 testis enhanced gene transcript (BAX inhibitor 1) /FL=gb:BC000916.1 gb:AF033095.1 gb:NM_003217.1	
213032_at		AL110126	Consensus includes gb:AI186739 /FEA=EST /DB_XREF=gi:3737377 /DB_XREF=est:qe79c01.x1 /CLONE=IMAGE:1745184 /UG=Hs.326416 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)	
65630_at		AI742455	Homo sapiens, Similar to RIKEN cDNA 5530601119 gene, clone MGC:9743 IMAGE:3854028, mRNA, complete cds	
212230_at	RPS20	AL576654	ribosomal protein S20	
219335_at		NM_022838	gb:NM_022838.1 /DEF=Homo sapiens hypothetical protein FLJ12969 (FLJ12969), mRNA. /FEA=mRNA /GEN=FLJ12969 /PROD=hypothetical protein FLJ12969 /DB_XREF=gi:12383085 /UG=Hs.119699 hypothetical protein FLJ12969 /FL=gb:NM_022838.1	
211026_s_at		BC006230	gb:BC006230.1 /DEF=Homo sapiens, lysophospholipase-like, clone MGC:10338, mRNA, complete cds. /FEA=mRNA /PROD=lysophospholipase-like /DB_XREF=gi:13623260 /FL=gb:BC006230.1	

208949_s_at		BC001120	gb:BC001120.1 /DEF=Homo sapiens, lectin, galactoside-binding, soluble, 3 (galectin 3), clone MGC:2058, mRNA, complete cds. /FEA=mRNA /PROD=lectin, galactoside-binding, soluble, 3(galectin 3) /DB_XREF=gi:12654570 /UG=Hs.621 lectin, galactoside-binding, soluble, 3 (galectin 3) /FL=gb:M35368.1 gb:BC001120.1 gb:M57710.1 gb:M36682.1 gb:AB006780.1 gb:NM_002306.1	
201142_at	EIF2S1	AA577698	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	
215146_s_at		AB028966	Consensus includes gb:AB028966.1 /DEF=Homo sapiens mRNA for KIAA1043 protein, partial cds. /FEA=mRNA /GEN=KIAA1043 /PROD=KIAA1043 protein /DB_XREF=gi:5689422 /UG=Hs.11390 KIAA1043 protein	
210563_x_at		U97075	gb:U97075.1 /DEF=Homo sapiens FLICE-like inhibitory protein short form mRNA, complete cds. /FEA=mRNA /PROD=FLICE-like inhibitory protein short form /DB_XREF=gi:2253680 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:U97075.1	
210718_s_at		AF119889	gb:AF119889.1 /DEF=Homo sapiens PRO2667 mRNA, complete cds. /FEA=mRNA /PROD=PRO2667 /DB_XREF=gi:7770214 /UG=Hs.321170 Homo sapiens PRO2667 mRNA, complete cds /FL=gb:AF119889.1	
221989_at	RPL10	AW057781	ribosomal protein L10	
205139_s_at		NM_005715	gb:NM_005715.1 /DEF=Homo sapiens uronyl 2-sulfotransferase (UST), mRNA. /FEA=mRNA /GEN=UST /PROD=uronyl 2-sulfotransferase /DB_XREF=gi:5032218 /UG=Hs.134015 uronyl 2-sulfotransferase /FL=gb:AB020316.1 gb:NM_005715.1	



221983_at	MGC3035	AL040896	hypothetical protein MGC3035	
205353_s_at		NM_002567	gb:NM_002567.1 /DEF=Homo sapiens prostatic binding protein (PBP), mRNA. /FEA=mRNA /GEN=PBP /PROD=prostatic binding protein /DB_XREF=gi:4505620 /UG=Hs.80423 prostatic binding protein /FL=gb:D16111.1 gb:NM_002567.1	
216862_s_at		Z24459	Consensus includes gb:Z24459 /DEF=H.sapiens MTCP1 gene, exons 2A to 7 (and joined mRNA) /FEA=mRNA_4 /DB_XREF=gi:2252491 /UG=Hs.3548 mature T-cell proliferation 1	
210949_s_at		BC000533	gb:BC000533.1 /DEF=Homo sapiens, Similar to eukaryotic translation initiation factor 3, subunit 8 (110kD), clone MGC:8693, mRNA, complete cds. /FEA=mRNA /PROD=Similar to eukaryotic translation initiationfactor 3, subunit 8 (110kD) /DB_XREF=gi:12653522 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kD) /FL=gb:BC000533.1	
209445_x_at	FLJ10803	AI765280	hypothetical protein FLJ10803	
215722_s_at		AJ130971	Consensus includes gb:AJ130971.1 /DEF=Homo sapiens mRNA for U2 snRNP-specific A protein, alternative transcript 4. /FEA=mRNA /PROD=U2 snRNP-specific A protein /DB_XREF=gi:3970726 /UG=Hs.80506 small nuclear ribonucleoprotein polypeptide A	
201331_s_at		BC004973	gb:BC004973.1 /DEF=Homo sapiens, signal transducer and activator of transcription 6, interleukin-4 induced, clone MGC:3649, mRNA, complete cds. /FEA=mRNA /PROD=signal transducer and activator of transcription6, interleukin-4 induced /DB_XREF=gi:13436385 /UG=Hs.181015 signal transducer and activator of transcription 6, interleukin-4 induced /FL=gb:BC004973.1	

			gb:NM_003153.1 gb:U16031.1	
221645_s_at		M27877	gb:M27877.1 /DEF=Homo sapiens HPF1 protein, complete cds. /FEA=mRNA /PROD=HPF1 protein /DB_XREF=gi:341790 /UG=Hs.305953 zinc finger protein 83 (HPF1) /FL=gb:M27877.1	
212343_at	GTF2A2	AA195936	general transcription factor IIA, 2, 12kDa	
212626_x_at	HNRPC	AA664258	heterogeneous nuclear ribonucleoprotein C (C1/C2)	
210694_s_at		AF041209	gb:AF041209.1 /DEF=Homo sapiens midline 1 fetal kidney isoform 2 (MID1) mRNA, complete cds. /FEA=mRNA /GEN=MID1 /PROD=midline 1 fetal kidney isoform 2 /DB_XREF=gi:3462508 /UG=Hs.27695 midline 1 (OpitzBBB syndrome) /FL=gb:AF041209.1	
209263_x_at		BC000389	gb:BC000389.1 /DEF=Homo sapiens, transmembrane 4 superfamily member 7, clone MGC:8437, mRNA, complete cds. /FEA=mRNA /PROD=transmembrane 4 superfamily member 7 /DB_XREF=gi:12653240 /UG=Hs.26518 transmembrane 4 superfamily member 7 /FL=gb:BC000389.1 gb:AF022813.1 gb:AF054841.1 gb:NM_003271.1	
200753_x_at	ET	BE866585	hypothetical protein ET	
203442_x_at	FLJ35827	AA478965	hypothetical protein FLJ35827	
204232_at		NM_004106	gb:NM_004106.1 /DEF=Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide (FCER1G), mRNA. /FEA=mRNA /GEN=FCER1G /PROD=Fc fragment of IgE, high affinity I, receptorfor, gamma polypeptide precursor	

			/DB_XREF=gi:4758343 /UG=Hs.743 Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide /FL=gb:M33195.1 gb:NM_004106.1	
208668_x_at		BC003689	gb:BC003689.1 /DEF=Homo sapiens, high-mobility group (nonhistone chromosomal) protein 17, clone MGC:5301, mRNA, complete cds. /FEA=mRNA /PROD=high- mobility group (nonhistone chromosomal)protein 17 /DB_XREF=gi:13277559 /UG=Hs.181163 high-mobility group (nonhistone chromosomal) protein 17 /FL=gb:BC003689.1 gb:M12623.1	
208673_s_at		AF107405	gb:AF107405.1 /DEF=Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds. /FEA=mRNA /GEN=SFRS3 /PROD=pre- mRNA splicing factor /DB_XREF=gi:5531903 /UG=Hs.167460 splicing factor, arginineserine-rich 3 /FL=gb:BC000914.1 gb:AF107405.1	
203860_at		NM_000282	gb:NM_000282.1 /DEF=Homo sapiens propionyl Coenzyme A carboxylase, alpha polypeptide (PCCA), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=PCCA /PROD=Propionyl-Coenzyme A carboxylase, alphapolypeptide precursor /DB_XREF=gi:4557832 /UG=Hs.80741 propionyl Coenzyme A carboxylase, alpha polypeptide /FL=gb:BC000140.1 gb:NM_000282.1	
200696_s_at		NM_000177	gb:NM_000177.1 /DEF=Homo sapiens gelsolin (amyloidosis, Finnish type) (GSN), mRNA. /FEA=mRNA /GEN=GSN /PROD=gelsolin (amyloidosis, Finnish type)	

			/DB_XREF=gi:4504164 /UG=Hs.290070 gelsolin (amyloidosis, Finnish type) /FL=gb:NM_000177.1	
204206_at		NM_020310	gb:NM_020310.1 /DEF=Homo sapiens MAX binding protein (MNT), mRNA. /FEA=mRNA /GEN=MNT /PROD=MAX binding protein /DB_XREF=gi:9945317 /UG=Hs.25497 MAX binding protein /FL=gb:NM_020310.1	
203666_at		NM_000609	gb:NM_000609.1 /DEF=Homo sapiens stromal cell-derived factor 1 (SDF1), mRNA. /FEA=mRNA /GEN=SDF1 /PROD=stromal cell-derived factor 1 /DB_XREF=gi:10834987 /UG=Hs.237356 stromal cell- derived factor 1 /FL=gb:NM_000609.1 gb:L36033.1 gb:U16752.1	
203606_at		NM_004553	gb:NM_004553.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase) (NDUFS6), mRNA. /FEA=mRNA /GEN=NDUFS6 /PROD=NADH dehydrogenase (ubiquinone) Fe-S protein 6(13kD) (NADH-coenzyme Q reductase) /DB_XREF=gi:4758791 /UG=Hs.49767 NADH dehydrogenase (ubiquinone) Fe- S protein 6 (13kD) (NADH- coenzyme Q reductase) /FL=gb:AF044959.1 gb:NM_004553.1	
221824_s_at	MGC26766	AA770170	hypothetical protein MGC26766	
212640_at		AV712602	ESTs, Weakly similar to T32252 hypothetical protein T15B7.2 - Caenorhabditis elegans [C.elegans]	
212599_at		AK025298	Consensus includes gb:AK025298.1 /DEF=Homo sapiens cDNA: FLJ21645 fis, clone COL08436. /FEA=mRNA /DB_XREF=gi:10437785 /UG=Hs.32168 KIAA0442 protein	

209332_s_at		BC003525	gb:BC003525.1 /DEF=Homo sapiens, Similar to Max, clone MGC:10775, mRNA, complete cds. /FEA=mRNA /PROD=Similar to Max /DB_XREF=gi:13097617 /UG=Hs.42712 MAX protein /FL=gb:BC003525.1	
221971_x_at	MRIP2	BE672818	ARF GTPase-activating protein	
203135_at		NM_003194	gb:NM_003194.1 /DEF=Homo sapiens TATA box binding protein (TBP), mRNA. /FEA=mRNA /GEN=TBP /PROD=TATA box binding protein /DB_XREF=gi:4507378 /UG=Hs.1100 TATA box binding protein /FL=gb:M34960.1 gb:M55654.1 gb:NM_003194.1	
208716_s_at		AB020980	gb:AB020980.1 /DEF=Homo sapiens mRNA for putative membrane protein, complete cds. /FEA=mRNA /PROD=membrane protein /DB_XREF=gi:6467174 /UG=Hs.93832 putative membrane protein /FL=gb:BC000104.1 gb:AB020980.1	
218781_at		NM_024624	gb:NM_024624.1 /DEF=Homo sapiens hypothetical protein FLJ22116 (FLJ22116), mRNA. /FEA=mRNA /GEN=FLJ22116 /PROD=hypothetical protein FLJ22116 /DB_XREF=gi:13375847 /UG=Hs.34497 hypothetical protein FLJ22116 /FL=gb:AL136544.1 gb:NM_024624.1	
221597_s_at		BC003080	gb:BC003080.1 /DEF=Homo sapiens, Similar to HSPC171 protein, clone MGC:770, mRNA, complete cds. /FEA=mRNA /PROD=Similar to HSPC171 protein /DB_XREF=gi:13111781 /UG=Hs.279593 HSPC171 protein /FL=gb:BC003080.1	
212848_s_at	FLJ14675	BG036668	hypothetical protein FLJ14675	
210638_s_at		AF176704	gb:AF176704.1 /DEF=Homo sapiens F-box protein FBX9 mRNA, complete cds. /FEA=mRNA /PROD=F-box	

			protein FBX9 /DB_XREF=gi:6103646 /UG=Hs.11050 F-box only protein 9 /FL=gb:AF176704.1	
202522_at		AL031591	Consensus includes gb:AL031591 /DEF=Human DNA sequence from clone RP3-353E16 on chromosome 22q11.22-12.3 Contains the 5 part of the MN1 gene for meningioma (disrupted in balanced translocation) 1, the PITPNB gene for phosphatidylinositol transfer protein beta, ESTs, STSs, GSSs and ... /FEA=mRNA /DB_XREF=gi:6006484 /UG=Hs.7370 phosphatidylinositol transfer protein, beta /FL=gb:D30037.1 gb:Nm_012399.1	
212261_at	TNRC15	AL045800	trinucleotide repeat containing 15	
218700_s_at		BC002585	gb:BC002585.1 /DEF=Homo sapiens, RAB7, member RAS oncogene family-like 1, clone MGC:1653, mRNA, complete cds. /FEA=mRNA /PROD=RAB7, member RAS oncogene family-like 1 /DB_XREF=gi:12803516 /UG=Hs.115325 RAB7, member RAS oncogene family-like 1 /FL=gb:BC002585.1 gb:D84488.1 gb:Nm_003929.1	
201647_s_at		NM_005506	gb:Nm_005506.1 /DEF=Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) (CD36L2), mRNA. /FEA=mRNA /GEN=CD36L2 /PROD=CD36 antigen (collagen type I receptor,thrombospondin receptor)-like 2 (lysosomal integralmembrane protein II) /DB_XREF=gi:5031630 /UG=Hs.323567 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) /FL=gb:D12676.1 gb:Nm_005506.1	

201744_s_at		NM_002345	gb:NM_002345.1 /DEF=Homo sapiens lumican (LUM), mRNA. /FEA=mRNA /GEN=LUM /PROD=lumican /DB_XREF=gi:4505046 /UG=Hs.79914 lumican /FL=gb:NM_002345.1 gb:U18728.1 gb:U21128.1	
201417_at		NM_003107	Consensus includes gb:AL136179 /DEF=Human DNA sequence from clone RP3-322L4 on chromosome 6. Contains the SOX4 gene for SRY (sex determining region Y)-box 4, a pseudogene similar to predicted fly, worm and yeast genes, ESTs, STSs, GSSs and four CpG islands /FEA=mRNA /DB_XREF=gi:8649149 /UG=Hs.83484 SRY (sex determining region Y)-box 4 /FL=gb:NM_003107.1	
160020_at	MMP14	Z48481	matrix metalloproteinase 14 (membrane-inserted)	NM_004995
201776_s_at		AK001487	Consensus includes gb:AK001487.1 /DEF=Homo sapiens cDNA FLJ10625 fis, clone NT2RP2005540, highly similar to Homo sapiens mRNA for KIAA0494 protein. /FEA=mRNA /DB_XREF=gi:7022773 /UG=Hs.62515 KIAA0494 gene product /FL=gb:BC002525.1 gb:AB007963.1 gb:NM_014774.1	
216652_s_at		AL137673	Consensus includes gb:AL137673.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872). /FEA=mRNA /DB_XREF=gi:6807841 /UG=Hs.306454 Homo sapiens mRNA; cDNA DKFZp434H0872 (from clone DKFZp434H0872)	
218241_at		NM_005113	gb:NM_005113.1 /DEF=Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA. /FEA=mRNA /GEN=GOLGA5 /PROD=golgi autoantigen, golgin subfamily a, 5 /DB_XREF=gi:4826747 /UG=Hs.241572 golgi autoantigen, golgin subfamily a,	

			5 /FL=gb:AF085199.1 gb:NM_005113.1	
214315_x_at	CALR	AI348935	calreticulin	
58780_s_at	FLJ10357	R42449	hypothetical protein FLJ10357	
206976_s_at		NM_006644	gb:NM_006644.1 /DEF=Homo sapiens heat shock 105kD (HSP105B), mRNA. /FEA=mRNA /GEN=HSP105B /PROD=heat shock 105kD /DB_XREF=gi:5729878 /UG=Hs.36927 heat shock 105kD /FL=gb:AB003333.1 gb:NM_006644.1	
218588_s_at		NM_018691	gb:NM_018691.1 /DEF=Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA. /FEA=mRNA /GEN=C5ORF3 /PROD=hypothetical protein /DB_XREF=gi:8922068 /UG=Hs.166551 chromosome 5 open reading frame 3 /FL=gb:NM_018691.1	
209363_s_at		U46837	gb:U46837.1 /DEF=Human RNA polymerase II holoenzyme component SRB7 (SRB7) mRNA, complete cds. /FEA=mRNA /GEN=SRB7 /PROD=SRB7 /DB_XREF=gi:1197662 /UG=Hs.286145 SRB7 (suppressor of RNA polymerase B, yeast) homolog /FL=gb:U46837.1 gb:U52960.1 gb:NM_004264.1	
204173_at		NM_002475	gb:NM_002475.1 /DEF=Homo sapiens myosin, light polypeptide 1, alkali; skeletal, fast (MYL1), mRNA. /FEA=mRNA /GEN=MYL1 /PROD=myosin, light polypeptide 1, alkali; skeletal,fast /DB_XREF=gi:4505302 /UG=Hs.90318 myosin, light polypeptide 1, alkali; skeletal, fast /FL=gb:M31211.1 gb:NM_002475.1	
202441_at	KEO4	AL568449	similar to Caenorhabditis elegans protein C42C1.9	



205644_s_at	NM_003096	gb:NM_003096.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA. /FEA=mRNA /GEN=SNRPG /PROD=small nuclear ribonucleoprotein polypeptide G /DB_XREF=gi:4507132 /UG=Hs.77496 small nuclear ribonucleoprotein polypeptide G /FL=gb:BC000070.1 gb:NM_003096.1
200847_s_at	NM_016127	gb:NM_016127.1 /DEF=Homo sapiens HSPC035 protein (LOC51669), mRNA. /FEA=mRNA /GEN=LOC51669 /PROD=HSPC035 protein /DB_XREF=gi:7706384 /UG=Hs.279921 HSPC035 protein /FL=gb:AF100748.1 gb:AF078855.1 gb:NM_016127.1
201298_s_at	BC003398	gb:BC003398.1 /DEF=Homo sapiens, hypothetical protein FLJ10788, clone MGC:4929, mRNA, complete cds. /FEA=mRNA /PROD=hypothetical protein FLJ10788 /DB_XREF=gi:13097287 /UG=Hs.196437 hypothetical protein FLJ10788 /FL=gb:AB016839.1 gb:BC003398.1 gb:NM_018221.1
207543_s_at	NM_000917	gb:NM_000917.1 /DEF=Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I (P4HA1), mRNA. /FEA=mRNA /GEN=P4HA1 /PROD=procollagen-proline, 2-oxoglutarate4-dioxygenase (proline 4-hydroxylase), alpha polypeptidel /DB_XREF=gi:4505564 /UG=Hs.76768 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I /FL=gb:M24486.1 gb:NM_000917.1

209790_s_at		BC000305	gb:BC000305.1 /DEF=Homo sapiens, caspase 6, apoptosis-related cysteine protease, clone MGC:8388, mRNA, complete cds. /FEA=mRNA /PROD=caspase 6, apoptosis-related cysteine protease /DB_XREF=gi:12653078 /UG=Hs.3280 caspase 6, apoptosis-related cysteine protease /FL=gb:BC000305.1 gb:BC004460.1 gb:NM_001226.1 gb:U20536.1	
215172_at		AL050040	Consensus includes gb:AL050040.1 /DEF=Homo sapiens mRNA; cDNA DKFZp566K0524 (from clone DKFZp566K0524); partial cds. /FEA=mRNA /GEN=DKFZp566K0524 /PROD=hypothetical protein /DB_XREF=gi:4884281 /UG=Hs.227651 DKFZP566K0524 protein	
213365_at	KIAA1504	N64622	KIAA1504 protein	
202951_at	STK38	BE048506	serine/threonine kinase 38	
203266_s_at		NM_003010	gb:NM_003010.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA. /FEA=mRNA /GEN=MAP2K4 /PROD=mitogen-activated protein kinase kinase 4 /DB_XREF=gi:4506888 /UG=Hs.75217 mitogen-activated protein kinase kinase 4 /FL=gb:NM_003010.1 gb:L36870.1 gb:U17743.1	
219869_s_at		NM_022154	gb:NM_022154.1 /DEF=Homo sapiens up-regulated by BCG-CWS (LOC64116), mRNA. /FEA=mRNA /GEN=LOC64116 /PROD=up-regulated by BCG-CWS /DB_XREF=gi:11545899 /UG=Hs.284205 up-regulated by BCG-CWS /FL=gb:NM_022154.1	
212200_at		AB014592	Consensus includes gb:AK025933.1 /DEF=Homo sapiens cDNA: FLJ22280 fis, clone HRC03841. /FEA=mRNA /DB_XREF=gi:10438600 /UG=Hs.100729 KIAA0692 protein	

201029_s_at		NM_002414	gb:NM_002414.1 /DEF=Homo sapiens antigen identified by monoclonal antibodies 12E7, F21 and O13 (MIC2), mRNA. /FEA=mRNA /GEN=MIC2 /PROD=antigen identified by monoclonal antibodies12E7, F21 and O13 /DB_XREF=gi:4505182 /UG=Hs.177543 antigen identified by monoclonal antibodies 12E7, F21 and O13 /FL=gb:BC002584.1 gb:BC003147.1 gb:M16279.1 gb:U82164.1 gb:NM_002414.1	
217839_at		NM_006070	gb:NM_006070.1 /DEF=Homo sapiens TRK-fused gene (TFG), mRNA. /FEA=mRNA /GEN=TFG /PROD=TRK-fused gene /DB_XREF=gi:5174718 /UG=Hs.250897 TRK-fused gene /FL=gb:NM_006070.1	
201444_s_at		NM_005765	gb:NM_005765.1 /DEF=Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (APT6M8-9), mRNA. /FEA=mRNA /GEN=APT6M8-9 /PROD=ATPase, H+ transporting, lysosomal (vacuolarproton pump) membrane sector associated protein M8-9 /DB_XREF=gi:5031590 /UG=Hs.183434 ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 /FL=gb:AF248966.1 gb:NM_005765.1	
221234_s_at		NM_021813	gb:NM_021813.1 /DEF=Homo sapiens BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA. /FEA=mRNA /GEN=BACH2 /PROD=BTB and CNC homology 1, basic leucine zippertranscription factor 2 /DB_XREF=gi:13540489 /FL=gb:NM_021813.1	
45633_at	FLJ13912	AI421812	hypothetical protein FLJ13912	
213937_s_at	FTSJ1	AV723177	FtsJ homolog 1 (E. coli)	

210109_at		AF191492	gb:AF191492.1 /DEF=Homo sapiens nasopharyngeal carcinoma associated gene protein-8 (NAG8) mRNA, complete cds. /FEA=mRNA /GEN=NAG8 /PROD=nasopharyngeal carcinoma associated gene protein-8 /DB_XREF=gi:11065903 /UG=Hs.26937 brain and nasopharyngeal carcinoma susceptibility protein /FL=gb:AF191492.1	
202485_s_at		NM_003927	gb:NM_003927.2 /DEF=Homo sapiens methyl-CpG binding domain protein 2 (MBD2), transcript variant 1, mRNA. /FEA=mRNA /GEN=MBD2 /PROD=methyl-CpG binding domain protein 2, isoform 1 /DB_XREF=gi:7710146 /UG=Hs.25674 methyl-CpG binding domain protein 2 /FL=gb:AF072242.1 gb:NM_003927.2	
201512_s_at		BC003633	gb:BC003633.1 /DEF=Homo sapiens, translocase of outer mitochondrial membrane 70 (yeast) homolog A, clone MGC:3766, mRNA, complete cds. /FEA=mRNA /PROD=translocase of outer mitochondrial membrane 70(yeast) homolog A /DB_XREF=gi:13177705 /UG=Hs.21198 translocase of outer mitochondrial membrane 70 (yeast) homolog A /FL=gb:BC003633.1 gb:AB018262.1 gb:NM_014820.1	
204122_at		NM_003332	gb:NM_003332.1 /DEF=Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP), mRNA. /FEA=mRNA /GEN=TYROBP /PROD=TYRO protein tyrosine kinase binding protein /DB_XREF=gi:4507754 /UG=Hs.9963 TYRO protein tyrosine kinase binding protein /FL=gb:AF019562.1 gb:NM_003332.1	

213204_at		AB014608	Consensus includes gb:AB014608.1 /DEF=Homo sapiens mRNA for KIAA0708 protein, partial cds. /FEA=mRNA /GEN=KIAA0708 /PROD=KIAA0708 protein /DB_XREF=gi:3327229 /UG=Hs.117177 KIAA0708 protein	
209232_s_at		BC004191	gb:BC004191.1 /DEF=Homo sapiens, dynactin 4, clone MGC:3248, mRNA, complete cds. /FEA=mRNA /PROD=dynactin 4 /DB_XREF=gi:13278857 /UG=Hs.111429 Homo sapiens, dynactin 4, clone MGC:3248, mRNA, complete cds /FL=gb:BC004191.1	
204241_at	ACOX3	BF055171	acyl-Coenzyme A oxidase 3, pristanoyl	
210205_at		AB026730	gb:AB026730.1 /DEF=Homo sapiens B3GALT4 mRNA for beta-1,3-galactosyltransferase-4, complete cds. /FEA=mRNA /GEN=B3GALT4 /PROD=beta-1,3-galactosyltransferase-4 /DB_XREF=gi:6683013 /UG=Hs.21495 UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4 /FL=gb:AF063595.1 gb:NM_003782.1 gb:AB026730.1	
213720_s_at	SMARCA4	AI831675	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	
201415_at		NM_000178	gb:NM_000178.1 /DEF=Homo sapiens glutathione synthetase (GSS), mRNA. /FEA=mRNA /GEN=GSS /PROD=glutathione synthetase /DB_XREF=gi:4504168 /UG=Hs.82327 glutathione synthetase /FL=gb:U34683.1 gb:NM_000178.1	
220672_at		NM_020958	gb:NM_020958.1 /DEF=Homo sapiens KIAA1622 protein (KIAA1622), mRNA. /FEA=mRNA /GEN=KIAA1622 /PROD=hypothetical protein MGC4163 /DB_XREF=gi:13124766 /UG=Hs.259599 KIAA1622	

			protein /FL=gb:BC002650.1 gb:Nm_020958.1	
218040_at		NM_018061	gb:Nm_018061.1 /DEF=Homo sapiens hypothetical protein FLJ10330 (FLJ10330), mRNA. /FEA=mRNA /GEN=FLJ10330 /PROD=hypothetical protein FLJ10330 /DB_XREF=gi:8922357 /UG=Hs.302267 hypothetical protein FLJ10330 /FL=gb:Nm_018061.1	
201376_s_at	HNRPF	AI591354	heterogeneous nuclear ribonucleoprotein F	
205255_x_at		NM_003202	gb:Nm_003202.1 /DEF=Homo sapiens transcription factor 7 (T-cell specific, HMG-box) (TCF7), mRNA. /FEA=mRNA /GEN=TCF7 /PROD=transcription factor 7 (T-cell specific,HMG-box) /DB_XREF=gi:4507402 /UG=Hs.169294 transcription factor 7 (T-cell specific, HMG-box) /FL=gb:Nm_003202.1	
202531_at		NM_002198	gb:Nm_002198.1 /DEF=Homo sapiens interferon regulatory factor 1 (IRF1), mRNA. /FEA=mRNA /GEN=IRF1 /PROD=interferon regulatory factor 1 /DB_XREF=gi:4504720 /UG=Hs.80645 interferon regulatory factor 1 /FL=gb:Nm_002198.1	
206078_at		NM_007064	gb:Nm_007064.1 /DEF=Homo sapiens serinethreonine kinase with Dbl- and pleckstrin homology domains (TRAD), mRNA. /FEA=mRNA /GEN=TRAD /PROD=serinethreonine kinase with Dbl- and pleckstrinhomology domains /DB_XREF=gi:5902139 /UG=Hs.162189 serinethreonine kinase with Dbl- and pleckstrin homology domains /FL=gb:AB011422.1 gb:Nm_007064.1	

211121_s_at		AF180527	gb:AF180527.1 /DEF=Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds. /FEA=mRNA /GEN=DOKDEL /PROD=p22Dokdel /DB_XREF=gi:6606314 /UG=Hs.103854 docking protein 1, 62kD (downstream of tyrosine kinase 1) /FL=gb:AF180527.1	
220975_s_at		NM_030968	gb:NM_030968.1 /DEF=Homo sapiens G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related (ZSIG37), mRNA. /FEA=mRNA /GEN=ZSIG37 /PROD=G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related /DB_XREF=gi:13569943 /FL=gb:NM_030968.1	
204163_at		NM_007046	gb:NM_007046.1 /DEF=Homo sapiens elastin microfibril interface located protein (EMILIN), mRNA. /FEA=mRNA /GEN=EMILIN /PROD=elastin microfibril interface located protein /DB_XREF=gi:5901943 /UG=Hs.63348 elastin microfibril interface located protein /FL=gb:AF088916.1	
206169_x_at		NM_025013	gb:NM_025013.1 /DEF=Homo sapiens KIAA1031 protein (KIAA1031), mRNA. /FEA=mRNA /GEN=KIAA1031 /PROD=hypothetical protein FLJ13787 /DB_XREF=gi:13430879 /UG=Hs.25347 KIAA1031 protein /FL=gb:NM_025013.1	
212786_at	KIAA0350	AA731693	KIAA0350 protein	
207767_s_at		NM_001965	gb:NM_001965.1 /DEF=Homo sapiens early growth response 4 (EGR4), mRNA. /FEA=mRNA /GEN=EGR4 /PROD=early growth response 4 /DB_XREF=gi:4503494 /UG=Hs.3052 early growth response 4 /FL=gb:NM_001965.1	

215495_s_at	AL117523	Consensus includes gb:AL117523.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434H0350 (from clone DKFZp434H0350); partial cds. /FEA=mRNA /GEN=DKFZp434H0350 /PROD=hypothetical protein /DB_XREF=gi:5912039 /UG=Hs.173571 KIAA1053 protein	
200661_at	NM_000308	gb:NM_000308.1 /DEF=Homo sapiens protective protein for beta-galactosidase (galactosialidosis) (PPGB), mRNA. /FEA=mRNA /GEN=PPGB /PROD=protective protein for beta-galactosidase /DB_XREF=gi:4505988 /UG=Hs.118126 protective protein for beta-galactosidase (galactosialidosis) /FL=gb:BC000597.1 gb:M22960.1 gb:NM_000308.1	
205080_at	NM_000965	gb:NM_000965.1 /DEF=Homo sapiens retinoic acid receptor, beta (RARB), mRNA. /FEA=mRNA /GEN=RARB /PROD=retinoic acid receptor, beta /DB_XREF=gi:4506420 /UG=Hs.171495 retinoic acid receptor, beta /FL=gb:NM_000965.1	
207388_s_at	NM_004878	gb:NM_004878.1 /DEF=Homo sapiens prostaglandin E synthase (PTGES), mRNA. /FEA=mRNA /GEN=PTGES /PROD=prostaglandin E synthase /DB_XREF=gi:4758909 /UG=Hs.146688 prostaglandin E synthase /FL=gb:AF027740.1 gb:NM_004878.1	
218915_at	NM_016418	gb:NM_016418.1 /DEF=Homo sapiens clone FLB5214 (LOC51219), mRNA. /FEA=mRNA /GEN=LOC51219 /PROD=clone FLB5214 /DB_XREF=gi:9994194 /UG=Hs.5486 clone FLB5214 /FL=gb:AF113694.1 gb:NM_016418.1	



210302_s_at	AF262032	gb:AF262032.1 /DEF=Homo sapiens MAB21L2 protein (MAB21L2) mRNA, complete cds. /FEA=mRNA /GEN=MAB21L2 /PROD=MAB21L2 protein /DB_XREF=gi:9964006 /UG=Hs.251390 mab-21 (C. elegans)-like 2 /FL=gb:NM_006439.2 gb:AF262032.1	
219518_s_at	NM_025165	gb:NM_025165.1 /DEF=Homo sapiens hypothetical protein FLJ22637 (FLJ22637), mRNA. /FEA=mRNA /GEN=FLJ22637 /PROD=hypothetical protein FLJ22637 /DB_XREF=gi:13376767 /UG=Hs.296178 hypothetical protein FLJ22637 /FL=gb:NM_025165.1	
204846_at	NM_000096	gb:NM_000096.1 /DEF=Homo sapiens ceruloplasmin (ferroxidase) (CP), mRNA. /FEA=mRNA /GEN=CP /PROD=ceruloplasmin (ferroxidase) /DB_XREF=gi:4557484 /UG=Hs.296634 ceruloplasmin (ferroxidase) /FL=gb:M13699.1 gb:NM_000096.1	
218986_s_at	NM_017631	gb:NM_017631.1 /DEF=Homo sapiens hypothetical protein FLJ20035 (FLJ20035), mRNA. /FEA=mRNA /GEN=FLJ20035 /PROD=hypothetical protein FLJ20035 /DB_XREF=gi:8923037 /UG=Hs.109309 hypothetical protein FLJ20035 /FL=gb:NM_017631.1	
219697_at	NM_006043	gb:NM_006043.1 /DEF=Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA. /FEA=mRNA /GEN=HS3ST2 /PROD=heparan sulfate D-glucosaminyl3-O-sulfotransferase 2 /DB_XREF=gi:5174462 /UG=Hs.115830 heparan sulfate (glucosamine) 3-O-sulfotransferase 2 /FL=gb:AF105374.1 gb:AF105375.1 gb:NM_006043.1	

211795_s_at		AF198052	gb:AF198052.1 /DEF=Homo sapiens EVH1 domain binding protein mRNA, complete cds. /FEA=CDS /PROD=EVH1 domain binding protein /DB_XREF=gi:7416992 /UG=Hs.58435 FYN-binding protein (FYB-120130) /FL=gb:AF198052.1	
205111_s_at		NM_016341	gb:NM_016341.1 /DEF=Homo sapiens pancreas-enriched phospholipase C (LOC51196), mRNA. /FEA=mRNA /GEN=LOC51196 /PROD=pancreas-enriched phospholipase C /DB_XREF=gi:7705940 /UG=Hs.6733 pancreas-enriched phospholipase C /FL=gb:AF190642.2 gb:AF117948.1 gb:NM_016341.1	
208124_s_at		NM_004263	gb:NM_004263.1 /DEF=Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (SEMA4F), mRNA. /FEA=mRNA /GEN=SEMA4F /PROD=semaphorin W /DB_XREF=gi:4759093 /UG=Hs.25887 sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F /FL=gb:AB022317.1 gb:NM_004263.1	
220422_at		NM_017481	gb:NM_017481.1 /DEF=Homo sapiens ubiquilin 3 (UBQLN3), mRNA. /FEA=mRNA /GEN=UBQLN3 /PROD=ubiquilin 3 /DB_XREF=gi:8567417 /UG=Hs.189184 ubiquilin 3 /FL=gb:AF230481.1 gb:NM_017481.1	
220465_at		NM_024988	gb:NM_024988.1 /DEF=Homo sapiens hypothetical protein FLJ12355 (FLJ12355), mRNA. /FEA=mRNA /GEN=FLJ12355 /PROD=hypothetical protein FLJ12355 /DB_XREF=gi:13376491 /UG=Hs.287521 hypothetical protein FLJ12355	

			/FL=gb:NM_024988.1	
202218_s_at		NM_004265	gb:NM_004265.1 /DEF=Homo sapiens delta-6 fatty acid desaturase (FADSD6), mRNA. /FEA=mRNA /GEN=FADSD6 /PROD=delta-6 fatty acid desaturase /DB_XREF=gi:4758333 /UG=Hs.184641 fatty acid desaturase 2 /FL=gb:AF084559.1 gb:AF126799.1 gb:NM_004265.1	
205130_at		NM_014226	gb:NM_014226.1 /DEF=Homo sapiens renal tumor antigen (RAGE), mRNA. /FEA=mRNA /GEN=RAGE /PROD=renal tumor antigen /DB_XREF=gi:7657497 /UG=Hs.104119 renal tumor antigen /FL=gb:AB022694.1 gb:NM_014226.1	
219567_s_at		NM_022774	gb:NM_022774.1 /DEF=Homo sapiens hypothetical protein FLJ21144 (FLJ21144), mRNA. /FEA=mRNA /GEN=FLJ21144 /PROD=hypothetical protein FLJ21144 /DB_XREF=gi:12232456 /UG=Hs.59584 hypothetical protein FLJ21144 /FL=gb:NM_022774.1	
203017_s_at	KIAA0923	AW136988	KIAA0923 protein	
38158_at	ESPL1	D79987	extra spindle poles like 1 (S. cerevisiae)	NM_012291
65133_i_at	PAPA-1	AI862454	PAP-1 binding protein	
201284_s_at		NM_001640	gb:NM_001640.2 /DEF=Homo sapiens N-acylaminoacyl-peptide hydrolase (APEH), mRNA. /FEA=mRNA /GEN=APEH /PROD=N-acylaminoacyl-peptide hydrolase /DB_XREF=gi:9951916 /UG=Hs.78223 N-acylaminoacyl-peptide hydrolase /FL=gb:BC000362.1 gb:BC001826.1 gb:J03068.1 gb:D38441.1 gb:AF141383.1 gb:NM_001640.2	

218512_at	NM_018256	gb:NM_018256.1 /DEF=Homo sapiens hypothetical protein FLJ10881 (FLJ10881), mRNA. /FEA=mRNA /GEN=FLJ10881 /PROD=hypothetical protein FLJ10881 /DB_XREF=gi:8922736 /UG=Hs.73291 hypothetical protein FLJ10881 /FL=gb:AF242546.1 gb:NM_018256.1	
218703_at	NM_012430	gb:NM_012430.1 /DEF=Homo sapiens sec22 homolog (SEC22A), mRNA. /FEA=mRNA /GEN=SEC22A /PROD=sec22 homolog /DB_XREF=gi:6912647 /UG=Hs.183655 sec22 homolog /FL=gb:AF100749.1 gb:NM_012430.1	
200683_s_at	NM_003347	Consensus includes gb:BE964689 /FEA=EST /DB_XREF=gi:11768267 /DB_XREF=est:601658226R1 /CLONE=IMAGE:3885630 /UG=Hs.108104 ubiquitin-conjugating enzyme E2L 3 /FL=gb:NM_003347.1	
219062_s_at	NM_017742	gb:NM_017742.1 /DEF=Homo sapiens hypothetical protein FLJ20281 (FLJ20281), mRNA. /FEA=mRNA /GEN=FLJ20281 /PROD=hypothetical protein FLJ20281 /DB_XREF=gi:8923259 /UG=Hs.18800 hypothetical protein FLJ20281 /FL=gb:NM_017742.1	
211621_at	M73069	gb:M73069.1 /DEF=Human androgen receptor mutant gene, mRNA, complete cds. /FEA=mRNA /GEN=AR /PROD=androgen receptor /DB_XREF=gi:178655 /FL=gb:M73069.1	
218023_s_at	NM_016605	gb:NM_016605.1 /DEF=Homo sapiens putative nuclear protein (LOC51307), mRNA. /FEA=mRNA /GEN=LOC51307 /PROD=putative nuclear protein /DB_XREF=gi:7706138 /UG=Hs.102469 putative nuclear protein /FL=gb:AF251040.1 gb:NM_016605.1	

218244_at		NM_017948	gb:NM_017948.1 /DEF=Homo sapiens hypothetical protein FLJ20736 (FLJ20736), mRNA. /FEA=mRNA /GEN=FLJ20736 /PROD=hypothetical protein FLJ20736 /DB_XREF=gi:8923662 /UG=Hs.48712 hypothetical protein FLJ20736 /FL=gb:NM_017948.1	
217989_at		NM_016245	gb:NM_016245.1 /DEF=Homo sapiens retinal short-chain dehydrogenasereductase retSDR2 (LOC51170), mRNA. /FEA=mRNA /GEN=LOC51170 /PROD=retinal short-chain dehydrogenasereductaseretSDR2 /DB_XREF=gi:7705904 /UG=Hs.12150 retinal short-chain dehydrogenasereductase retSDR2 /FL=gb:AF126780.1 gb:NM_016245.1	
211982_x_at	KIAA0370	AL546600	KIAA0370 protein	
218385_at		NM_018135	gb:NM_018135.1 /DEF=Homo sapiens hypothetical protein FLJ10548 (FLJ10548), mRNA. /FEA=mRNA /GEN=FLJ10548 /PROD=hypothetical protein FLJ10548 /DB_XREF=gi:8922510 /UG=Hs.9622 hypothetical protein FLJ10548 /FL=gb:NM_018135.1	
218424_s_at		NM_018234	gb:NM_018234.1 /DEF=Homo sapiens hypothetical protein FLJ10829 (FLJ10829), mRNA. /FEA=mRNA /GEN=FLJ10829 /PROD=hypothetical protein FLJ10829 /DB_XREF=gi:8922696 /UG=Hs.57655 hypothetical protein FLJ10829 /FL=gb:NM_018234.1	
74694_s_at	FLJ23282	AA907940	hypothetical protein FLJ23282	
200709_at		NM_000801	gb:NM_000801.1 /DEF=Homo sapiens FK506-binding protein 1A (12kD) (FKBP1A), mRNA. /FEA=mRNA /GEN=FKBP1A /PROD=FK506-binding protein 1A (12kD) /DB_XREF=gi:4503724 /UG=Hs.752 FK506-binding protein 1A (12kD) /FL=gb:BC001925.1	

			gb:M34539.1 gb:NM_000801.1	
221898_at	T1A-2	BF337209	lung type-I cell membrane-associated glycoprotein	
200602_at		NM_000484	gb:NM_000484.1 /DEF=Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA. /FEA=mRNA /GEN=APP /PROD=amyloid beta (A4) precursor protein (proteasenexin-II, Alzheimer disease) /DB_XREF=gi:4502166 /UG=Hs.177486 amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) /FL=gb:NM_000484.1	
37232_at	TIMM9	AB011158	translocase of inner mitochondrial membrane 9 homolog (yeast)	NM_014749
44563_at	FLJ10385	AI858000	hypothetical protein FLJ10385	
211047_x_at		BC006337	gb:BC006337.1 /DEF=Homo sapiens, clone MGC:12798, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:12798) /DB_XREF=gi:13623468 /FL=gb:BC006337.1	
219472_at		NM_024322	gb:NM_024322.1 /DEF=Homo sapiens hypothetical protein MGC11266 (MGC11266), mRNA. /FEA=mRNA /GEN=MGC11266 /PROD=hypothetical protein MGC11266 /DB_XREF=gi:13236564 /UG=Hs.293943 hypothetical protein MGC11266 /FL=gb:BC002870.1 gb:NM_024322.1	
221247_s_at		NM_030798	gb:NM_030798.1 /DEF=Homo sapiens hypothetical protein DKFZp434D0421 (DKFZP434D0421), mRNA. /FEA=mRNA /GEN=DKFZP434D0421 /PROD=hypothetical protein DKFZp434D0421 /DB_XREF=gi:13540581 /FL=gb:NM_030798.1	

200649_at		BC002356	gb:BC002356.1 /DEF=Homo sapiens, nucleobindin 1, clone MGC:8479, mRNA, complete cds. /FEA=mRNA /PROD=nucleobindin 1 /DB_XREF=gi:12803104 /UG=Hs.172609 nucleobindin 1 /FL=gb:BC002356.1 gb:M96824.1 gb:NM_006184.1	
59631_at	TR2	AI247566	thioredoxin reductase 2	
213306_at	MPDZ	AA917899	multiple PDZ domain protein	
213754_s_at	PAIP1	AW613203	polyadenylate binding protein-interacting protein 1	
213791_at		NM_006211	Consensus includes gb:NM_006211.1 /DEF=Homo sapiens proenkephalin (PENK), mRNA. /FEA=CDS /GEN=PENK /PROD=proenkephalin /DB_XREF=gi:5453875 /UG=Hs.93557 proenkephalin /FL=gb:NM_006211.1	
213853_at		AL050199	Consensus includes gb:AL050199.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586D0923 (from clone DKFZp586D0923). /FEA=mRNA /DB_XREF=gi:4884438 /UG=Hs.62669 Homo sapiens mRNA; cDNA DKFZp586D0923 (from clone DKFZp586D0923)	
213246_at	DKFZP564F1123	AI346504	DKFZP564F1123 protein	
201103_x_at	DJ328E19.C1.1	BE299495	hypothetical protein DJ328E19.C1.1	
213729_at	FNBP3	Z78308	formin binding protein 3	
212403_at		AL096740	Consensus includes gb:AI749193 /FEA=EST /DB_XREF=gi:5127457 /DB_XREF=est:at40e04.x1 /CLONE=IMAGE:2374494 /UG=Hs.17639 Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, partial cds	
201038_s_at		BE560202	ESTs, Highly similar to putative human HLA class II associated protein I; cerebellar leucine rich acidic nuclear protein [Homo sapiens] [H.sapiens]	
217901_at	DSG2	BF031829	desmoglein 2	

221688_s_at		AL136913	gb:AL136913.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L0118 (from clone DKFZp586L0118); complete cds. /FEA=mRNA /GEN=DKFZp586L0118 /PROD=hypothetical protein /DB_XREF=gi:12053320 /UG=Hs.6118 hypothetical protein FLJ10968 /FL=gb:AL136913.1	
216092_s_at		AL365347	Consensus includes gb:AL365347.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 298948. /FEA=mRNA /DB_XREF=gi:9187134 /UG=Hs.22891 solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	
214293_at	FLJ10849	AI539361	hypothetical protein FLJ10849	
212093_s_at		AL096842	Consensus includes gb:AI695017 /FEA=EST /DB_XREF=gi:4982917 /DB_XREF=est:we45d07.x1 /CLONE=IMAGE:2344045 /UG=Hs.7946 KIAA1288 protein	
214722_at		AW516297	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	
214109_at	LRBA	AI659561	LPS-responsive vesicle trafficking, beach and anchor containing	
214499_s_at		AF249273	Consensus includes gb:AF249273.1 /DEF=Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds. /FEA=CDS /PROD=Bcl-2-associated transcription factor shortform /DB_XREF=gi:7582385 /UG=Hs.80338 KIAA0164 gene product /FL=gb:AF249273.1	
209387_s_at		M90657	gb:M90657.1 /DEF=Human tumor antigen (L6) mRNA, complete cds. /FEA=mRNA /GEN=L6 /DB_XREF=gi:186803 /UG=Hs.3337 transmembrane 4 superfamily member 1 /FL=gb:M90657.1	



205294_at		NM_017450	gb:NM_017450.1 /DEF=Homo sapiens BAI1-associated protein 2 (BAIAP2), transcript variant 1, mRNA. /FEA=mRNA /GEN=BAIAP2 /PROD=BAI1-associated protein 2, isoform 1 /DB_XREF=gi:9257196 /UG=Hs.7936 BAI1-associated protein 2 /FL=gb:AB015019.1 gb:AB017120.1 gb:NM_017450.1	
203159_at		NM_014905	gb:NM_014905.1 /DEF=Homo sapiens glutaminase (GLS), mRNA. /FEA=mRNA /GEN=GLS /PROD=glutaminase C /DB_XREF=gi:7662327 /UG=Hs.239189 glutaminase /FL=gb:AF327434.1 gb:AB020645.1 gb:AF097493.1 gb:AF223943.1 gb:NM_014905.1	
209284_s_at		AF180425	Consensus includes gb:AI922509 /FEA=EST /DB_XREF=gi:5658473 /DB_XREF=est:wh13g11.x1 /CLONE=IMAGE:2380676 /UG=Hs.23440 KIAA1105 protein /FL=gb:AF180425.2	
203053_at		NM_005872	gb:NM_005872.1 /DEF=Homo sapiens breast carcinoma amplified sequence 2 (BCAS2), mRNA. /FEA=mRNA /GEN=BCAS2 /PROD=breast carcinoma amplified sequence 2 /DB_XREF=gi:5031652 /UG=Hs.22960 breast carcinoma amplified sequence 2 /FL=gb:BC005285.1 gb:AF081788.1 gb:AB020623.1 gb:NM_005872.1	
205225_at		NM_000125	gb:NM_000125.1 /DEF=Homo sapiens estrogen receptor 1 (ESR1), mRNA. /FEA=mRNA /GEN=ESR1 /PROD=estrogen receptor 1 /DB_XREF=gi:4503602 /UG=Hs.1657 estrogen receptor 1 /FL=gb:NM_000125.1	
209838_at		AA496247	ESTs	
202194_at		AL117354	Consensus includes gb:AL117354 /DEF=Human DNA sequence from clone RP5-976O13 on chromosome 1p21.2-22.2 Contains part of the gene for CGI-100 protein, 3 isoforms of the gene for	

			M96 protein, ESTs, STSs, GSSs and a CpG Island /FEA=mRNA_1 /DB_XREF=gi:6822199 /UG=Hs.296155 CGI-100 protein /FL=gb:AF151858.1 gb:NM_016040.1	
202139_at		NM_003689	gb:NM_003689.1 /DEF=Homo sapiens aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) (AKR7A2), mRNA. /FEA=mRNA /GEN=AKR7A2 /PROD=aldo-keto reductase family 7, member A2(aflatoxin aldehyde reductase) /DB_XREF=gi:4502020 /UG=Hs.6980 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) /FL=gb:BC004111.1 gb:AF026947.1 gb:NM_003689.1	
209778_at		AF007217	gb:AF007217.1 /DEF=Homo sapiens Trip230 mRNA, complete cds. /FEA=mRNA /GEN=Trip230 /PROD=Trip230 /DB_XREF=gi:2253416 /UG=Hs.85092 thyroid hormone receptor interactor 11 /FL=gb:NM_004239.1 gb:AF007217.1	
202557_at	STCH	AI718418	stress 70 protein chaperone, microsome-associated, 60kDa	
202544_at		NM_004124	gb:NM_004124.1 /DEF=Homo sapiens glia maturation factor, beta (GMFB), mRNA. /FEA=mRNA /GEN=GMFB /PROD=glia maturation factor, beta /DB_XREF=gi:4758441 /UG=Hs.151413 glia maturation factor, beta /FL=gb:BC005359.1 gb:M86492.1 gb:AB001106.1 gb:NM_004124.1	
207176_s_at		NM_005191	gb:NM_005191.1 /DEF=Homo sapiens CD80 antigen (CD28 antigen ligand 1, B7-1 antigen) (CD80), mRNA. /FEA=mRNA /GEN=CD80 /PROD=CD80 antigen (CD28 antigen ligand 1, B7-1 antigen) /DB_XREF=gi:4885122 /UG=Hs.838 CD80 antigen (CD28 antigen ligand 1, B7-1 antigen) /FL=gb:NM_005191.1	

209681_at		AF153330	gb:AF153330.1 /DEF=Homo sapiens thiamine carrier 1 (TC1) mRNA, complete cds. /FEA=mRNA /GEN=TC1 /PROD=thiamine carrier 1 /DB_XREF=gi:5453325 /UG=Hs.30246 solute carrier family 19 (thiamine transporter), member 2 /FL=gb:AF153330.1 gb:AF135488.1 gb:AF160812.1	
202471_s_at		NM_004135	gb:NM_004135.1 /DEF=Homo sapiens isocitrate dehydrogenase 3 (NAD+) gamma (IDH3G), mRNA. /FEA=mRNA /GEN=IDH3G /PROD=isocitrate dehydrogenase 3 (NAD+) gamma /DB_XREF=gi:4758581 /UG=Hs.75253 isocitrate dehydrogenase 3 (NAD+) gamma /FL=gb:BC001902.1 gb:BC000933.2 gb:U40272.1 gb:NM_004135.1	
203504_s_at		NM_005502	gb:NM_005502.1 /DEF=Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1), mRNA. /FEA=mRNA /GEN=ABCA1 /PROD=ATP-binding cassette, sub-family A member 1 /DB_XREF=gi:5915657 /UG=Hs.211562 ATP-binding cassette, sub-family A (ABC1), member 1 /FL=gb:AF165281.1 gb:NM_005502.1 gb:AF285167.1	
208760_at		NM_003345	Consensus includes gb:AL031714 /DEF=Human DNA sequence from clone LA16-358B7 on chromosome 16 Contains the UBE21 gene for ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9), and an RPS20 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSs. GSSs and a putative CpG is... /FEA=mRNA /DB_XREF=gi:4775608 /UG=Hs.84285 ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9) /FL=gb:U45328.1 gb:U31933.1 gb:BC000427.1 gb:BC004429.1 gb:U31882.1 gb:U66818.1 gb:U66867.1 gb:U38785.1	

			gb:NM_003345.1 gb:U29092.1	
204336_s_at		NM_005873	gb:NM_005873.1 /DEF=Homo sapiens regulator of G-protein signalling 19 (RGS19), mRNA. /FEA=mRNA /GEN=RGS19 /PROD=G protein signalling regulator 19 /DB_XREF=gi:5031704 /UG=Hs.22698 regulator of G-protein signalling 19 /FL=gb:NM_005873.1	
209153_s_at		M31523	gb:M31523.1 /DEF=Human transcription factor (E2A) mRNA, complete cds. /FEA=mRNA /GEN=TCF3 /DB_XREF=gi:339477 /UG=Hs.101047 transcription factor 3 (E2A immunoglobulin enhancer binding factors E12E47) /FL=gb:M31523.1	
204491_at	PDE4D	R40917	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	
208816_x_at		M62898	gb:M62898.1 /DEF=Human lipocortin (LIP) 2 pseudogene mRNA, complete cds-like region. /FEA=mRNA /DB_XREF=gi:187147 /UG=Hs.217493 annexin A2 /FL=gb:M62898.1	
201586_s_at		NM_005066	gb:NM_005066.1 /DEF=Homo sapiens splicing factor prolineglutamine rich (polypyrimidine tract-binding protein-associated) (SFPQ), mRNA. /FEA=mRNA /GEN=SFPQ /PROD=splicing factor prolineglutamine rich(polypyrimidine tract-binding protein-associated) /DB_XREF=gi:4826997 /UG=Hs.180610 splicing factor prolineglutamine rich	

			(polypyrimidine tract-binding protein-associated) /FL=gb:NM_005066.1	
204059_s_at		NM_002395	gb:NM_002395.2 /DEF=Homo sapiens malic enzyme 1, NADP(+)-dependent, cytosolic (ME1), mRNA. /FEA=mRNA /GEN=ME1 /PROD=cytosolic malic enzyme 1 /DB_XREF=gi:13435400 /UG=Hs.14732 malic enzyme 1, NADP(+)-dependent, cytosolic /FL=gb:NM_002395.2	
203255_at		NM_018693	gb:NM_018693.1 /DEF=Homo sapiens vitiligo-associated protein VIT-1 (VIT1), mRNA. /FEA=mRNA /GEN=VIT1 /PROD=vitiligo-associated protein VIT-1 /DB_XREF=gi:10048403 /UG=Hs.284289 vitiligo-associated protein VIT-1 /FL=gb:NM_018693.1 gb:AF264714.1	
209186_at		M23114	gb:M23114.1 /DEF=Homo sapiens calcium-ATPase (HK1) mRNA, complete cds. /FEA=mRNA /GEN=HK1 /DB_XREF=gi:184100 /UG=Hs.1526 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 /FL=gb:M23114.1	
204671_s_at	ANKRD6	BE677131	ankyrin repeat domain 6	
201672_s_at		NM_005151	gb:NM_005151.1 /DEF=Homo sapiens ubiquitin specific protease 14 (tRNA-guanine transglycosylase) (USP14), mRNA. /FEA=mRNA /GEN=USP14 /PROD=ubiquitin specific protease 14 (tRNA-guaninetransglycosylase) /DB_XREF=gi:4827049 /UG=Hs.75981 ubiquitin specific protease 14 (tRNA-guanine transglycosylase) /FL=gb:BC003556.1 gb:NM_005151.1 gb:U30888.1	
201836_s_at	STAF65(gamma)	AU154740	SPTF-associated factor 65 gamma	

202105_at		NM_001551	gb:NM_001551.1 /DEF=Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1), mRNA. /FEA=mRNA /GEN=IGBP1 /PROD=immunoglobulin-binding protein 1 /DB_XREF=gi:4557662 /UG=Hs.3631 immunoglobulin (CD79A) binding protein 1 /FL=gb:BC004137.1 gb:NM_001551.1	
206960_at		NM_005296	gb:NM_005296.1 /DEF=Homo sapiens G protein-coupled receptor 23 (GPR23), mRNA. /FEA=mRNA /GEN=GPR23 /PROD=G protein-coupled receptor 23 /DB_XREF=gi:4885310 /UG=Hs.27812 G protein-coupled receptor 23 /FL=gb:U90322.1 gb:NM_005296.1	
201994_at		NM_012286	gb:NM_012286.1 /DEF=Homo sapiens MORF-related gene X (KIAA0026), mRNA. /FEA=mRNA /GEN=KIAA0026 /PROD=MORF-related gene X /DB_XREF=gi:6912447 /UG=Hs.173714 MORF-related gene X /FL=gb:D14812.1 gb:AF100620.1 gb:NM_012286.1 gb:AF167174.1	
201870_at		NM_006809	gb:NM_006809.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 34 (TOM34), mRNA. /FEA=mRNA /GEN=TOM34 /PROD=translocase of outer mitochondrial membrane 34 /DB_XREF=gi:5803204 /UG=Hs.76927 translocase of outer mitochondrial membrane 34 /FL=gb:BC001763.1 gb:U58970.1 gb:NM_006809.1	

201783_s_at		NM_021975	gb:NM_021975.1 /DEF=Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA. /FEA=mRNA /GEN=RELA /PROD=v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) /DB_XREF=gi:11496238 /UG=Hs.75569 v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) /FL=gb:NM_021975.1 gb:L19067.1	
215643_at		AU145680	ESTs, Highly similar to SM3D_HUMAN Semaphorin 3D precursor [H.sapiens]	
203718_at		NM_006702	gb:NM_006702.1 /DEF=Homo sapiens neuropathy target esterase (NTE), mRNA. /FEA=mRNA /GEN=NTE /PROD=neuropathy target esterase /DB_XREF=gi:5729950 /UG=Hs.5038 neuropathy target esterase /FL=gb:NM_006702.1	
202514_at		NM_004087	Consensus includes gb:AW139131 /FEA=EST /DB_XREF=gi:6143449 /DB_XREF=est:UI-H-BI1-aet-a-12-0-UI.s1 /CLONE=IMAGE:2720183 /UG=Hs.154294 discs, large (Drosophila) homolog 1 /FL=gb:NM_004087.1 gb:U13896.1	
208238_x_at		NM_013344	gb:NM_013344.1 /DEF=Homo sapiens leucine zipper-like protein (LZLP), mRNA. /FEA=mRNA /GEN=LZLP /PROD=leucine zipper-like protein /DB_XREF=gi:7106350 /UG=Hs.278952 leucine zipper-like protein /FL=gb:AF159055.1 gb:NM_013344.1	

210212_x_at		BC002600	gb:BC002600.1 /DEF=Homo sapiens, mature T-cell proliferation 1, clone MGC:2069, mRNA, complete cds. /FEA=mRNA /PROD=mature T-cell proliferation 1 /DB_XREF=gi:12803540 /UG=Hs.3548 mature T-cell proliferation 1 /FL=gb:BC002600.1	
218252_at		NM_018204	gb:NM_018204.1 /DEF=Homo sapiens cytoskeleton associated protein 2 (CKAP2), mRNA. /FEA=mRNA /GEN=CKAP2 /PROD=cytoskeleton associated protein 2 /DB_XREF=gi:8922641 /UG=Hs.24641 cytoskeleton associated protein 2 /FL=gb:AL136848.1 gb:NM_018204.1	
47550_at	LZTS1	N21184	leucine zipper, putative tumor suppressor 1	
213793_s_at	SYN47	BE550452	Homer, neuronal immediate early gene, 1B	
215545_at		AK024185	Consensus includes gb:AK024185.1 /DEF=Homo sapiens cDNA FLJ14123 fis, clone MAMMA1002155. /FEA=mRNA /DB_XREF=gi:10436502 /UG=Hs.269314 Homo sapiens cDNA FLJ14123 fis, clone MAMMA1002155	
36499_at	CELSR2	D87469	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	NM_001408
35846_at	THRA	M24899	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	NM_003250
216561_x_at	SOX29	AF032454	Homo sapiens SOX-29 protein (SOX29) gene, partial cds.	



209732_at		BC005254	gb:BC005254.1 /DEF=Homo sapiens, Similar to C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced), clone MGC:12289, mRNA, complete cds. /FEA=mRNA /PROD=Similar to C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) /DB_XREF=gi:13528920 /UG=Hs.85201 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced) /FL=gb:BC005254.1 gb:AB015628.1 gb:NM_005127.1	
205877_s_at		NM_017590	gb:NM_017590.1 /DEF=Homo sapiens hypothetical protein DKFZp434K0920 (DKFZp434K0920), mRNA. /FEA=mRNA /GEN=DKFZp434K0920 /PROD=hypothetical protein DKFZp434K0920 /DB_XREF=gi:8922144 /UG=Hs.279922 hypothetical protein DKFZp434K0920 /FL=gb:NM_017590.1	
202902_s_at		NM_004079	gb:NM_004079.1 /DEF=Homo sapiens cathepsin S (CTSS), mRNA. /FEA=mRNA /GEN=CTSS /PROD=cathepsin S /DB_XREF=gi:4758097 /UG=Hs.181301 cathepsin S /FL=gb:BC002642.1 gb:M86553.1 gb:NM_004079.1 gb:M90696.1	
211488_s_at		BC002630	gb:BC002630.1 /DEF=Homo sapiens, Similar to integrin, beta 8, clone MGC:3946, mRNA, complete cds. /FEA=mRNA /PROD=Similar to integrin, beta 8 /DB_XREF=gi:12803590 /UG=Hs.52620 integrin, beta 8 /FL=gb:BC002630.1	
213696_s_at	MED8	AA421957	mediator of RNA polymerase II transcription subunit MED8	

212911_at		AB023179	Consensus includes gb:AB023179.1 /DEF=Homo sapiens mRNA for KIAA0962 protein, partial cds. /FEA=mRNA /GEN=KIAA0962 /PROD=KIAA0962 protein /DB_XREF=gi:4589567 /UG=Hs.9059 KIAA0962 protein	
210556_at		U85430	gb:U85430.1 /DEF=Human transcription factor NFATx4 mRNA, complete cds. /FEA=mRNA /PROD=transcription factor NFATx4 /DB_XREF=gi:1835590 /UG=Hs.172674 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 /FL=gb:U85430.1	
205199_at		NM_001216	gb:NM_001216.1 /DEF=Homo sapiens carbonic anhydrase IX (CA9), mRNA. /FEA=mRNA /GEN=CA9 /PROD=carbonic anhydrase IX precursor /DB_XREF=gi:9955947 /UG=Hs.63287 carbonic anhydrase IX /FL=gb:NM_001216.1	
217626_at	AKR1C1	BF508244	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	
218464_s_at		NM_018182	gb:NM_018182.1 /DEF=Homo sapiens hypothetical protein FLJ10700 (FLJ10700), mRNA. /FEA=mRNA /GEN=FLJ10700 /PROD=hypothetical protein FLJ10700 /DB_XREF=gi:8922595 /UG=Hs.295909 hypothetical protein FLJ10700 /FL=gb:NM_018182.1	
203372_s_at		AB004903	gb:AB004903.1 /DEF=Homo sapiens mRNA for STAT induced STAT inhibitor-2, complete cds. /FEA=mRNA /PROD=STAT induced STAT inhibitor-2 /DB_XREF=gi:2443360 /UG=Hs.110776 STAT induced STAT inhibitor-2 /FL=gb:AB004903.1 gb:AB006966.1 gb:AF037989.1 gb:AF020590.1 gb:NM_003877.1	

210635_s_at		BC005253	gb:BC005253.1 /DEF=Homo sapiens, Similar to Kelch motif containing protein, clone MGC:12288, mRNA, complete cds. /FEA=mRNA /PROD=Similar to Kelch motif containing protein /DB_XREF=gi:13528917 /UG=Hs.106290 Kelch motif containing protein /FL=gb:BC005253.1	
204834_at		NM_006682	gb:NM_006682.1 /DEF=Homo sapiens fibrinogen-like 2 (FGL2), mRNA. /FEA=mRNA /GEN=FGL2 /PROD=fibrinogen-like 2 /DB_XREF=gi:5730074 /UG=Hs.2659 fibrinogen-like 2 /FL=gb:NM_006682.1	
213272_s_at		AF070596	Consensus includes gb:AF070596.1 /DEF=Homo sapiens clone 24796 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3387973 /UG=Hs.27191 hypothetical protein from clone 24796	
210306_at		U89358	gb:U89358.1 /DEF=Human I(3)mbt protein homolog mRNA, complete cds. /FEA=mRNA /PROD=I(3)mbt protein homolog /DB_XREF=gi:3811110 /UG=Hs.300863 lethal (3) malignant brain tumor I(3)mbt protein (Drosophila) homolog /FL=gb:U89358.1	
200747_s_at		NM_006185	gb:NM_006185.1 /DEF=Homo sapiens nuclear mitotic apparatus protein 1 (NUMA1), mRNA. /FEA=mRNA /GEN=NUMA1 /PROD=nuclear mitotic apparatus protein 1 /DB_XREF=gi:5453819 /UG=Hs.301512 nuclear mitotic apparatus protein 1 /FL=gb:NM_006185.1	
36545_s_at	KIAA0542	AB011114	KIAA0542 gene product	
213409_s_at	RHEB2	BF593727	Ras homolog enriched in brain 2	
202116_at		NM_006268	gb:NM_006268.2 /DEF=Homo sapiens requiem, apoptosis response zinc finger gene (REQ), mRNA. /FEA=mRNA /GEN=REQ /PROD=requiem /DB_XREF=gi:10862706 /UG=Hs.13495 requiem, apoptosis response zinc finger	

			gene /FL=gb:NM_006268.2 gb:U94585.1 gb:AF001433.1	
213823_at		H94842	ESTs	
59375_at	MYO15B	AI825877	myosin XVB, pseudogene	
218659_at		NM_018263	gb:NM_018263.1 /DEF=Homo sapiens hypothetical protein FLJ10898 (FLJ10898), mRNA. /FEA=mRNA /GEN=FLJ10898 /PROD=hypothetical protein FLJ10898 /DB_XREF=gi:8922749 /UG=Hs.13801 KIAA1685 protein /FL=gb:NM_018263.1	
200766_at		NM_001909	gb:NM_001909.1 /DEF=Homo sapiens cathepsin D (lysosomal aspartyl protease) (CTSD), mRNA. /FEA=mRNA /GEN=CTSD /PROD=cathepsin D (lysosomal aspartyl protease) /DB_XREF=gi:4503142 /UG=Hs.79572 cathepsin D (lysosomal aspartyl protease) /FL=gb:M11233.1 gb:NM_001909.1	
211452_x_at		AF130054	gb:AF130054.1 /DEF=Homo sapiens clone FLB4816 PRO1252 mRNA, complete cds. /FEA=mRNA /PROD=PRO1252 /DB_XREF=gi:11493414 /UG=Hs.326159 leucine rich repeat (in FLII) interacting protein 1 /FL=gb:AF130054.1	
201398_s_at		BC000687	gb:BC000687.1 /DEF=Homo sapiens, translocating chain-associating membrane protein, clone MGC:784, mRNA, complete cds. /FEA=mRNA /PROD=translocating chain-associating membraneprotein /DB_XREF=gi:12653796 /UG=Hs.4147 translocating chain-associating membrane protein /FL=gb:BC000687.1 gb:NM_014294.1	
200849_s_at	FCGR2B	AA479488	Fc fragment of IgG, low affinity IIb, receptor for (CD32)	

200816_s_at		NM_000430	gb:NM_000430.2 /DEF=Homo sapiens platelet-activating factor acetylhydrolase, isoform lb, alpha subunit (45kD) (PAFAH1B1), mRNA. /FEA=mRNA /GEN=PAFAH1B1 /PROD=platelet-activating factor acetylhydrolase, isoform lb, alpha subunit (45kD) /DB_XREF=gi:6031206 /UG=Hs.77318 platelet-activating factor acetylhydrolase, isoform lb, alpha subunit (45kD) /FL=gb:L13385.1 gb:L13386.1 gb:NM_000430.2	
202589_at		NM_001071	gb:NM_001071.1 /DEF=Homo sapiens thymidylate synthetase (TYMS), mRNA. /FEA=mRNA /GEN=TYMS /PROD=thymidylate synthetase /DB_XREF=gi:4507750 /UG=Hs.82962 thymidylate synthetase /FL=gb:BC002567.1 gb:NM_001071.1	
201964_at	KIAA0625	N64643	KIAA0625 protein	
204020_at	PURA	BF739943	purine-rich element binding protein A	
216960_s_at		AL049646	Consensus includes gb:AL049646 /DEF=Human DNA sequence from clone RP4-568F9 on chromosome 20 Contains the ZNF133 (zinc finger protein 133 (clone pHZ-13)) gene, part of a gene for a novel protein, ESTs, STSs, GSSs and CpG islands /FEA=mRNA_2 /DB_XREF=gi:11121205 /UG=Hs.78434 zinc finger protein 133 (clone pHZ-13)	
213213_at		AL035669	Consensus includes gb:AL035669 /DEF=Human DNA sequence from clone RP5-885L7 on chromosome 20q13.2-13.33 Contains ESTs, STSs, GSSs and eight CpG islands. Contains the 3 end of the NTSR1 gene for high affinity neurotensin receptor 1, a putative novel gene, a novel gene similar to a f... /FEA=mRNA_3 /DB_XREF=gi:8979786 /UG=Hs.155313 death	

			associated transcription factor 1	
218473_s_at		NM_024656	gb:NM_024656.1 /DEF=Homo sapiens hypothetical protein FLJ22329 (FLJ22329), mRNA. /FEA=mRNA /GEN=FLJ22329 /PROD=hypothetical protein FLJ22329 /DB_XREF=gi:13375904 /UG=Hs.61478 hypothetical protein FLJ22329 /FL=gb:NM_024656.1	
202896_s_at		NM_004648	gb:NM_004648.1 /DEF=Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA. /FEA=mRNA /GEN=PTPNS1 /PROD=protein tyrosine phosphatase, non-receptor typesubstrate 1 /DB_XREF=gi:4758977 /UG=Hs.156114 protein tyrosine phosphatase, non-receptor type substrate 1 /FL=gb:D86043.1 gb:NM_004648.1 gb:AB023430.1	
208905_at		BC005299	gb:BC005299.1 /DEF=Homo sapiens, cytochrome c, clone MGC:12367, mRNA, complete cds. /FEA=mRNA /PROD=cytochrome c /DB_XREF=gi:13529022 /UG=Hs.169248 cytochrome c /FL=gb:NM_018947.1 gb:BC005299.1	
201585_s_at	SFPQ	BG035151	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	
204049_s_at		NM_014721	gb:NM_014721.1 /DEF=Homo sapiens KIAA0680 gene product (KIAA0680), mRNA. /FEA=mRNA /GEN=KIAA0680 /PROD=KIAA0680 gene product /DB_XREF=gi:7662247 /UG=Hs.102471 KIAA0680 gene product /FL=gb:AB014580.1 gb:NM_014721.1	

201866_s_at		NM_000176	gb:NM_000176.1 /DEF=Homo sapiens nuclear receptor subfamily 3, group C, member 1 (NR3C1), mRNA. /FEA=mRNA /GEN=NR3C1 /PROD=nuclear receptor subfamily 3, group C, member 1 /DB_XREF=gi:4504132 /UG=Hs.75772 nuclear receptor subfamily 3, group C, member 1 /FL=gb:M10901.1 gb:NM_000176.1	
213051_at	ZAP	AI133727	likely ortholog of rat zinc-finger antiviral protein	
214948_s_at		AL050136	Consensus includes gb:AL050136.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141). /FEA=mRNA /DB_XREF=gi:4884346 /UG=Hs.140945 Homo sapiens mRNA; cDNA DKFZp586L141 (from clone DKFZp586L141)	
203874_s_at		NM_003069	gb:NM_003069.1 /DEF=Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1), mRNA. /FEA=mRNA /GEN=SMARCA1 /PROD=SWISNF related, matrix associated, actindependent regulator of chromatin, subfamily a, member 1 /DB_XREF=gi:4507066 /UG=Hs.152292 SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 /FL=gb:M88163.1 gb:NM_003069.1	
201579_at		NM_005245	gb:NM_005245.1 /DEF=Homo sapiens FAT tumor suppressor (Drosophila) homolog (FAT), mRNA. /FEA=mRNA /GEN=FAT /PROD=FAT tumor suppressor precursor /DB_XREF=gi:4885228 /UG=Hs.166994 FAT tumor suppressor (Drosophila) homolog /FL=gb:NM_005245.1	

202388_at		NM_002923	gb:NM_002923.1 /DEF=Homo sapiens regulator of G-protein signalling 2, 24kD (RGS2), mRNA. /FEA=mRNA /GEN=RGS2 /PROD=regulator of G-protein signalling 2, 24kD /DB_XREF=gi:4506516 /UG=Hs.78944 regulator of G-protein signalling 2, 24kD /FL=gb:L13463.1 gb:NM_002923.1	
202709_at		NM_002023	gb:NM_002023.2 /DEF=Homo sapiens fibromodulin (FMOD), mRNA. /FEA=mRNA /GEN=FMOD /PROD=fibromodulin precursor /DB_XREF=gi:5016093 /UG=Hs.230 fibromodulin /FL=gb:NM_002023.2	
201277_s_at		NM_004499	gb:NM_004499.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein AB (HNRPAB), mRNA. /FEA=mRNA /GEN=HNRPAB /PROD=heterogeneous nuclear ribonucleoprotein AB /DB_XREF=gi:4758541 /UG=Hs.81361 heterogeneous nuclear ribonucleoprotein AB /FL=gb:BC002625.1 gb:BC004561.1 gb:M65028.1 gb:NM_004499.1	
220094_s_at		NM_022102	gb:NM_022102.1 /DEF=Homo sapiens hypothetical protein FLJ20958 (FLJ20958), mRNA. /FEA=mRNA /GEN=FLJ20958 /PROD=hypothetical protein FLJ20958 /DB_XREF=gi:13430855 /UG=Hs.261023 hypothetical protein FLJ20958 /FL=gb:NM_022102.1	
203024_s_at		NM_020199	gb:NM_020199.1 /DEF=Homo sapiens HTGN29 protein (HTGN29), mRNA. /FEA=mRNA /GEN=HTGN29 /PROD=HTGN29 protein /DB_XREF=gi:9910277 /UG=Hs.283437 HTGN29 protein /FL=gb:AF226055.1 gb:NM_020199.1	



209934_s_at		AF225981	gb:AF225981.1 /DEF=Homo sapiens calcium transport ATPase ATP2C1 (ATP2C1) mRNA, complete cds. /FEA=mRNA /GEN=ATP2C1 /PROD=calcium transport ATPase ATP2C1 /DB_XREF=gi:7021496 /UG=Hs.106778 ATPase, Ca++ transporting, type 2C, member 1 /FL=gb:AF225981.1	
212539_at	FLJ22530	AI422099	hypothetical protein FLJ22530	
32091_at	KIAA0446	AB007915	KIAA0446 gene product	
221511_x_at		AB033080	Consensus includes gb:AB033080.1 /DEF=Homo sapiens mRNA for KIAA1254 protein, partial cds. /FEA=mRNA /GEN=KIAA1254 /PROD=KIAA1254 protein /DB_XREF=gi:6330892 /UG=Hs.82506 KIAA1254 protein /FL=gb:AF212228.1	
215754_at		AU148040	AU148040 MAMMA1 Homo sapiens cDNA clone MAMMA1002428 3', mRNA sequence.	
206261_at		NM_005674	gb:NM_005674.1 /DEF=Homo sapiens zinc finger protein 239 (ZNF239), mRNA. /FEA=mRNA /GEN=ZNF239 /PROD=zinc finger protein 239 /DB_XREF=gi:5032244 /UG=Hs.25040 zinc finger protein 239 /FL=gb:NM_005674.1	
202126_at	PRPF4B	AA156948	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	
205812_s_at		NM_006588	gb:NM_006588.1 /DEF=Homo sapiens sulfotransferase family, cytosolic, 1C, member 2 (SULT1C2), mRNA. /FEA=mRNA /GEN=SULT1C2 /PROD=SULT1C sulfotransferase /DB_XREF=gi:5730070 /UG=Hs.312644 sulfotransferase family, cytosolic, 1C, member 2 /FL=gb:AF055584.1 gb:NM_006588.1	
214085_x_at	GLIPR	AI912583	glioma pathogenesis-related protein	

207128_s_at		NM_013361	gb:NM_013361.1 /DEF=Homo sapiens zinc finger protein 223 (ZNF223), mRNA. /FEA=mRNA /GEN=ZNF223 /PROD=zinc finger protein 223 /DB_XREF=gi:7019588 /UG=Hs.279782 zinc finger protein 223 /FL=gb:AF187989.1 gb:NM_013361.1	
207163_s_at		NM_005163	gb:NM_005163.1 /DEF=Homo sapiens v-akt murine thymoma viral oncogene homolog 1 (AKT1), mRNA. /FEA=mRNA /GEN=AKT1 /PROD=serinethreonine protein kinase /DB_XREF=gi:4885060 /UG=Hs.71816 v-akt murine thymoma viral oncogene homolog 1 /FL=gb:M63167.1 gb:NM_005163.1	
202133_at	TAZ	AA081084	transcriptional co-activator with PDZ-binding motif (TAZ)	
209883_at		AF288389	gb:AF288389.1 /DEF=Homo sapiens C1orf17 mRNA, complete cds. /FEA=mRNA /PROD=C1orf17 /DB_XREF=gi:12620187 /UG=Hs.106794 KIAA0584 protein /FL=gb:AF288389.1	
210312_s_at		BC002640	gb:BC002640.1 /DEF=Homo sapiens, Similar to uterine protein, clone MGC:4279, mRNA, complete cds. /FEA=mRNA /PROD=Similar to uterine protein /DB_XREF=gi:12803610 /UG=Hs.4187 hypothetical protein 24636 /FL=gb:BC002640.1	
213293_s_at	TRIM22	AA083478	tripartite motif-containing 22	
208745_at	ATP5L	AA917672	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit g	
205141_at		NM_001145	gb:NM_001145.1 /DEF=Homo sapiens angiogenin, ribonuclease, RNase A family, 5 (ANG), mRNA. /FEA=mRNA /GEN=ANG /PROD=angiogenin, ribonuclease, RNase A family, 5precursor /DB_XREF=gi:4557312 /UG=Hs.154730 angiogenin, ribonuclease, RNase A family, 5 /FL=gb:NM_001145.1	

218001_at		NM_016034	gb:NM_016034.1 /DEF=Homo sapiens CGI-91 protein (LOC51116), mRNA. /FEA=mRNA /GEN=LOC51116 /PROD=CGI-91 protein /DB_XREF=gi:7705804 /UG=Hs.20776 CGI-91 protein /FL=gb:AF151849.1 gb:NM_016034.1	
208812_x_at		BC004489	gb:BC004489.1 /DEF=Homo sapiens, major histocompatibility complex, class I, C, clone MGC:11039, mRNA, complete cds. /FEA=mRNA /PROD=major histocompatibility complex, class I, C /DB_XREF=gi:13325360 /UG=Hs.277477 major histocompatibility complex, class I, C /FL=gb:NM_002117.1 gb:M99388.1 gb:U06487.1 gb:BC002463.1 gb:BC004489.1 gb:D64145.1 gb:D38526.1 gb:D49552.1 gb:D49819.1 gb:M24097.1 gb:M84171.1 gb:M84172.1 gb:M84173.1 gb:M84174.1 gb:M26429.1 gb:M26430.1 gb:M26431.1 gb:U41420.1 gb:U41386.1 gb:D50852.1 gb:D50853.1 gb:D50854.1 gb:D83031.1 gb:U57028.1 gb:U06695.1 gb:U06696.1 gb:M99389.1 gb:M99390.1 gb:M28160.1 gb:U09853.1 gb:AF168611.1 gb:L38251.1 gb:D31817.1	
206929_s_at		NM_005597	gb:NM_005597.1 /DEF=Homo sapiens nuclear factor IC (CCAAT-binding transcription factor) (NFIC), mRNA. /FEA=mRNA /GEN=NFIC /PROD=nuclear factor IC (CCAAT-binding transcriptionfactor) /DB_XREF=gi:10835080 /UG=Hs.184771 nuclear factor IC (CCAAT-binding transcription factor) /FL=gb:NM_005597.1	
212151_at	PSMB5	BF967998	proteasome (prosome, macropain) subunit, beta type, 5	
210092_at		AF067173	gb:AF067173.1 /DEF=Homo sapiens Mago homolog mRNA, complete cds. /FEA=mRNA /PROD=Mago homolog /DB_XREF=gi:4894379 /UG=Hs.57904 mago-nashi	

			(Drosophila) homolog, proliferation-associated /FL=gb:AF035940.1 gb:AF067173.1 gb:NM_002370.2	
212372_at		AK026977	Consensus includes gb:AK026977.1 /DEF=Homo sapiens cDNA: FLJ23324 fis, clone HEP12482, highly similar to HUMMYOHCB Human nonmuscle myosin heavy chain- B (MYH10) mRNA. /FEA=mRNA /DB_XREF=gi:10439970 /UG=Hs.296842 Homo sapiens, clone IMAGE:3357927, mRNA, partial cds	
202761_s_at		NM_015180	gb:NM_015180.1 /DEF=Homo sapiens synaptic nuclei expressed gene 2; KIAA1011 protein (KIAA1011), mRNA. /FEA=mRNA /GEN=KIAA1011 /PROD=KIAA1011 protein /DB_XREF=gi:11056019 /UG=Hs.57749 synaptic nuclei expressed gene 2; KIAA1011 protein /FL=gb:NM_015180.1 gb:AL080133.1	
218640_s_at		NM_024613	gb:NM_024613.1 /DEF=Homo sapiens hypothetical protein FLJ13187 (FLJ13187), mRNA. /FEA=mRNA /GEN=FLJ13187 /PROD=hypothetical protein FLJ13187 /DB_XREF=gi:13375826 /UG=Hs.29724 hypothetical protein FLJ13187 /FL=gb:NM_024613.1	
218398_at		NM_016640	gb:NM_016640.1 /DEF=Homo sapiens programmed cell death 9 (PDCD9), mRNA. /FEA=mRNA /GEN=PDCD9 /PROD=(HSA)PAP protein /DB_XREF=gi:7706187 /UG=Hs.28555 programmed cell death 9 /FL=gb:AL136706.1 gb:BC002460.1 gb:AF146192.2 gb:AF217523.1 gb:NM_016640.1	

211458_s_at		AF180519	gb:AF180519.1 /DEF=Homo sapiens GABA-A receptor-associated protein mRNA, complete cds. /FEA=mRNA /PROD=GABA-A receptor-associated protein /DB_XREF=gi:13241283 /UG=Hs.326776 Homo sapiens GABA-A receptor-associated protein mRNA, complete cds /FL=gb:AF180519.1	
218769_s_at		NM_023039	gb:NM_023039.1 /DEF=Homo sapiens ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA. /FEA=mRNA /GEN=ANKRA2 /PROD=ankyrin repeat, family A (RFXANK-like), 2 /DB_XREF=gi:12746411 /UG=Hs.239154 ankyrin repeat, family A (RFXANK-like), 2 /FL=gb:AF314032.1 gb:NM_023039.1	
203438_at	STC2	AI435828	stanniocalcin 2	
206937_at		NM_003126	gb:NM_003126.1 /DEF=Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), mRNA. /FEA=mRNA /GEN=SPTA1 /PROD=spectrin, alpha, erythrocytic 1 (elliptocytosis2) /DB_XREF=gi:4507188 /UG=Hs.1985 spectrin, alpha, erythrocytic 1 (elliptocytosis 2) /FL=gb:M61877.1 gb:NM_003126.1	
215948_x_at	ZNF237	AI522311	zinc finger protein 237	
217919_s_at	MRPL42	BE782148	mitochondrial ribosomal protein L42	
201543_s_at		NM_020150	gb:NM_020150.1 /DEF=Homo sapiens SAR1 protein (SAR1), mRNA. /FEA=mRNA /GEN=SAR1 /PROD=SAR1 protein /DB_XREF=gi:9910541 /UG=Hs.110796 SAR1 protein /FL=gb:AY008268.1 gb:AL136724.1 gb:AF261717.1 gb:NM_020150.1	
213296_at	PEX10	BF339133	peroxisome biogenesis factor 10	

204346_s_at		NM_007182	gb:NM_007182.2 /DEF=Homo sapiens Ras association (RalGDSAF-6) domain family 1 (RASSF1), mRNA. /FEA=mRNA /GEN=RASSF1 /PROD=Ras association (RalGDSAF-6) domain family 1 /DB_XREF=gi:9256633 /UG=Hs.26931 Ras association (RalGDSAF-6) domain family 1 /FL=gb:AF061836.1 gb:AF132676.1 gb:AF040703.2 gb:NM_007182.2	
204772_s_at		NM_007344	gb:NM_007344.1 /DEF=Homo sapiens transcription termination factor, RNA polymerase I (TTF1), mRNA. /FEA=mRNA /GEN=TTF1 /PROD=transcription termination factor, RNA polymerase I /DB_XREF=gi:6678454 /UG=Hs.54780 transcription termination factor, RNA polymerase I /FL=gb:NM_007344.1	
204510_at		NM_003503	gb:NM_003503.2 /DEF=Homo sapiens CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1 (CDC7L1), mRNA. /FEA=mRNA /GEN=CDC7L1 /PROD=CDC7-like 1 /DB_XREF=gi:11038647 /UG=Hs.28853 CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1 /FL=gb:NM_003503.2 gb:AB003698.1 gb:AF005209.1 gb:AF015592.1	
206129_s_at		NM_000046	gb:NM_000046.1 /DEF=Homo sapiens arylsulfatase B (ARSB), mRNA. /FEA=mRNA /GEN=ARSB /PROD=arylsulfatase B precursor /DB_XREF=gi:4557332 /UG=Hs.1256 arylsulfatase B /FL=gb:J05225.1 gb:NM_000046.1	
215195_at		AF035594	Consensus includes gb:AF035594.1 /DEF=Homo sapiens protein kinase C-alpha mRNA, partial 3 UTR. /FEA=mRNA /DB_XREF=gi:3168857 /UG=Hs.279856 Homo sapiens	

			protein kinase C-alpha mRNA, partial 3 UTR	
219074_at		NM_018241	gb:NM_018241.1 /DEF=Homo sapiens hypothetical protein FLJ10846 (FLJ10846), mRNA. /FEA=mRNA /GEN=FLJ10846 /PROD=hypothetical protein FLJ10846 /DB_XREF=gi:8922706 /UG=Hs.32271 hypothetical protein FLJ10846 /FL=gb:NM_018241.1	
205978_at		NM_004795	gb:NM_004795.1 /DEF=Homo sapiens klotho (KL), mRNA. /FEA=mRNA /GEN=KL /PROD=klotho /DB_XREF=gi:4758653 /UG=Hs.94592 klotho /FL=gb:AB005142.1 gb:NM_004795.1	
200619_at		NM_006842	gb:NM_006842.1 /DEF=Homo sapiens splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA. /FEA=mRNA /GEN=SF3B2 /PROD=splicing factor 3b, subunit 2, 145kD /DB_XREF=gi:5803154 /UG=Hs.75916 splicing factor 3b, subunit 2, 145kD /FL=gb:U41371.1 gb:NM_006842.1	
206315_at		NM_004750	gb:NM_004750.1 /DEF=Homo sapiens cytokine receptor-like factor 1 (CRLF1), mRNA. /FEA=mRNA /GEN=CRLF1 /PROD=cytokine receptor-like factor 1 /DB_XREF=gi:4758061 /UG=Hs.114948 cytokine receptor-like factor 1 /FL=gb:AF059293.1 gb:NM_004750.1 gb:AF073515.1 gb:AF178684.1	
37005_at	NBL1	D28124	neuroblastoma, suppression of tumorigenicity 1	NM_005380
206385_s_at		NM_020987	gb:NM_020987.1 /DEF=Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA. /FEA=mRNA /GEN=ANK3 /PROD=ankyrin 3, isoform 1 /DB_XREF=gi:10947055	

			/UG=Hs.75893 ankyrin 3, node of Ranvier (ankyrin G) /FL=gb:NM_020987.1 gb:U13616.1	
202010_s_at		NM_021188	gb:NM_021188.1 /DEF=Homo sapiens clones 23667 and 23775 zinc finger protein (LOC57862), mRNA. /FEA=mRNA /GEN=LOC57862 /PROD=clones 23667 and 23775 zinc finger protein /DB_XREF=gi:10863994 /UG=Hs.7137 clones 23667 and 23775 zinc finger protein /FL=gb:NM_021188.1 gb:U90919.1	
202295_s_at		NM_004390	gb:NM_004390.1 /DEF=Homo sapiens cathepsin H (CTSH), mRNA. /FEA=mRNA /GEN=CTSH /PROD=cathepsin H /DB_XREF=gi:4758095 /UG=Hs.288181 cathepsin H /FL=gb:BC002479.1 gb:NM_004390.1	
201883_s_at		D29805	gb:D29805.1 /DEF=Human mRNA for beta-1,4-galactosyltransferase, complete cds. /FEA=mRNA /PROD=beta-1,4-galactosyltransferase /DB_XREF=gi:474986 /UG=Hs.198248 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1 /FL=gb:NM_001497.1 gb:D29805.1	
206101_at		NM_001393	gb:NM_001393.1 /DEF=Homo sapiens extracellular matrix protein 2, female organ and adipocyte specific (ECM2), mRNA. /FEA=mRNA /GEN=ECM2 /PROD=extracellular matrix protein 2 /DB_XREF=gi:4557542 /UG=Hs.35094 extracellular matrix protein 2, female organ and adipocyte specific /FL=gb:AB011792.1 gb:NM_001393.1	



206159_at		NM_004962	gb:NM_004962.2 /DEF=Homo sapiens growth differentiation factor 10 (GDF10), mRNA. /FEA=mRNA /GEN=GDF10 /PROD=growth differentiation factor 10 precursor /DB_XREF=gi:11641417 /UG=Hs.2171 growth differentiation factor 10 /FL=gb:NM_004962.2	
203625_x_at	SKP2	BG105365	S-phase kinase-associated protein 2 (p45)	
203305_at		NM_000129	gb:NM_000129.2 /DEF=Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA. /FEA=mRNA /GEN=F13A1 /PROD=coagulation factor XIII A1 subunit precursor /DB_XREF=gi:9961355 /UG=Hs.80424 coagulation factor XIII, A1 polypeptide /FL=gb:M14354.1 gb:NM_000129.2	
218193_s_at		NM_016072	gb:NM_016072.1 /DEF=Homo sapiens CGI-141 protein (LOC51026), mRNA. /FEA=mRNA /GEN=LOC51026 /PROD=CGI-141 protein /DB_XREF=gi:7705635 /UG=Hs.62275 CGI-141 protein /FL=gb:AF151899.1 gb:AL136571.1 gb:NM_016072.1	
204076_at		AB002390	Consensus includes gb:AB002390.1 /DEF=Human mRNA for KIAA0392 gene, partial cds. /FEA=mRNA /GEN=KIAA0392 /DB_XREF=gi:2280487 /UG=Hs.201377 apyrase, lysosomal /FL=gb:AF016032.1 gb:NM_004901.1	
204221_x_at		U16307	gb:U16307.1 /DEF=Human glioma pathogenesis-related protein (GliPR) mRNA, complete cds. /FEA=mRNA /GEN=GliPR /PROD=glioma pathogenesis-related protein /DB_XREF=gi:1100927 /UG=Hs.64639 glioma pathogenesis-related protein /FL=gb:U16307.1 gb:NM_006851.1	

203066_at		NM_014863	gb:NM_014863.1 /DEF=Homo sapiens B cell RAG associated protein (BRAG), mRNA. /FEA=mRNA /GEN=BRAG /PROD=KIAA0598 gene product /DB_XREF=gi:7662195 /UG=Hs.6079 B cell RAG associated protein /FL=gb:AB011170.1 gb:AF026477.1 gb:NM_014863.1 gb:NM_015892.1	
205194_at		NM_004577	gb:NM_004577.1 /DEF=Homo sapiens phosphoserine phosphatase (PSPH), mRNA. /FEA=mRNA /GEN=PSPH /PROD=phosphoserine phosphatase /DB_XREF=gi:4758971 /UG=Hs.56407 phosphoserine phosphatase /FL=gb:NM_004577.1	
219563_at		NM_024633	gb:NM_024633.1 /DEF=Homo sapiens hypothetical protein FLJ21276 (FLJ21276), mRNA. /FEA=mRNA /GEN=FLJ21276 /PROD=hypothetical protein FLJ21276 /DB_XREF=gi:13375863 /UG=Hs.41502 hypothetical protein FLJ21276 /FL=gb:NM_024633.1	
202582_s_at		AF306510	gb:AF306510.1 /DEF=Homo sapiens RANBPM mRNA, complete cds. /FEA=mRNA /PROD=RANBPM /DB_XREF=gi:13194575 /UG=Hs.279886 RAN binding protein 9 /FL=gb:AF306510.1 gb:AB008515.1 gb:NM_005493.1	
203247_s_at		BC003566	gb:BC003566.1 /DEF=Homo sapiens, zinc finger protein 24 (KOX 17), clone MGC:2057, mRNA, complete cds. /FEA=mRNA /PROD=zinc finger protein 24 (KOX 17) /DB_XREF=gi:13097725 /UG=Hs.183593 zinc finger protein 24 (KOX 17) /FL=gb:BC003566.1 gb:U68536.1 gb:AF038964.1 gb:NM_006965.1	

203232_s_at		NM_000332	gb:NM_000332.1 /DEF=Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA. /FEA=mRNA /GEN=SCA1 /PROD=ataxin 1 /DB_XREF=gi:4506792 /UG=Hs.74520 spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) /FL=gb:NM_000332.1	
205120_s_at		U29586	gb:U29586.1 /DEF=Human beta-sarcoglycan dystrophin-associated glycoprotein mRNA, complete cds. /FEA=mRNA /PROD=dystrophin-associated glycoprotein /DB_XREF=gi:1794188 /UG=Hs.77501 sarcoglycan, beta (43kD dystrophin-associated glycoprotein) /FL=gb:U31116.1 gb:U29586.1 gb:NM_000232.1	
213447_at		AI672541	ESTs, Weakly similar to S41161 keratin 9, cytoskeletal - human [H.sapiens]	
209122_at		BC005127	gb:BC005127.1 /DEF=Homo sapiens, adipose differentiation-related protein, clone MGC:10598, mRNA, complete cds. /FEA=mRNA /PROD=adipose differentiation-related protein /DB_XREF=gi:13477306 /UG=Hs.3416 adipose differentiation-related protein /FL=gb:BC005127.1 gb:NM_001122.1	
214066_x_at	NPR2	AA565715	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	
209827_s_at		NM_004513	Consensus includes gb:NM_004513.1 /DEF=Homo sapiens interleukin 16 (lymphocyte chemoattractant factor) (IL16), mRNA. /FEA=CDS /GEN=IL16 /PROD=interleukin 16 /DB_XREF=gi:4758595 /UG=Hs.82127 interleukin 16 (lymphocyte chemoattractant factor) /FL=gb:S81601.1 gb:U82972.1 gb:AF053412.1 gb:M90391.1 gb:NM_004513.1	

208415_x_at		NM_005537	gb:NM_005537.1 /DEF=Homo sapiens inhibitor of growth 1 family, member 1 (ING1), mRNA. /FEA=mRNA /GEN=ING1 /PROD=inhibitor of growth 1 family, member 1 /DB_XREF=gi:5031792 /UG=Hs.46700 inhibitor of growth 1 family, member 1 /FL=gb:AF001954.1 gb:NM_005537.1	
212572_at		AB023182	Consensus includes gb:AW779556 /FEA=EST /DB_XREF=gi:7794159 /DB_XREF=est:hn81f05.x1 /CLONE=IMAGE:3034305 /UG=Hs.184523 KIAA0965 protein	
208632_at	RNF10	AL578551	ring finger protein 10	
212330_at	TFDP1	R60866	transcription factor Dp-1	
213707_s_at		NM_005221	Consensus includes gb:NM_005221.3 /DEF=Homo sapiens distal-less homeo box 5 (DLX5), mRNA. /FEA=CDS /GEN=DLX5 /PROD=distal-less homeo box 5 /DB_XREF=gi:6224974 /UG=Hs.99348 distal-less homeo box 5 /FL=gb:NM_005221.3	
210183_x_at		AF112222	gb:AF112222.1 /DEF=Homo sapiens nuclear protein SDK3 mRNA, complete cds. /FEA=mRNA /PROD=nuclear protein SDK3 /DB_XREF=gi:6563229 /UG=Hs.44499 pinin, desmosome associated protein /FL=gb:AF112222.1	
210555_s_at		U85430	gb:U85430.1 /DEF=Human transcription factor NFATx4 mRNA, complete cds. /FEA=mRNA /PROD=transcription factor NFATx4 /DB_XREF=gi:1835590 /UG=Hs.172674 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 /FL=gb:U85430.1	
210105_s_at		M14333	gb:M14333.1 /DEF=Homo sapiens c-syn protooncogene mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:181171	

			/UG=Hs.169370 FYN oncogene related to SRC, FGR, YES /FL=gb:M14333.1 gb:M14676.1 gb:NM_002037.1	
213249_at	FBXL7	AU145127	F-box and leucine-rich repeat protein 7	
213134_x_at	BTG3	AI765445	BTG family, member 3	
202907_s_at		NM_002485	gb:NM_002485.2 /DEF=Homo sapiens Nijmegen breakage syndrome 1 (nibrin) (NBS1), mRNA. /FEA=mRNA /GEN=NBS1 /PROD=nibrin /DB_XREF=gi:6996019 /UG=Hs.25812 Nijmegen breakage syndrome 1 (nibrin) /FL=gb:AF058696.1 gb:AF051334.1 gb:NM_002485.2	
212753_at	MGC40413	AI692203	hypothetical protein MGC40413	
201972_at		AF113129	gb:AF113129.1 /DEF=Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds. /FEA=mRNA /PROD=vacuolar ATPase isoform VA68 /DB_XREF=gi:6523820 /UG=Hs.281866 ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, isoform 1 /FL=gb:L09235.1 gb:NM_001690.1 gb:AF113129.1	
208817_at		BC000419	gb:BC000419.1 /DEF=Homo sapiens, catechol-O-methyltransferase, clone MGC:8663, mRNA, complete cds. /FEA=mRNA /PROD=catechol-O-methyltransferase /DB_XREF=gi:12653300 /UG=Hs.240013 catechol-O-methyltransferase /FL=gb:BC000419.1 gb:M58525.1 gb:M65212.1 gb:NM_007310.1 gb:NM_000754.2	
201769_at		NM_014666	gb:NM_014666.1 /DEF=Homo sapiens KIAA0171 gene product (KIAA0171), mRNA. /FEA=mRNA /GEN=KIAA0171 /PROD=KIAA0171 gene product /DB_XREF=gi:7661967 /UG=Hs.155623 KIAA0171 gene product /FL=gb:D79993.1 gb:BC004467.1	

			gb:NM_014666.1	
217788_s_at		NM_004481	gb:NM_004481.2 /DEF=Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2), mRNA. /FEA=mRNA /GEN=GALNT2 /PROD=polypeptide N-acetylgalactosaminyltransferase 2 /DB_XREF=gi:9945385 /UG=Hs.130181 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) /FL=gb:NM_004481.2	
41856_at		AL049370	EST	
214917_at		AK024252	Consensus includes gb:AK024252.1 /DEF=Homo sapiens cDNA FLJ14190 fis, clone NT2RP2006534, moderately similar to 5-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-). /FEA=mRNA /DB_XREF=gi:10436581 /UG=Hs.288546 Homo sapiens cDNA FLJ14190 fis, clone NT2RP2006534, moderately similar to 5-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-)	
218486_at	TIEG2	AA149594	TGFB inducible early growth response 2	
201848_s_at		U15174	gb:U15174.1 /DEF=Homo sapiens BCL2adenovirus E1B 19kD-interacting protein 3 (BNIP3) mRNA, complete cds. /FEA=mRNA /GEN=BNIP3 /PROD=BCL2adenovirus E1B 19kD-interacting protein 3 /DB_XREF=gi:558845 /UG=Hs.79428 BCL2adenovirus E1B 19kD-interacting protein 3 /FL=gb:AF002697.1 gb:U15174.1 gb:NM_004052.2	
89948_at	C20orf67	AI743331	chromosome 20 open reading frame 67	

216197_at		AK021569	Consensus includes gb:AK021569.1 /DEF=Homo sapiens cDNA FLJ11507 fis, clone HEMBA1002160. /FEA=mRNA /DB_XREF=gi:10432775 /UG=Hs.314347 Homo sapiens cDNA FLJ11507 fis, clone HEMBA1002160	
208200_at		NM_000575	gb:NM_000575.1 /DEF=Homo sapiens interleukin 1, alpha (IL1A), mRNA. /FEA=mRNA /GEN=IL1A /PROD=interleukin 1, alpha /DB_XREF=gi:13236493 /UG=Hs.1722 interleukin 1, alpha /FL=gb:NM_000575.1 gb:M28983.1	
212365_at		AK000160	Consensus includes gb:BF215996 /FEA=EST /DB_XREF=gi:11109582 /DB_XREF=est:601881549F1 /CLONE=IMAGE:4093740 /UG=Hs.121576 Homo sapiens cDNA FLJ20153 fis, clone COL08656, highly similar to AJ001381 Homo sapiens incomplete cDNA for a mutated allele	
219289_at		NM_017939	gb:NM_017939.1 /DEF=Homo sapiens hypothetical protein FLJ20718 (FLJ20718), mRNA. /FEA=mRNA /GEN=FLJ20718 /PROD=hypothetical protein FLJ20718 /DB_XREF=gi:8923644 /UG=Hs.50579 hypothetical protein FLJ20718 /FL=gb:NM_017939.1	
219698_s_at		NM_022840	gb:NM_022840.1 /DEF=Homo sapiens hypothetical protein FLJ23017 (FLJ23017), mRNA. /FEA=mRNA /GEN=FLJ23017 /PROD=hypothetical protein FLJ23017 /DB_XREF=gi:12383089 /UG=Hs.122546 hypothetical protein FLJ23017 /FL=gb:NM_022840.1	
212608_s_at		W85912	ESTs, Moderately similar to Z254_HUMAN Zinc finger protein 254 (Bone marrow zinc finger 5) (BMZF-5) (Hematopoietic cell derived zinc finger protein 1) (HD-ZNF1) [H.sapiens]	

217801_at		NM_006886	gb:NM_006886.1 /DEF=Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), mRNA. /FEA=mRNA /GEN=ATP5E /PROD=ATP synthase, H <sup>+</sup> transporting, mitochondrial F1complex, epsilon subunit /DB_XREF=gi:5901895 /UG=Hs.177530 ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, epsilon subunit /FL=gb:BC001690.1 gb:BC003671.1 gb:AF077045.1 gb:NM_006886.1 gb:AF052955.1	
219520_s_at		NM_018458	gb:NM_018458.1 /DEF=Homo sapiens uncharacterized bone marrow protein BM042 (BM042), mRNA. /FEA=mRNA /GEN=BM042 /PROD=uncharacterized bone marrow protein BM042 /DB_XREF=gi:8922101 /UG=Hs.324136 uncharacterized bone marrow protein BM042 /FL=gb:AF217518.1 gb:NM_018458.1	
209080_x_at		AF118652	gb:AF118652.1 /DEF=Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds. /FEA=mRNA /GEN=PKCOT /PROD=PKCq-interacting protein PICOT /DB_XREF=gi:6840952 /UG=Hs.42644 thioredoxin-like /FL=gb:BC005289.1 gb:AF118649.1 gb:AF118652.1	
213604_at		AW451236	ESTs, Highly similar to FINC_HUMAN Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) [H.sapiens]	
219178_at		NM_024638	gb:NM_024638.1 /DEF=Homo sapiens hypothetical protein FLJ12960 (FLJ12960), mRNA. /FEA=mRNA /GEN=FLJ12960 /PROD=hypothetical protein FLJ12960 /DB_XREF=gi:13375871 /UG=Hs.45005 hypothetical protein FLJ12960 /FL=gb:NM_024638.1	



218019_s_at		NM_021941	gb:NM_021941.1 /DEF=Homo sapiens hypothetical protein FLJ21324 (FLJ21324), mRNA. /FEA=mRNA /GEN=FLJ21324 /PROD=hypothetical protein FLJ21324 /DB_XREF=gi:11345479 /UG=Hs.4746 hypothetical protein FLJ21324 /FL=gb:NM_021941.1 gb:BC003651.1	
210095_s_at		M31159	gb:M31159.1 /DEF=Human growth hormone-dependent insulin-like growth factor-binding protein mRNA, complete cds. /FEA=mRNA /GEN=IGFBP1 /DB_XREF=gi:183115 /UG=Hs.77326 insulin-like growth factor binding protein 3 /FL=gb:BC000013.1 gb:M31159.1	
202534_x_at		NM_000791	gb:NM_000791.2 /DEF=Homo sapiens dihydrofolate reductase (DHFR), mRNA. /FEA=mRNA /GEN=DHFR /PROD=dihydrofolate reductase /DB_XREF=gi:7262376 /UG=Hs.83765 dihydrofolate reductase /FL=gb:BC000192.1 gb:BC003584.1 gb:NM_000791.2	
212271_at	MAPK1	AA195999	mitogen-activated protein kinase 1	
209668_x_at		D50579	gb:D50579.1 /DEF=Homo sapiens mRNA for carboxylesterase, complete cds. /FEA=mRNA /PROD=carboxylesterase precursor /DB_XREF=gi:2641989 /UG=Hs.282975 carboxylesterase 2 (intestine, liver) /FL=gb:U60553.1 gb:D50579.1 gb:NM_003869.2	
209635_at		BC003561	gb:BC003561.1 /DEF=Homo sapiens, Similar to adaptor-related protein complex 1, sigma 1 subunit, clone MGC:1929, mRNA, complete cds. /FEA=mRNA /PROD=Similar to adaptor-related protein complex 1,sigma 1 subunit /DB_XREF=gi:13097710 /UG=Hs.57600 adaptor-related	

			protein complex 1, sigma 1 subunit /FL=gb:BC003561.1	
221751_at	TMSB10	AL565516	thymosin, beta 10	
221652_s_at		AF274950	gb:AF274950.1 /DEF=Homo sapiens PNAS-25 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-25 /DB_XREF=gi:12751064 /UG=Hs.22595 hypothetical protein FLJ10637 /FL=gb:AF274950.1	
222371_at		AI732802	ESTs	
201136_at		NM_002668	gb:NM_002668.1 /DEF=Homo sapiens proteolipid protein 2 (colonic epithelium-enriched) (PLP2), mRNA. /FEA=mRNA /GEN=PLP2 /PROD=proteolipid protein 2 (colonic epithelium-enriched) /DB_XREF=gi:4505892 /UG=Hs.77422 proteolipid protein 2 (colonic epithelium-enriched) /FL=gb:L09604.1 gb:NM_002668.1	
220076_at		NM_019847	gb:NM_019847.2 /DEF=Homo sapiens ankylosis, progressive (mouse) homolog (ANKH), mRNA. /FEA=mRNA /GEN=ANKH /PROD=homolog of mouse Ank /DB_XREF=gi:10947057 /UG=Hs.168640 ankylosis, progressive (mouse) homolog /FL=gb:NM_019847.2	
209443_at		J02639	gb:J02639.1 /DEF=Human plasma serine protease (protein C) inhibitor mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:180549 /UG=Hs.76353 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5 /FL=gb:NM_000624.1 gb:U35464.1 gb:J02639.1 gb:S58545.1	
217540_at		AA721025	ESTs, Moderately similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	

201690_s_at	TPD52	BE974098	tumor protein D52	
213905_x_at	BGN	AA845258	biglycan	
204222_s_at		NM_006851	gb:NM_006851.1 /DEF=Homo sapiens glioma pathogenesis-related protein (RTVP1), mRNA. /FEA=mRNA /GEN=RTVP1 /PROD=glioma pathogenesis-related protein /DB_XREF=gi:5803150 /UG=Hs.64639 glioma pathogenesis-related protein /FL=gb:U16307.1	
212517_at		AL132773	gb:NM_006851.1 Consensus includes gb:AL132773 /DEF=Human DNA sequence from clone RP4-741H3 on chromosome 20 Contains parts of isoform 1 and isoform 2 (KIAA0548) of the ATRN (attractin (with dipeptidylpeptidase IV activity)) gene, ESTs, STSs and GSSs /FEA=mRNA_1 /DB_XREF=gi:7159777 /UG=Hs.194019 attractin	
202141_s_at		BC003090	gb:BC003090.1 /DEF=Homo sapiens, COP9 homolog, clone MGC:1297, mRNA, complete cds. /FEA=mRNA /PROD=COP9 homolog /DB_XREF=gi:13111846 /UG=Hs.75193 COP9 homolog /FL=gb:BC003090.1	
203932_at		NM_002118	gb:U51205.1 gb:NM_006710.1 gb:NM_002118.1 /DEF=Homo sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA. /FEA=mRNA /GEN=HLA-DMB /PROD=major histocompatibility complex, class II, DMbeta /DB_XREF=gi:4504398 /UG=Hs.1162 major histocompatibility complex, class II, DM beta /FL=gb:NM_002118.1	
212612_at		D31888	gb:U15085.1 Consensus includes gb:D31888.1 /DEF=Human mRNA for KIAA0071 gene, partial cds. /FEA=mRNA /GEN=KIAA0071 /DB_XREF=gi:506340 /UG=Hs.78398 KIAA0071	

			protein /FL=gb:AF155595.1 gb:NM_015156.1	
209862_s_at		BC001233	gb:BC001233.1 /DEF=Homo sapiens, Similar to KIAA0092 gene product, clone MGC:4896, mRNA, complete cds. /FEA=mRNA /PROD=Similar to KIAA0092 gene product /DB_XREF=gi:12654780 /UG=Hs.134158 Homo sapiens, Similar to KIAA0092 gene product, clone MGC:4896, mRNA, complete cds /FL=gb:BC001233.1	
212914_at		AV648364	ESTs, Highly similar to potassium voltage-gated channel, Isk-related subfamily, gene 4; potassium voltage-gated channel-like protein, Isk-related subfamily [Homo sapiens] [H.sapiens]	
212249_at		M61906	Consensus includes gb:AI934473 /FEA=EST /DB_XREF=gi:5673433 /DB_XREF=est:wp58d05.x1 /CLONE=IMAGE:2465961 /UG=Hs.6241 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	
204806_x_at		NM_018950	gb:NM_018950.1 /DEF=Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA. /FEA=mRNA /GEN=HLA-F /PROD=major histocompatibility complex, class I, F /DB_XREF=gi:9665231 /UG=Hs.110309 major histocompatibility complex, class I, F /FL=gb:NM_018950.1	
205726_at		NM_006729	gb:NM_006729.1 /DEF=Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA. /FEA=mRNA /GEN=DIAPH2 /PROD=diaphanous 2 isoform 156 /DB_XREF=gi:5803002 /UG=Hs.226483 diaphanous (Drosophila, homolog) 2 /FL=gb:NM_006729.1	

201036_s_at		NM_005327	gb:NM_005327.1 /DEF=Homo sapiens L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA. /FEA=mRNA /GEN=HADHSC /PROD=L-3-hydroxyacyl-Coenzyme A dehydrogenase, shortchain /DB_XREF=gi:4885386 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:BC000306.1 gb:NM_005327.1	
211263_s_at		D87994	gb:D87994.1 /DEF=Homo sapiens mRNA for PACE4E-II, complete cds. /FEA=mRNA /PROD=PACE4E-II /DB_XREF=gi:2330550 /UG=Hs.170414 paired basic amino acid cleaving system 4 /FL=gb:D87994.1	
217667_at		AV761014	ESTs, Moderately similar to SC14_HUMAN SEC14-like protein 1 [H.sapiens]	
205833_s_at	PART1	AI770098	prostate androgen-regulated transcript 1	
47105_at	FLJ20399	AA886893	hypothetical protein FLJ20399	
208015_at		NM_015583	gb:NM_015583.1 /DEF=Homo sapiens DKFZP586M0622 protein (DKFZP586M0622), mRNA. /FEA=mRNA /GEN=DKFZP586M0622 /PROD=DKFZP586M0622 protein /DB_XREF=gi:7661687 /UG=Hs.241544 DKFZP586M0622 protein /FL=gb:NM_015583.1	
202847_at		NM_004563	gb:NM_004563.1 /DEF=Homo sapiens phosphoenolpyruvate carboxykinase 2 (mitochondrial) (PCK2), mRNA. /FEA=mRNA /GEN=PCK2 /PROD=phosphoenolpyruvate carboxykinase 2(mitochondrial) /DB_XREF=gi:4758885 /UG=Hs.75812 phosphoenolpyruvate carboxykinase 2 (mitochondrial) /FL=gb:BC001454.1 gb:NM_004563.1	

219631_at		NM_024937	gb:NM_024937.1 /DEF=Homo sapiens hypothetical protein FLJ12929 (FLJ12929), mRNA. /FEA=mRNA /GEN=FLJ12929 /PROD=hypothetical protein FLJ12929 /DB_XREF=gi:13376412 /UG=Hs.278956 hypothetical protein FLJ12929 /FL=gb:NM_024937.1	
222311_s_at		AA648521	ESTs, Highly similar to SRA4_HUMAN CTD-binding SR-like protein RA4 [H.sapiens]	
219384_s_at		NM_012091	gb:NM_012091.2 /DEF=Homo sapiens adenosine deaminase, tRNA-specific 1 (ADAT1), mRNA. /FEA=mRNA /GEN=ADAT1 /PROD=adenosine deaminase, tRNA-specific 1 /DB_XREF=gi:7382475 /UG=Hs.188661 adenosine deaminase, tRNA-specific 1 /FL=gb:BC002758.1 gb:AF125188.1 gb:NM_012091.2	
203224_at	FLJ11149	BF340123	hypothetical protein FLJ11149	
217196_s_at		AL110158	Consensus includes gb:AL110158.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586F0424 (from clone DKFZp586F0424); partial cds. /FEA=mRNA /GEN=DKFZp586F0424 /PROD=hypothetical protein /DB_XREF=gi:5817061 /UG=Hs.23585 KIAA1078 protein	
217805_at		NM_004516	gb:NM_004516.1 /DEF=Homo sapiens interleukin enhancer binding factor 3, 90kD (ILF3), mRNA. /FEA=mRNA /GEN=ILF3 /PROD=interleukin enhancer binding factor 3, 90kD /DB_XREF=gi:4758603 /UG=Hs.256583 interleukin enhancer binding factor 3, 90kD /FL=gb:BC003086.1 gb:NM_004516.1 gb:U10324.1 gb:AF167570.1 gb:NM_012218.1	
200822_x_at		NM_000365	gb:NM_000365.1 /DEF=Homo sapiens triosephosphate isomerase 1 (TPI1), mRNA. /FEA=mRNA /GEN=TPI1 /PROD=triosephosphate	

			isomerase 1 /DB_XREF=gi:4507644 /UG=Hs.83848 triosephosphate isomerase 1 /FL=gb:BC004230.1 gb:Nm_000365.1	
209476_at		AL080080	Consensus includes gb:AL080080.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564E1962 (from clone DKFZp564E1962); partial cds. /FEA=mRNA /GEN=DKFZp564E1962 /PROD=hypothetical protein /DB_XREF=gi:5262491 /UG=Hs.24766 thioredoxin- related transmembrane protein /FL=gb:AB048246.1	
215314_at		AU146646	ESTs, Weakly similar to 2109260A B cell growth factor [Homo sapiens] [H.sapiens]	
37892_at	COL11A1	J04177	collagen, type XI, alpha 1	NM_001854; NM_080629; NM_080630
55662_at	FLJ13114	H27225	hypothetical protein FLJ13114	
91816_f_at		C18318	Homo sapiens mRNA for OK/SW- CL.4, complete cds	
202051_s_at		NM_005095	gb:Nm_005095.1 /DEF=Homo sapiens zinc finger protein 262 (ZNF262), mRNA. /FEA=mRNA /GEN=ZNF262 /PROD=zinc finger protein 262 /DB_XREF=gi:4827068 /UG=Hs.150390 zinc finger protein 262 /FL=gb:AB007885.1 gb:Nm_005095.1	
221249_s_at		NM_030802	gb:Nm_030802.1 /DEF=Homo sapiens CEBP-induced protein (LOC81558), mRNA. /FEA=mRNA /GEN=LOC81558 /PROD=CEBP-induced protein /DB_XREF=gi:13540589 /FL=gb:Nm_030802.1	
202478_at		NM_021643	gb:Nm_021643.1 /DEF=Homo sapiens GS3955 protein (GS3955), mRNA. /FEA=mRNA /GEN=GS3955 /PROD=GS3955 protein /DB_XREF=gi:11056053 /UG=Hs.155418 GS3955 protein /FL=gb:Nm_021643.1 gb:BC002637.1 gb:D87119.1	

200609_s_at		NM_017491	gb:NM_017491.1 /DEF=Homo sapiens WD repeat domain 1 (WDR1), transcript variant 1, mRNA. /FEA=mRNA /GEN=WDR1 /PROD=WD repeat-containing protein 1, isoform 1 /DB_XREF=gi:9257256 /UG=Hs.85100 WD repeat domain 1 /FL=gb:BC000201.1 gb:BC002489.1 gb:AF020056.1 gb:AB010427.2 gb:NM_017491.1	
208842_s_at	GORASP2	W93787	golgi reassembly stacking protein 2, 55kDa	
204320_at		NM_001854	gb:NM_001854.1 /DEF=Homo sapiens collagen, type XI, alpha 1 (COL11A1), mRNA. /FEA=mRNA /GEN=COL11A1 /PROD=collagen, type XI, alpha 1 /DB_XREF=gi:4502938 /UG=Hs.82772 collagen, type XI, alpha 1 /FL=gb:J04177.1 gb:NM_001854.1	
217984_at		NM_003730	gb:NM_003730.2 /DEF=Homo sapiens ribonuclease 6 precursor (RNASE6PL), mRNA. /FEA=mRNA /GEN=RNASE6PL /PROD=ribonuclease 6 precursor /DB_XREF=gi:5231227 /UG=Hs.8297 ribonuclease 6 precursor /FL=gb:BC001660.1 gb:BC001819.1 gb:U85625.2 gb:NM_003730.2	
215246_at		AK000089	Consensus includes gb:AK000089.1 /DEF=Homo sapiens cDNA FLJ20082 fis, clone COL03245. /FEA=mRNA /DB_XREF=gi:7019950 /UG=Hs.323797 Homo sapiens cDNA FLJ20082 fis, clone COL03245	
221967_at	NXPH4	AI933199	neurexophilin 4	
217921_at	MAN1A2	H97940	mannosidase, alpha, class 1A, member 2	
213184_at		N48361	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]	
218377_s_at		NM_016940	gb:NM_016940.1 /DEF=Homo sapiens chromosome 21 open reading frame 6 (C21ORF6), mRNA. /FEA=mRNA /GEN=C21ORF6 /PROD=chromosome 21 open	



			reading frame 6 /DB_XREF=gi:8393017 /UG=Hs.34136 chromosome 21 open reading frame 6 /FL=gb:AF212232.1 gb:NM_016940.1	
212818_s_at		AF055024	Consensus includes gb:AF055024.1 /DEF=Homo sapiens clone 24763 mRNA sequence. /FEA=mRNA /DB_XREF=gi:3005752 /UG=Hs.153489 ASB-1 protein /FL=gb:AF156777.1 gb:NM_016114.1	
222270_at		BG540048	ESTs	
216012_at		U43604	Consensus includes gb:U43604.1 /DEF=Human unidentified mRNA, partial sequence. /FEA=mRNA /DB_XREF=gi:1171236 /UG=Hs.159901 Human unidentified mRNA, partial sequence	
208837_at		BC000027	gb:BC000027.1 /DEF=Homo sapiens, integral type I protein, clone MGC:1302, mRNA, complete cds. /FEA=mRNA /PROD=integral type I protein /DB_XREF=gi:12652570 /UG=Hs.179516 integral type I protein /FL=gb:BC000027.1 gb:NM_007364.1	
221827_at	C20orf18	BE788439	chromosome 20 open reading frame 18	
221767_x_at		AK026138	Consensus includes gb:AA515560 /FEA=EST /DB_XREF=gi:2255160 /DB_XREF=est:ni42c09.s1 /CLONE=IMAGE:979504 /UG=Hs.283473 hypothetical protein PRO2900	
202241_at		NM_025195	gb:NM_025195.1 /DEF=Homo sapiens phosphoprotein regulated by mitogenic pathways (C8FW), mRNA. /FEA=mRNA /GEN=C8FW /PROD=G-protein-coupled receptor induced protein /DB_XREF=gi:13399327 /UG=Hs.7837 phosphoprotein regulated by mitogenic pathways /FL=gb:AF205437.1 gb:NM_025195.1	

202201_at		NM_000713	gb:NM_000713.1 /DEF=Homo sapiens biliverdin reductase B (flavin reductase (NADPH)) (BLVRB), mRNA. /FEA=mRNA /GEN=BLVRB /PROD=biliverdin reductase B (flavin reductase(NADPH)) /DB_XREF=gi:4502418 /UG=Hs.76289 biliverdin reductase B (flavin reductase (NADPH)) /FL=gb:D26308.1 gb:NM_000713.1	
203745_at	HCCS	AI801013	holocytochrome c synthase (cytochrome c heme-lyase)	
201952_at		NM_001627	Consensus includes gb:AA156721 /FEA=EST /DB_XREF=gi:1728335 /DB_XREF=est:z118b04.s1 /CLONE=IMAGE:502255 /UG=Hs.10247 activated leucocyte cell adhesion molecule /FL=gb:NM_001627.1 gb:L38608.1	
215034_s_at	TM4SF1	AI189753	transmembrane 4 superfamily member 1	
201876_at		NM_000305	gb:NM_000305.1 /DEF=Homo sapiens paraoxonase 2 (PON2), mRNA. /FEA=mRNA /GEN=PON2 /PROD=paraoxonase 2 /DB_XREF=gi:4505952 /UG=Hs.169857 paraoxonase 2 /FL=gb:L48513.1 gb:AF001601.1 gb:NM_000305.1	
210511_s_at		M13436	gb:M13436.1 /DEF=Human ovarian beta-A inhibin mRNA, complete cds. /FEA=mRNA /GEN=INHBA /DB_XREF=gi:186414 /UG=Hs.727 inhibin, beta A (activin A, activin AB alpha polypeptide) /FL=gb:M13436.1	
202071_at		NM_002999	gb:NM_002999.1 /DEF=Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4), mRNA. /FEA=mRNA /GEN=SDC4 /PROD=syndecan 4 (amphiglycan, ryudocan) /DB_XREF=gi:4506860 /UG=Hs.252189 syndecan 4 (amphiglycan, ryudocan) /FL=gb:NM_002999.1	
202050_s_at	ZNF262	AA521508	zinc finger protein 262	

219922_s_at		NM_021070	gb:NM_021070.1 /DEF=Homo sapiens latent transforming growth factor beta binding protein 3 (LTBP3), mRNA. /FEA=mRNA /GEN=LTBP3 /PROD=latent transforming growth factor beta bindingprotein 3 /DB_XREF=gi:10835104 /UG=Hs.289019 latent transforming growth factor beta binding protein 3 /FL=gb:NM_021070.1 gb:AF135960.2	
209281_s_at		M95541	gb:M95541.1 /DEF=Homo sapiens adenosine triphosphatase mRNA, complete cds. /FEA=mRNA /PROD=adenosine triphosphatase /DB_XREF=gi:184269 /UG=Hs.78546 ATPase, Ca++ transporting, plasma membrane 1 /FL=gb:M95541.1 gb:NM_001682.1 gb:J04027.1	
201063_at		NM_002901	gb:NM_002901.1 /DEF=Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA. /FEA=mRNA /GEN=RCN1 /PROD=reticulocalbin 1 precursor /DB_XREF=gi:4506454 /UG=Hs.167791 reticulocalbin 1, EF-hand calcium binding domain /FL=gb:D42073.1 gb:NM_002901.1	
202515_at		NM_004087	Consensus includes gb:BG251175 /FEA=EST /DB_XREF=gi:12760991 /DB_XREF=est:602364982F1 /CLONE=IMAGE:4473165 /UG=Hs.154294 discs, large (Drosophila) homolog 1 /FL=gb:NM_004087.1 gb:U13896.1	
201261_x_at		BC002416	gb:BC002416.1 /DEF=Homo sapiens, biglycan, clone MGC:2298, mRNA, complete cds. /FEA=mRNA /PROD=biglycan /DB_XREF=gi:12803216 /UG=Hs.821 biglycan /FL=gb:BC002416.1 gb:BC004244.1 gb:J04599.1	

			gb:NM_001711.1	
200647_x_at		NM_003752	gb:NM_003752.2 /DEF=Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA. /FEA=mRNA /GEN=EIF3S8 /PROD=eukaryotic translation initiation factor 3,subunit 8 (110kD) /DB_XREF=gi:5579457 /UG=Hs.4835 eukaryotic translation initiation factor 3, subunit 8 (110kD) /FL=gb:NM_003752.2	
218730_s_at		NM_014057	gb:NM_014057.1 /DEF=Homo sapiens osteoglycin (osteoinductive factor, mimecan) (OGN), mRNA. /FEA=mRNA /GEN=OGN /PROD=osteoglycin /DB_XREF=gi:7661703 /UG=Hs.109439 osteoglycin (osteoinductive factor, mimecan) /FL=gb:NM_024416.1 gb:AF100758.1 gb:AL110267.1 gb:NM_014057.1 gb:AF202167.1	

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